# From genes to plant architecture: the shoot apical meristem in all its states

Jessica Bertheloot, Jean-Louis Durand, Christophe Godin

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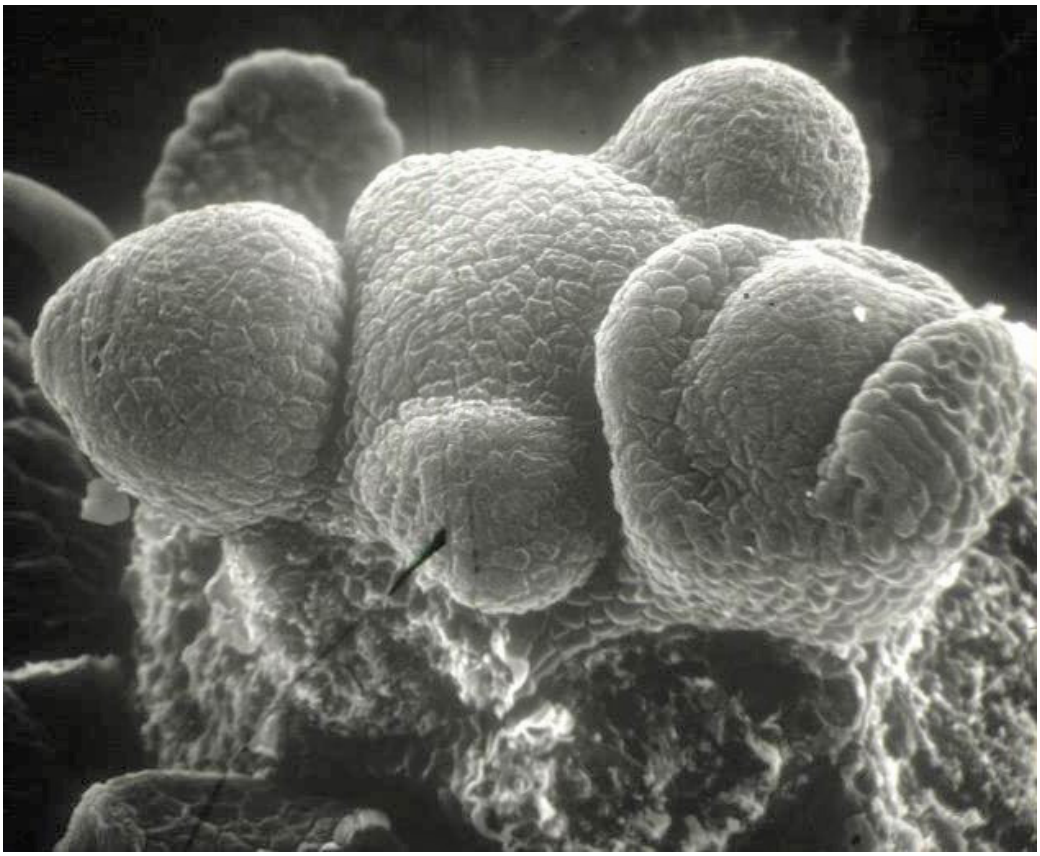
**Abstracts**

# FROM GENES TO PLANT ARCHITECTURE THE SHOOT APICAL MERISTEM IN ALL ITS STATES

Coordinators: Jessica Bertheloot, Jean-Louis Durand, Christophe Godin



Metaprogramme DIGIT-BIO

# From genes to plant architecture
# The Shoot Apical Meristem in all its states

Abstracts IFM2A2
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# Introduction

It is a pleasure to introduce this series of 28 contributions to a topic that still is a dream of many of us: integrate knowledge from the level of cell to that of the whole plant to explain morphogenesis. For 40 years now, substantial progress has been made at the sub-cellular level as well as at the whole plant level. On the one hand, much more is known on the key processes regulating cell proliferation in the meristem, as well as water, nitrogen, carbon, hormones, and mechanical processes that contribute to organ formation... On the other hand, functional-structural plant models allow to increasingly better understanding plant architecture dynamics at the scale of individuals and its response to the biotic and abiotic environment. At both levels, genetics has explored in depth the connection between genes and phenotypes to improve our selection strategies and the development of a profound understanding, piece after piece, of how shapes make themselves.

However, building such an integrating view of the various scales, from genes to whole organisms, through temporal and spatial dimensions, and encompassing genetic and environmental regulations remains a major challenge. To address this, the different scientific communities working at different scales on plant morphogenesis must meet and debate about their views, understanding and approaches. The INRAE – INRIA metaprogramme DIGIT-BIO is an excellent framework for that. We hope that this book of abstract testifies for that fruitful interdisciplinary exercise.

Jessica Bertheloot Jean-Louis Durand Christophe Godin

# SUMMARY

## Opening keynote:



## Session 1: The functioning of SAM

## Session 2: Determination and regulation of SAM fate in the plant



## Session 3: Toward FSPM integrating SAM functions

# Morphogenesis at the shoot meristem: a challenging problem

## OPENING KEYNOTE

Jan Traas
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Work during the last three decades has revealed a complex network of molecular regulators, which controls both shoot meristem maintenance and the production of different types of organs. The behavior of this network in time and space is defined by the local interactions between regulators, but involves also the action of hormones and in particular auxin and cytokinin are intimately implicated in the dynamic coordination of gene expression patterns. To control growth patterns at the SAM the individual components of the network influence local directions and rates of cell expansion and division. This in turn requires interference with the mechanical properties of the cells. How this occurs, remains largely an open question, but recently developed tools offer interesting (albeit challenging) perspectives.

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# SESSION 1.
# THE FUNCTIONING OF SAM

# On the initiation and maintenance of shoot meristems

**KEYNOTE**

Henrik Jönsson
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The inflorescence shoot apical meristem inherits its patterning from the embryo while reorganisations are required at the transition to flowering. We have developed models that can explain the maintenance and plasticity of the inflorescence meristem patterning. These models are also very robust to the initial condition of the patterns. Still, this relies on the geometry of the meristem, and the initiation of the patterns and geometrical structure in parallel is less understood. I will discuss some dynamics related to the initiation of novel meristems with examples from flowers and regeneration of shoot meristems from other tissues.

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# Tight control of division plane orientation is necessary to optimize the growth capacity of tissues and organs in *Arabidopsis thaliana*

Magalie Uyttewaal, Marie-Ludivine De Tauzia, Coralie Goncalves, Katia Belcram, Martine Pastuglia and David Bouchez
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The shape and size of the fruit vary greatly among Angiosperms, even within the same species. Fruit shape results from spatiotemporal coordination of cell division, expansion and differentiation during flower and fruit development, especially from the initiation of floral primordia at the flank of the shoot apical meristem to the mature gynoecium. Several genetic components control fruit morphology, among them the TRM gene family, which has been shown in rice, maize, tomato, melon to determine fruit size and shape. The TRM proteins belong to the TTP (TON1-PP2A-TRM) protein complex, involved in cortical microtubule (cMT) array organization.
In this study, we investigated the cellular role of TRM 1, 2, 3, and 4 during gynoecium development in *Arabidopsis*. We first showed that the quadruple mutation trm1234 impairs the spatial organization of the interphasic cortical MT array, affecting both the co-alignment of MTs and their average orientation in several tissues.
We then quantify cellular morphometrics parameters during fruit development from stage 8 to stage 12, with a particular focus on the replum, a tissue at the margin between the two carpels, where epidermal cells are organized in files. In the WT, we identified 3 phases: at Phase 1, cells divide at a very high rate, and as a consequence the mean cell area decreases. At Phase 2, divisions slow down, and cell size remains constant. At Phase 3, divisions gradually stop and a sharp increase of cell area is observed. Although slightly smaller, the trm1234 mutant cells follow the same decrease in division rate and U-shaped growth dynamics. However, trm1234 cells are significantly less elongated, especially at later stages, showing that the mutant is strongly impaired in its capacity to control anisotropic growth.
In the wild-type, transverse wall orientation is constant and perpendicular to the cell file's axis at all stages. The pattern is markedly different in the trm1234 mutant: at stages 8 and 9, it is indistinguishable from the wild-type, but progressively diverges from the wild-type. By analyzing recently divided cells and division figures, we showed that the elongation defect of trm1234 produces small deviations from transversality upon division, and that these small deviations are dramatically amplified during the active growth phase.
We conclude that in plants, slight deviations in the initial orientation of the division plane can have dramatic consequences on the growth capacity of cells and organs. We previously showed that the PPB acts as a filter to suppress noise in division plane positioning: we propose that this spatial control of division orientation has evolved to optimize the growth capacity of plants at various scales.

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# Can U-Net replace CLV3? Machine learning for the identification of biological landmarks in shoot apical meristem images

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Main engine of plant phyllotaxis, the Shoot Apical Meristem (SAM) is a tightly regulated tissue that presents striking spatiotemporal periodicity properties, and due to that, a high level of inter-individual similarity at tissue scale. It is possible to take advantage of this shape similarity to align a population of SAMs imaged using confocal microscopy onto a common reference frame. In previous work, we performed such an alignment by identifying key biological landmarks on the surface of the SAM (Galvian Ampudia *et al.* 2020).
Among these landmarks, an essential one is the precise position of the center of the Central Zone (CZ) of the SAM. It is usually accessed by adding a transcriptional reporter for the CLAVATA3 peptide (CLV3) in the genetic construct of the observed plants. However, the crossing and selection of plant lines generally involves a significant amount of time. In this work, we study whether the geometry of the SAM itself could be sufficient to predict accurately the location of the CZ, and therefore avoid the time-consuming development of crossed reporter lines.
We used 3D confocal SAM images containing both a CLV3 fluorescent reporter and a geometry reference marker (either a nuclei-targeted marker under a ubiquitous promoter, or an external cell wall staining). We trained various Machine Learning approaches on both image and surface mesh data to predict the CZ membership based only on geometrical cues. The best performing method among those we tested was the convolutional neural network model U-Net (Ronneberger *et al.* 2015) applied on down sampled 2D projections of the reference images (Figure 1.A). The prediction classifies image pixels into 3 classes: background, meristem or central zone (Figure 1.B) from which it is possible to derive a 2D position for the center of the CZ.
We evaluated the different methods on an independent set of images of wild-type SAMs grown under the same conditions, and we show that the trained 2D U-Net model is able to position the CZ center with an error of less than 1 cell relatively to the CLV3 center (Figure 1.C). It outperforms the surface-based methods, including the recently proposed paraboloid approximation of the SAM surface (Åhl *et al.* 2022). Moreover, although the performance drops on images of tilted meristems, it proves to be robust to different growth conditions and to the type of geometry marker used. This tool could constitute a first step towards the aggregation of quantitative SAM data from various experiments without having to rely on CLV3.

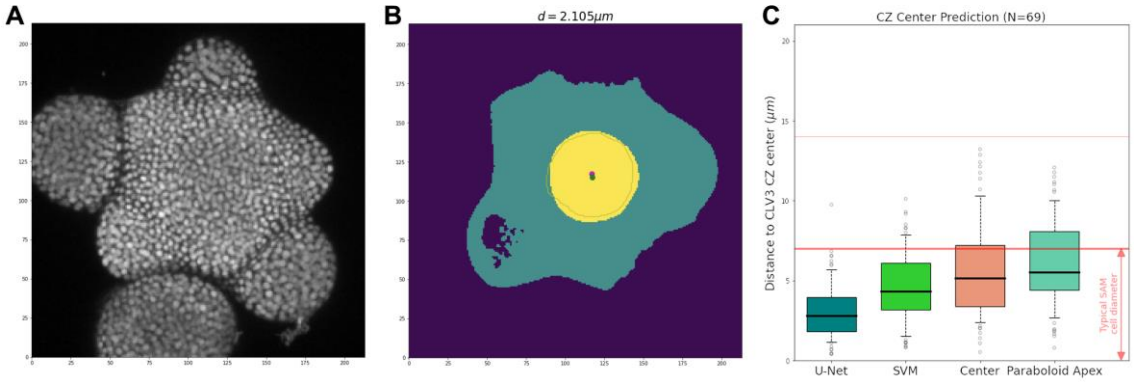


**Figure 1**: The trained U-Net model takes as input a downsampled 2D projection of the confocal image stack (**A**) and returns a 2D image where each pixel belongs either to the background (■), to the meristem (■) or to the central zone (■), allowing to determine a position for the center of the CZ (**B**). When compared with the actual center of the CLV3 domain, the predicted point lies at a distance lesser than the typical SAM cell diameter of 7µm, showing a better precision than the other surface-based methods that we evaluated (**C**).

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# *De novo* stem cell establishment in meristems requires repression of organ boundary cell fate

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Meristems are the ultimate source of all plant organs and tissues, whether roots, stems, leaves or flowers. These multicellular structures are either formed during embryogenesis or arise throughout the life of the plant. In particular, axillary meristems that produce lateral shoots arise from the division of boundary domain cells at the leaf base. The CUP-SHAPED COTYLEDON (CUC) genes are major determinants of the boundary domain and are required for axillary meristem initiation. However, how axillary meristems get structured and how stem cells become established *de novo* remain elusive. Here, we show that two NGATHA-LIKE transcription factors, DPA4 and SOD7, redundantly repress CUC expression in initiating axillary meristems of *Arabidopsis thaliana*. Ectopic boundary fate leads to abnormal growth and organisation of the axillary meristem and prevents *de novo* stem cell establishment. Floral meristems of the dpa4 sod7 double mutant show a similar delay in de novo stem cell establishment. Although the shoot apical meristem shares with axillary meristem a phase of CUC gene repression during the early stages of their formation, we found that stem cell specification is not affected in dpa4 sod7 double mutant. Altogether, our work reveals a pathway facilitating stem cell formation in post-embryonic formed meristems and stresses the difference in the regulatory networks leading to meristem formation during the embryonic and post-embryonic phases.

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# How mechanical signals contribute to plant resilience after drastic pruning: the case of pollard trees

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The resilience shown by tree species, where all upper and lateral branches are pruned highlights the adaptation to shoot loss. Such pruned trees, called pollards, share a characteristic phenotype of massive branching and increased thickening of the trunk. We hypothesize that, as part of the wounding response, pruning also changes the mechanical status of meristems and their activity. To test this, emergence of new shoots and covering bulge after pruning will be described in poplars. We will focus on the mechanical and hormonal interplays after pruning by bending poplar stems. In parallel, the contribution of hormonal signals and mechanical forces to the activity of meristems after pruning will be investigated in a perennial *Arabidopsis* mutant sharing anatomical features with woody stems. In other words, we will investigate the long-term consequences of pruning on meristems and what makes trees robust to repeated traumatic events.

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# Analysis of natural variation in meristematic conversion

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The ability of plant cells to recreate an entire organism has been widely exploited for in vitro regeneration, a key step in plant transformation or genome editing. In addition, this property is used to understand complex phenomena of cell determination/differentiation and genetic reprogramming. Regeneration from an explant can be direct or indirect depending on whether the cells form a callus (mass of undifferentiated cells). In *Arabidopsis*, a hormonal treatment of auxin at high concentration induces the division of root pericycle cells, similar to what drives the induction of young lateral root primordia (LRP). This tissue proliferates into a callus that can give rise to roots or leaves, depending on the hormonal balance between auxin and cytokinin. On the other hand, during direct regeneration an explant turns into an organ without passing through a callus stage. This meristematic conversion of a young root meristem into a shoot meristem after treatment with cytokinin has been described in *Arabidopsis* and can take place in a few days compared to a few weeks for indirect regeneration. During this trans-differentiation phenomenon, cytokinin treatment represses the expression of genes regulating root stem cells (*WOX5*, *PLT1*) and induces, among others, the expression of genes regulating shoot stem cells (*WUS*, *STM*, *CLV3*). Here we present data on the natural variation of this process among *Arabidopsis* accession and the identification of QTLs involved in such variation in an *Arabidopsis* Bur-0 x Col-0 RIL population.

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# Hydraulic stress at the meristem-organ boundaries

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Plant development is shaped by physical variables that either promote or restrict growth. One of these variables is the water status of cells, which can be heterogenous in neighboring cells even when water is sufficiently available. Here we investigate how mechanical conflict between differentially growing tissues can impact water status, and thus, in turn, the ability of cells to grow. In shoot apical meristems (SAM), the emergence of new organs deforms cells at the meristem-organ boundaries creating a saddle-shaped domain of anisotropic forces. We speculated this could also have hydraulic implications for boundary cells. In order to understand these volumetric and morphological deformations, we performed a 4D image segmentation analysis over the whole SAM. Our results suggest water flux out of the boundary domain. Consistently, we also found a bias in water-stress gene expression. Through artificially deforming meristems and modifying meristem osmotic conditions, we further show that hydraulic stress activates a growth cessation response in late stages of boundary development. Investigating this response in vegetative meristems, we relate this slowed life response to the dormancy of axillary meristems. Taken together, our integratory analysis suggests that SAM boundary identity is defined by mechanical as well as hydraulic stress.

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# Computational analysis of cell division patterns in the shoot apical meristem

Sandrine Lefranc, Chie Kodera, Eric Biot, Ayoub Ouddah, Alexandre Durrmeyer, Magalie Uyttewaal, David Bouchez and Philippe Andrey
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How the division plane is positioned during plant cell division plays an important role in the building of specific tissue architectures and organ shapes. Much is known about the molecular and cellular machinery involved in the different steps of cell division but how the positioning and orientation of the division plane is selected remains unclear. Several phenomenological rules have been proposed to relate the geometry of the mother cell to the selection of the division plane. Among these, Errera's rule is generally accepted as a default principle, according to which cells divide into two daughter cells of equal volumes with a minimum contact interface area. Deviations from this default regime would result from specific signals such as hormonal and mechanical cues. However, much of this view has been derived essentially from 2D analyses of volume-symmetric divisions. Recently, we introduced an original image-based 3D model of cell division that allows to address both symmetric and asymmetric partitionings of the mother cell space. Using this model, we showed that a single rule linking the positioning of the division plane to cell geometry accounted for both stereotyped and variable, symmetric and asymmetric, division patterns in *A. thaliana* early embryo, thus unifying a range of distinct division patterns. Here, we examined the potential of this approach to decipher division patterns in the shoot apical meristem. A large collection of 3D time-lapse images of developing meristems with fluorescently labeled cell membranes were acquired using confocal microscopy. We designed original image processing pipelines under the BIP software (see companion poster by Biot *et al.*) to quantify topological, morphological, and geometrical features of tissues, cells and cell divisions. The 3D cell division model was run in mother cells from automatically identified cell divisions and model predictions were compared to observed daughter cell patterns. We report the first results of the quantitative image analyses and model simulations we obtained on meristems from wild-type and from *trm678* mutant plants in which the absence of preprophase band alters division patterns.

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# Changing SAM geometry and generation of phyllotactic patterns

**KEYNOTE**

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Two fundamental SAM functions, the self-maintenance and primordium initiation, require cyclic changes in SAM geometry due to differential growth. A geometric landmark during primordium formation is SAM surface partitioning that takes place at the moment of the appearance of SAM/primordium boundary, *i.e.* the crease characterized by negative Gaussian curvature. Depending on the developmental phase a single or double boundary is formed. In *Arabidopsis*, the cyclic geometry changes match the phyllotactic pattern generated at the SAM periphery but in general this relationship depends on the relative size of primordia. If primordia generated on the SAM periphery are relatively small the apical dome remains nearly axisymmetric throughout the plastochron. However, the dome shape of SAMs generating relatively large primordia depends on phyllotaxis and undergoes spatiotemporal changes. For example, the dome has bilateral symmetry in the case of decussate phyllotaxy but is asymmetric if phyllotaxy is spiral. Relative size of primordia influences also the primordia packing, as shown by comparison of various *Arabidopsis* ecotypes and *cup-shaped cotyledons* mutant. One of the consequences of primordia packing is the phyllotaxy of elongated shoots. In *Arabidopsis* this phyllotaxy is strongly affected by imprecisions in spatiotemporal patterning at the SAM to which other species seem to be more resistant.

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# From phyllotaxis to Homogalacturonan and back: exploring the origins of plant growth

## KEYNOTE

Alexis Peaucelle
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We will present a perspective on our work that permitted us to explore the role of cell wall components in plant morphogenesis. Using the meristem as a model we observed that a chemical modification of one of the polymers of the cell wall (the methyl esterification of the HG) is necessary and sufficient for organ formation. Then we discovered that this modification gives a native growth capacity to the cell wall revealing an alternative growth model for plant cells. Finally, we will present our work on the element regulating this chemical modification and its implication in the generation of beautiful patterns in plants such as pavement cells and the phyllotaxic pattern.

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# How meristem cells measure themselves and why it matters

**KEYNOTE**

Robert Sablowski
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Across biological kingdoms, cell size has important developmental and physiological roles, but its regulation remains unclear (D'Ario and Sablovski, 2019). In the *Arabidopsis* shoot stem cell niche, cell size is one of the features that is maintained in a steady state over long periods of cell proliferation. We have found that meristem cell size is maintained by a feedback between cell growth and cell cycle progression (Serrano Mislata *et al.* 2015), and more recently, we have revealed the underlying mechanism (D'Ario *et al.*2021). Specifically, the size of recently divided cells determines the growth period (G1) from mitosis to the next DNA synthesis phase (S). The KRP4 protein, which inhibits the G1-S transition, binds to chromosomes before mitosis, while the F-box protein FBL17 maintains low steady-state levels of KRP4. As a consequence, sister cells are born with comparable amounts of KRP4, so after asymmetric cell divisions, the smaller sister cell needs to grow for a longer period to dilute KRP4 sufficiently and progress to S-phase. In this way, cell size is regulated using chromatin content as a size-independent standard, which is read by a cell cycle regulator that is stabilized when bound to mitotic chromosomes. One of our next questions is whether and how this mechanism may be modified during the development of different cell types. For this, we focus on the stomatal lineage, which includes a well-studied transition from meristem-like identity to specific cell fates, and where cell size has important physiological consequences. Current results in this area will be presented and their implications will be discussed.

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# The distribution of sugars and amino acids between source and sink organs: more than just a transporters' game

## KEYNOTE

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The distribution of organic materials within the plant mainly relies on the function of the phloem, which controls the allocation of nutrients from source to sink organs (Braun, 2022). The mass flow in the phloem is driven by osmotic pressure differences between sources and sinks. The concentration in the sieve tubes of sugars and ions, such as potassium, is responsible for creating phloem pressure. As a consequence, phloem transport also relies on the osmotic exchange of water with the xylem system, and the water status of the plant has a major impact on phloem flow (Sevanto, 2018).
The entry, leakage or release of amino acids and sucrose along the phloem pathway is regulated by the opening status of plasmodesmata and the activity of transporters, with a key role of members of the SUC/SUT and SWEET sugar transporters, and AAP and UmamiT amino acid transporters families (Kim *et al.*, 2021; van Bel, 2021). The symplasmic steps through plasmodesmata further contribute to the diffusion of sugars and amino acids in terminal sink tissues, such as root apices, or during the development of the embryos, where they contribute to creating the sink strength. The mechanisms of phloem loading have been studied in detail, but the mechanisms of phloem unloading and sugar use and storage in sink organs, including meristems, are less understood. Sink strength corresponds to the ability of an organ to import photoassimilates. The transport of photoassimilates is intimately coupled to cellular metabolism and compartmentation in sink cells. The classical model for determining sink strength relies on the cleavage and resynthesis of sucrose, a scenario in which sucrose is metabolized by a combination of cell-wall and vacuolar invertases (INV) in the phloem-unloading zone, and resynthesized in sink tissues to support sugar storage and use. Recent evidence also supports a role of sucrose synthases (SUSY) in the control of sink strength in many species (Stein and Granot, 2019). Sucrose synthase may also play another, less-studied role in the shoot apical meristem (SAM), influencing plant growth and leaf morphogenesis, as recently described in tomato (Goren *et al*., 2017).

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# Model-based reconstruction of whole organ growth dynamics reveals invariant patterns in leaf morphogenesis

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Morphogenesis is a process that spans several orders of magnitude in both time and space. Because it is generally impossible to follow developing organs all along growth, analyses typically rely on static data sampled at different developmental stages. We propose a model-based approach for the accurate dating of organs, allowing spatio-temporal reconstruction of organ morphogenesis over unlimited time windows, based on static data collected from different individuals. Although considered leaves in wild-type and mutant plants displayed contrasted final shapes and sizes, we revealed invariant, iterated developmental schemes, and identical critical time points, suggesting conserved morphogenetic modules. We provided evidence that modules determining local features may act independently of global leaf growth. In particular, we showed that serrations developing at different times and/or in different leaves grow in a remarkably synchronized way. In addition, graded differences in growth dynamics and final shapes of successive leaves suggest continuous variations in module expression. Altogether, we illustrated that our strategy is powerful to finely dissect multi-scale morphogenetic processes.

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# Statistical spatio-temporal atlasing of gene expression patterns during organ growth

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Plant development requires spatio-temporal coordination of gene expression. Gene expression programs are continuously adjusted through feedbacks to ensure reproducible output at the organ level. This is especially true in a growing organ - such as the leaf - which is dramatically changing in size and shape during development. Hence understanding how dynamics of gene expression is coordinated with growth and morphogenesis requires the development of innovative methods to follow gene expression over long time period in a quantitative way. Here we propose to build precise, integrative, statistical, spatio-temporal atlases of gene expression patterns observed in growing organ relying on fluorescent reporter lines. We exploit series of static images sampled at different developmental stages on different individuals to infer the continuous dynamics of gene expression in an evolving, growing shape. Our strategy consists in three steps: 1) building an average growing organ shape, 2) projecting individual expression pattern images in this evolving framework, 3) computing mean expression patterns at any time point, to reconstruct the continuous developmental dynamics, as a "movie" monitoring pattern evolution during growth. It not only allows to take inter-individual variability into account, but also to simultaneously analyze patterns of distinct genes in a common framework. The methodology is currently used in the context of plant leaf morphogenesis. A gene regulatory network centered on the CUP-SHAPED COTYLEDON 2 transcription factor controls leaf shaping and tooth emergence at its margin. CUC2 TF acts through molecular relays but the dynamics of these regulations as well as the architecture of the network remain unclear. Using our methodology, we conjointly quantify dynamics of the different actors involved in the network, analyze network behavior and predict putative network interactions.

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# BIP, a new software design for batch analysis of biological images

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Biological imaging is one of the major tools used to decipher the functioning of meristems in plant morphogenesis. Extracting quantitative information from microscopy images typically requires complex image processing and analysis pipelines, designed by combining elementary operations such as signal enhancement, object segmentation, and object measurements. Moreover, integrating data through the processing of large image datasets is required to model variability and ensure robust analyses. Existing image analysis software solutions fall into two categories that come with their respective limitations. On the one hand, dedicated libraries such as ITK provide collections of basic components that can be assembled into possibly complex image processing pipelines. This requires a strong computer programming expertise. On the other hand, embedded software such as Fiji provide user-friendly graphical interfaces that allow end users with little or no programming expertise to perform a wide range of predefined image processing operations. The possibilities for automation and batch processing are however often limited, and generally do not eliminate the need for the user to do some programming.
We address these limitations by proposing a new software, called BIP, for batch processing and analysis of biological images. BIP integrates many standard algorithms and specific algorithms developed in the framework of our research projects for quantifying images of plant cells and tissues. BIP fills-in an empty niche in the ecosystem of bioimaging software, by relying on a simple yet powerful command line interface. Furthermore, integrating BIP within frameworks for high-throughput, distributed computing is straightforward. BIP allows users to easily specify sets of images to be processed and to readily chain basic operations into complex analysis pipelines. BIP offers transparent support for images of arbitrary dimensions (2D to 5D) and numerical types (integer and floating numbers, signed and unsigned, from 8 to 32 bits), thus breaking the compatibility barriers often encountered between implementations of different algorithms in existing software. This performance is achieved thanks to a single, unified templated data structure to represent multi-dimensional images and a generic design pattern for the automatic detection of the numerical data type in input images. In addition, these design principles allow minimizing the number of implementations of each algorithm, thus easying code maintenance, evolution, and optimization. Here, we illustrate through several examples the benefits and potential of BIP for processing and quantifying image datasets of plant cells and tissues, including 3D time-lapse confocal images of A. thaliana shoot apical meristems.

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# Bract inhibition at floral transition in *Arabidopsis thaliana*

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Flowering plant architecture results from the continuous production of phytomers at the shoot apex. These basic developmental units are composed of an internode and an axillary meristem subtended by a leaf. Phytomer composition can be remodelled during plant development, resulting in a modification of plant architecture. In *Arabidopsis thaliana,* reproductive transition leads both to the production of flowers and the loss of its subtending leaf: the bract. Contrary to flower production, bract loss mechanism is poorly understood. We show that in several natural accessions of *Arabidopsis thaliana*, but not the reference *Col-0*, presence of bracts are common on the first flowers. In *Tsu-0*, bractflowers are frequent and robust to different photoperiodic condition. Using Recombinant Imbred Lines (RILs), we fine mapped two major loci controlling bract inhibition in chromosome 1. We then profiled the transcriptome of finely-dissected shoot meristems over time in the two accessions. Gene expression divergence strikingly peaks at floral transition, because of complex heterochronic shifts in both directions. Unexpectedly, master regulators of floral identity or previously bract-associated genes are unaffected. And paradoxically, the transcriptome of bract-making meristem at floral transition is more similar to the one of older flowering meristems. Altogether, our data already demonstrate an unprecedented mechanism of bract formation in *Arabidopsis*, acting at floral transition. Our results will contribute to understand how cell fates are coordinated in the shoot apex. They may also enlighten the evolutionary origin of bract loss in *Brassicaceæ*.

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# Revisiting PIN1 polarity interpretation at the SAM based on automated PIN1 map reconstruction

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The shoot apical meristem (SAM) produces new aerial organs such as leaves and flowers, patterning the shoot in an arrangement called phyllotaxis. Phyllotaxis is driven by the spatiotemporal dynamics of the auxin hormone at the SAM. It has been shown that auxin accumulation emerges from auxin polar transport, and triggers organ differentiation. In particular, the PIN1 membrane protein is a polar auxin exporter necessary to a functional auxin dynamical patterning. Auxin feedbacks on PIN1 polarity that in turn transports auxin and thus changes its pattern. This feedback loop has been widely modeled to explain the emergence of phyllotactic patterns (Smith *et al.* 2006, Jönsson *et al.* 2006, Stoma *et al.* 2008, Bayer *et al.* 2009). Most of the studies detect PIN1 polarity direction in tissues by human inspection of fluorescent images (Reinhardt *et al.* 2003, Heisler *et al.* 2005, de Reuille *et al.* 2006). Based on analysis of the direction of PIN1 polarity, it was proposed that auxin accumulation results from locally converging PIN1 polarities. PIN1 polarity quantitative extraction remains challenging in vivo because PIN1 are located at the cell membranes, separated by the cell wall whose thickness is below optical resolution. A first automated technique was proposed in (Jönson *et al.* 2006) The authors have shown a partial change of PIN1 polarity direction at the initiation site as observed in (Heisler *et al.* 2005). In a recently published work (Galvan Ampudia *et al.* 2020), an automated quantitative technique provides high resolution spatiotemporal PIN1 maps, and makes it possible to reanalyse PIN1 polarity patterns. It appears that PIN1 polarity directions globally converge toward the central zone with only limited reorientation over time and space. This work emphasizes the need to revisit the interpretation of PIN1 polarity direction as the unique factor determining auxin accumulation. Here, we propose a new analysis of PIN1 polarity based on the above quantitative technique to understand the formation of auxin accumulation. Using a modeling approach, we study the influence of the PIN1 expression level and the polarity direction on the auxin pattern, and show that both could be regulated to achieve auxin accumulation spots. Our approach clarifies the qDII auxin reporter and PIN1 polarity spatiotemporal observations in (Galvan Ampudia *et al.* 2020). We explain why auxin can accumulate locally without strict PIN1 polarity directional convergence due to the effect of a gradient of the PIN1 expression level. New phyllotaxis models proposing both regulations of the PIN1 polarity direction and level of expression could lead to a better understanding of the biological observations.

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# SESSION 2.
# DETERMINATION AND REGULATION OF SAM FATE IN THE PLANT

# Off with their head: a tale of decapitation and auxin

**KEYNOTE**

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A key aim in biology is to identify which genetic changes contributed to the evolution of form through time. Apical dominance, the inhibitory effect exerted by shoot apices on the initiation or outgrowth of distant lateral buds, is a major regulatory mechanism of plant form. Nearly a century of studies in the sporophyte of flowering plants have established the phytohormone auxin as a front-runner in the search for key factors controlling apical dominance, identifying critical roles for long-range polar auxin transport and local auxin biosynthesis in modulating shoot branching. A capacity for lateral branching evolved by convergence in the gametophytic shoot of mosses and primed its diversification; however the extent of conservation in apical dominance regulation within the land plants remains largely unknown. To fill this knowledge gap, we sought to identify genetic determinants of apical dominance in haploid leafy shoot of the moss *Physcomitrium* patens. We identified shared mechanisms between *Physcomitrium* and *Arabidopsis*, indicating deep homology in the regulation of apical dominance within the land plants.

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# Representation and functions of shoot apical meristems in FSPMs

## KEYNOTE

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Functional Structural Plant Models (FSPM) are individual-based models that explicitly account for the interactions between plant architecture and its abiotic and biotic environment. Plant morphogenesis, growth and grain or fruit production are among the most represented processes in FSPMs. These biological processes are largely determined at the Shoot Apical Meristem (SAM) level as it drives the rate of leaf initiation, phyllotaxy, leaf geometry, floral induction and the production of reproductive organs. Nevertheless, not all FSPMs are based on an explicit representation of SAMs, their functioning is then ignored in the case of non-dynamic models or embedded in parametric or statistical functions of plant morphogenesis in dynamic models. For FSPMs that include an explicit representation of SAMs, they are mainly constructed on the L-systems formalism which is well suited to describe plant development (Boudon *et al.*, 2012). First, one of the main functions of SAMs in these FSPMs is the production of new leaves or growth units, usually at a constant rate expressed in thermal unit. In some cases, the rate of leaf production by SAMs is coordinated with the rate of leaf emergence, leading to the concept of self-regulated architecture. However, the effect of substrate or water availability on the functioning of the SAM in terms of the size or properties of the emitted primordia is not accounting for. Secondly, the representation of apices in models is also used to simulate axillary bud break and the production of tillers, branches or new growth units. In these cases, the transition from a latent to an active SAM is controlled by light intensity and its spectrum (Verdenal *et al.*, 2008; Faverjon *et al.*, 2019), or temperature or hormones (Prusinkiewicz *et al.*, 2009) or is based on stochastic approaches. Finally, some FSPMs also account for the production of reproductive organs like grains and fruits by SAMs (Boudon *et al.*, 2020; Rouet *et al.*, 2022). Nevertheless, this aspect of SAM functioning remains poorly described in FSPMs despite its importance in plant production, yield and ecology. We believe that a better integration of SAMs functioning and control in FSPMs is a promising way to assess functional hypotheses and predict plant plasticity to the environment.

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# What did we learn on meristem fates by modelling fruit tree development?

## KEYNOTE

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In polycarpic perennial plants, meristem fate varies within individuals in a given year and between consecutive years and among genotypes of a given species. The different meristems composing those plants exhibit different activity levels regarding the periods of organogenesis and organ extension, latency, growth and growth cessation and their transition from vegetative to floral state.
The comprehension of tree development through a precise description of meristem fates depending on time and position allows building the structural part of so called Functional-Structural models (FSPM). Building such a model in the apple tree case led us to highlight strong organization of meristem fates at shoot, branch and tree levels with remarkable regularities and gradients despite variations among genotypes. Observations of other fruit tree species, especially in the *Prunus* genus, led us to similar findings and highlighted regular patterns and gradients during tree ontogeny that were specific to each species. Those regularities *versus* variations question the physiological and molecular processes that might control the perception of environment as well as the timing and state of meristem activities as well as their coordination within plants for appropriate organogenesis, elongation, bursting and blooming.
Focusing on floral induction (FI) in apple tree meristems, we observed occurrences in a given year at specific positions in tree structures and recurrence over consecutive years that drives tree production (ir)regularity. We analyzed the tryptic between tree architectural development, physiology and FI occurrence in different varieties with contrasted behaviors. A linear model common to all genotypes, combined four main factors - cytokinins and gibberellins content in meristems, starch content in leaves and the proportion of long shoots in trees - to predict FI proportion. However, each factor had a different weight in FI determination, depending on the genotype, suggesting a genotype-specific architectural and physiological profile linked to flowering behavior. These results combined with literature and previous findings obtained by genetic and transcriptomic approaches, lead us to assume that the GA-mediated pathway already known to be involved in *Arabidopsis thaliana* flowering could also act in the apple tree FI. Future research in our group will aim at a more in-depth comprehension of the role of gibberellins in FI, in the apple tree study case.

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# Detecting dormancy dynamics in woody plants by characterizing hydraulic connectivity between stem and bud

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In late summer, the buds of temperate woody plants become dormant, being unable to grow under favourable conditions. Accurate characterization of the dormancy state is an important limitation in predicting the phenology of woody species and leads to increased uncertainty in prediction models under climate change. Different phenological stages are visible during the transition from growth to dormancy (e.g. growth cessation, leaf fall, lignification, or bud set), while others are cryptic (e.g. endodormancy induction and release, ecodormancy release). Indirect methods to measure these cryptic stages are based on measuring the intensity of growth inhibition using forcing tests. The reference methods are based on single node cuttings or set of buds on a stem exposed to non-limiting conditions (i.e. warm temperature of about 20-25°C and a long photoperiod 16:8 D/N). However, these methods are time and plant intensive, limiting their use for high-resolution temporal dynamics.
Here, we describe the development of a new method based on the change in the hydraulic connectivity between the stem and the bud to measure dormancy stage. The hypothesis of this method is that disruption and recovery of water flows between stems and buds will be indicative of the endodormancy induction and release, respectively. In order to analyze xylem conductance at the stem-bud junction, we propose to study the dynamics of ice propagation by initiating ice nucleation within the wood and measuring the subsequent propagation to the bud. Using the exothermic properties of ice formation, we were able to characterize the change in the hydraulic connectivity between the stem and the bud in four contrasted species: walnut *Juglans regia* cv Franquette, peach *Prunus persica* cv Red Haven, ash *Fraxinus excelsior* and beech *Fagus sylvatica*. Comparison with the standard forcing test showed specific patterns of bud isolation compared to the classical dormancy stages (endodormancy induction, endodormancy release and ecodormancy). This new phenotyping method should help to define the phenological stages and consequences of climate change on phenological cycles of temperate woody species.

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# Temperature heterogeneity at crown scale possible impact on tree architecture after late spring frost

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Trees are exposed to large spatio-temporal thermal variation. Temperature heterogeneity can induce intra-crown discrepancies in the onset and the dynamic of primary and secondary growth and, furthermore, in meristem frost resistance. In late spring, freezing events could be more detrimental to the southern part of the tree, which is likely to exhibit advanced growth and reduced frost resistance. Would intra-crown thermal heterogeneity have lagged effects on tree growth and thus modify tree crown shape? Are there compensatory mechanisms between branches at the crown level during the growing season?
We conducted a differential warming experiment on young *Juglans regia* trees in greenhouse. From February to August, the average difference in temperature during the day between warmed and control parts was 4°C. We explored the responses between warmed and control parts in primary (budburst date through visual observation and time-lapse photography) and secondary growth (through Linear Variable Differential Transformer measurements and cytological analysis). Physiological changes in relative water content and soluble carbohydrates were also measured in buds and branches. Bud burst occurs two weeks earlier in warmed branches. The difference between warmed and control branches as well as the correlation between budburst and secondary growth were explored. On a secondary experiment, a controlled freezing event was performed to assess the effect of a false spring event. Preliminary results show a frost dehardening difference and no compensatory mechanisms at tree scale, resulting in branches ramification difference between warm and control part.

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# Axillary meristem is central to the trade-off between flowering and runnering in strawberry

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Plant architecture is central in determining crop yield. In strawberry, sexual and asexual reproductions take place jointly and affect plant architecture. Each reproduction habit displays an agronomical interest: sexual reproduction controls fruit yield via flowering and asexual reproduction is essential to cultivar propagation via the production of an aerial stolon (elongated stem produced in the runnering process). These two reproduction habits are in competition and the trade-off between the two takes place in the axillary meristem (AXM), which can produce either an inflorescence-bearing branch or a stolon. Changing the balance between sexual and asexual reproduction by playing on AXM fate modulates plant architecture and therefore fruit and daughter-plant yield.
Our objective is to decipher the mechanisms that regulate the AXM fate and so the plant architecture in strawberry. To do so, we aim at identifying new molecular actors involved in the gene network regulating AXM fate. To this end, we focused on the diploid *Fragaria vesca* strawberry model. Indeed, insights from the *F. vesca* diploid strawberry can be easily transferred to the octoploid cultivated strawberry because physiological processes and their key regulators are well conserved between these two species.
Using large scale gene expression analyses targeted to specific stages of AXM development and functional approaches, we identified and characterized key actors involved in the gene network regulating the balance between flowering and runnering in strawberry, e.g members of the FT/TFL1 family and BRANCHED1. Our findings offer potential breeding targets to modulate flowering and runnering responses in cultivated strawberry. As an example, we showed that overexpression of a specific FT gene in F. vesca increased fruit yield by more than 3.5-fold (Gaston *et al.*, New Phytol. 2021).

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# Control of lateral meristems: how is sugar availability involved in the environmental control of axillary bud outgrowth?

## KEYNOTE

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Axillary bud outgrowth is a major process allowing the plant to adapt its architecture to environmental constraints. Indeed, the dormant buds formed at each leaf axil contain meristems, which depending on the environment, remain quiescent or resume activity leading to bud outgrowth and the development of a new axis (Rameau *et al.* 2015). Studies on apical dominance, *i.e.* the inhibition of buds by the growing apical zone, have highlighted the opposite roles of auxin and sugar, which is involved in a signaling and trophic regulation of bud activity (Mason *et al.* 2014, Barbier *et al.* 2015, Schneider *et al.* 2019). However, understanding the interaction between the environment and the mechanisms of apical dominance is a major issue (Schneider *et al.* 2019). Our study tests the long-standing hypothesis that sugar availability is involved in the mediation of light effect on bud outgrowth at plant-level. We combined experimental studies and computer simulations, using rose as a plant model.

First, using buds grown *in vitro*, high sugar availability was demonstrated to reduce auxin repressing effect on bud outgrowth, indicating that it could reduce the auxin-related apical dominance *in planta*. Sugar effect was highlighted to be due to a repression of a pathway downstream of auxin by testing different possible scenarios in a model (Bertheloot *et al.* 2020).

Then, we demonstrated the ability of sugar availability to modulate bud outgrowth rate and to explain, at least partly, light effect *in planta*. Plants were grown under comfort light conditions, or under permanent or temporary light limitation. Physiological and morphological analyses showed a positive relationship between bud outgrowth rate and sugar contents in stems. Moreover, the exogenous supply of sugar stimulated bud outgrowth under unfavorable light conditions. Calculating photosynthesis and carbohydrate (C) demand highlighted that, compared to high light, continuous and temporary low light altered sugar contents through a predominant effect on photosynthesis and on C demand, respectively.

These results highlight that light, by controlling C sources and sinks, modulates the availability of sugar for buds and thus the repressive effect of auxin on axillary bud activity. They pave the way for a better consideration of the mechanisms controlling the control of lateral meristems in plant models.

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# Sugar signaling modulates SHOOT MERISTEMLESS expression and meristem function in *Arabidopsis*

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In plants, development of all above-ground tissues is controlled by the shoot apical meristem (SAM) which finely balances cell proliferation and differentiation to allow life-long growth. To maximize fitness and survival, meristem activity is adjusted to the prevailing conditions through a poorly understood integration of developmental signals with environmental and nutritional information. Here, we show that sugar signals play a central role in SAM function through post-transcriptional regulation of the key regulator of meristem maintenance, SHOOT MERISTEMLESS (STM). STM protein is less abundant in the inflorescence meristem of plants grown under limiting light conditions or transferred from optimal irradiance to darkness for up to three days, with lower STM expression correlating with lower sugar content in these meristems compared to control plants. We further show that STM accumulation requires sucrose rather than light *per se*. Subjecting plants to prolonged darkness activates the sugar sensing protein kinase SUCROSE-NON-FERMENTING1-RELATED KINASE 1 (SnRK1) in the SAM, where SnRK1 is particularly abundant. Plants overexpressing SnRK1α1 have decreased STM levels under optimal light conditions, despite a higher sugar accumulation in the SAM. In contrast, SnRK1α silencing in the meristem leads to reduced STM expression and severe developmental phenotypes previously associated with STM loss-of-function. Altogether, we demonstrate that sugars promote STM accumulation and that the SnRK1 sugar sensor plays a dual role in the SAM, limiting STM abundance under unfavorable conditions but being required for overall meristem organization and integrity. This highlights the importance of sugar signaling for the proper coordination of meristem activities.

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# A hydraulically based model framework for the grass leaf meristem

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The rate with which lateral buds/meristems in grasses are formed is likely under control of the apical meristem. But as far as initiation and outgrowth, and the appearance of successive leaves and tillers are concerned, grasses display a remarkable level of coordination of leaf and tiller initiation and appearance, which are associated to onset and cessation of leaf cell division. Therefore, the growth kinetics of a specific leaf have propagated, 'downstream' effects on growth dynamics of successive leaves, and, consequently, largely impact plant productivity.
Furthermore, the grass leaf is an interesting model to study meristem behavior, because cell division, elongation and maturation occur simultaneously in spatially distinct zones. The kinetics of leaf growth are complex and are impacted by environmental variables such as air temperature and relative humidity, availability of water, nitrogen and phosphorus.
We now present a model that integrates short-term leaf growth dynamics (minutes-to-hours) to whole-leaf growth rate patterns (days-to-weeks). Thereto, we conceived four zones in a growing grass leaf, differing in hydraulic, visco-elastic and meristematic properties. Closest to the leaf base, there is the cell division zone (DZ), which is meristematic, highly elastic, a strong sink for carbohydrates and fully enclosed by the the pseudostem, shaped by the sheaths of the older leaves of the tiller (and hence, not transpiring). Distal to the cell division zone, there is the cell elongation zone, where cells have stopped dividing, but are still highly elastic, are elongating, are strong sinks and fully enclosed. In the following zone, cells are maturing, whereby growth has stopped, and cells have become less elastic, but are still enclosed and not transpiring. In the most distal zone, cells are mature (and thus no longer growing and less elastic), but are exposed to the atmosphere, and therefore transpiring and photosynthetically active.
A crucial feature in this model is the timing of cell division cessation, which is triggered by the appearance of the leaf tip. As a result, from tip appearance, final (maximum) leaf length is approximately fixed, and leaves which are enclosed in larger pseudostems, become larger, as has been documented by many observations of leaf growth coordination in grasses.
This model provides a framework to investigate putative (molecular) mechanisms underlying this coordination, which appears not to be controlled by the apex, and explore dynamics in sink metabolism underpinning leaf growth.

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# SESSION 3.
# TOWARD FSPM INTEGRATING SAM FUNCTIONS

# Cauliflowers and the genetic origin of fractals in plants

**KEYNOTE**

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Fractals forms are ubiquitous in nature, clouds, lightenings, coastlines, snowflakes in the inorganic world, but also trees, ferns, lungs, and corals in the living world. One of the most iconic example of a biological fractal is certainly the cauliflower, whose fractal appearance culminates in the Romanesco variety. A bit more than 10 years ago, I met François Parcy, a specialist of the genetic regulation of the passage from inflorescences to flowers during plant growth. We both were very intrigued by this ability of plants to make so remarkable fractals. François knew already that the cauliflower was the result of the failure of a plant to make flowers, due to a couple of mutations. However, why and how the change in the gene activity would produce a fractal-like shape remained a mystery. In this talk, I will explain what we understood, *i.e.* basically that such fractal forms are produced because, despite their failure to make flowers, the growing tissues keep memory of their transient passage in a floral state. Additional mutations affecting growth can induce the production of conical structures reminiscent of the conspicuous fractal Romanesco shape. Interestingly, the way plants produce fractals has commonalities with the way mathematical fractals are constructed, but they are not exactly similar. This study reveals how fractal-like forms may emerge from the combination of specific perturbations of floral developmental programs and growth dynamics.

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# The SAM and the leaf series in grasses: a new model

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The leaves of grass tillers begin their life on the shoot apical meristem (SAM) as primordia. Each leaf elongates from an intercalary meristem followed by an extension zone only and by the mature zone. The complete elongation of a leaf takes place in the sheath of the previous leaf. Durand *et al*. (1999*)* implemented a model of leaf elongation based on the conservation and growth equations relating the tissues fluxes between the three compartments. With time, the proportion of tissues leaving the intercalary meristem and the extension only zone increases. In a further version of that model, Durand *et al.* (2000) implemented the response to temperature and water deficits in order to simulate the response of the grass tiller morphogenesis to dry conditions in summer. Also they used the morphological observations by Skinner *et al* (1994) on a series of leaves at different stages of development to introduce coordination rules between the successive leaves on the tiller. When leaf *n* length was equal to the length of the including sheath, *i.e.* when the tip of leaf *n* emerged, the intercalary meristem started producing sheath cells only. At the same time, the leaf *n+ 2* started to elongate from the shoot apical meristem. That supposed the existence of a primordium with no explicit consideration to the functioning of the SAM itself. In the work exposed here, we further introduced a new compartment to simulate the shoot apical meristem, in order to simulate the production of primordia, adding a new condition to- or replacing the coordination rule described above. In the new version of the model, the SAM is supposed to grow at a rate, which is proportional to the rate of other meristems, and similarly sensitive to environment. A part of the tissues produced by the SAM accumulates in a compartment, simulating the gradual production of successive primordia. Every time the length of meristematic tissues accumulated reach the length of a primordium, the appearance of the n-2 leaf allows for the elongation of the newly formed leaf. In this version, two conditions must be met to start the elongation of leaves: production of a primordium *n+2* and emergence of leaf *n*. The rate at which the SAM grows, is used to build a new primordium and the length of a primordium are related using allometric relationships reducing the number of parameters involved and insuring the consistency of the tiller architecture. A first set of parameters were derived from *ex situ* observations of SAM on vegetative tillers of perennial ryegrass. A first verification of the consistency of the model was tested using experimental data of successive leaves elongation on tall fescue in the field.

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# Linking genes to plant global morphogenesis: the role of tropisms just beyond the SAM

Bruno Moulia
*UMR 547 PIAF, INRAE, University Clermont Auvergne, France*

Shoot morphogenetic plasticity is crucial to the adaptation of plants to their fluctuating environments. Major insights into shoot morphogenesis have been compiled studying the shoot apical meristem (SAM) through a methodological effort in multiscale systems biology and biophysics (Vernoux *et al.* 2021). However, morphogenesis at the SAM is robust to environmental variability. Plasticity emerges later on during post-SAM development. The purpose of this talk is to show that multiscale systems biology and biophysics is insightful for the shaping of the whole plant as well. More specifically, I will review the shaping of axes and crowns through tropisms and elasticity, combining the recent advances in morphogenetic control using physical cues and by genes. I will focus on land angiosperms, with growth habits ranging from small herbs to big trees. Generic morphogenetic processes have been identified, revealing feedforward and feedback effects of global shape on the local morphogenetic process, involving proprioception (Moulia *et al.* 2021). Major advances have also been made in the analysis of the major genes involved in shaping axes and crowns, revealing conserved genic networks (Hill and Hollender 2019, Hollender *et al.* 2020). These two approaches are now starting to converge through the definition of a quadruplet of dimensionless morphogenetic numbers (B,M,W,El) that fully defines the control over axis and crown shaping at the scale of the tropic control apparatus (i.e. a segment of stem in the growth zone below the apical meristem) . These dimensionless numbers are quantitative macro-characters that can be more readily related to multi-cellular models and to relative expressions of genes and/or to QTLs (Moulia *et al.* 2022)

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# Towards the integration of cellular scales in individual plant models

## KEYNOTE

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Predicting quantitatively the behavior of living organisms from the finest scales to the individual scale in normal and complex environmental conditions remains highly challenging for the systems biology community (Goelzer and Fromion. 2017). Part of the difficulty consists in integrating the scales where the decisions of the adaptation to the environment take place, i.e. the cellular and infra-cellular scales, in the context of the individual. Over the last ten years, a significant step has been achieved in the modeling of cellular and infra-cellular scales in prokaryotic cells. We developed and validated experimentally on microbial cells a new modeling method, named Resource Balance Analysis (RBA) [Goelzer *et al.* 2011, Goelzer *et al.* 2015). RBA predicts, for a specific environment, the set of possible cellular configurations (growth rate, metabolic fluxes, abundances of molecular machines, including ribosomes, enzymes, transporters) compatible with the available external resources, and has the potential to predict the cell response to a large set of complex environmental conditions (Tournier *et al.* 2017). Recently, the RBA theoretical framework was extended to eukaryotic cells (Goelzer *et al.* 2019) and used to generate a RBA model for the shoot compartment of the plant *Arabidopsis thaliana.* In this talk, we introduce the RBA modeling framework and illustrate its ability to predict plant cell phenotypes in normal and complex environmental conditions – *i.e.* conditions where abiotic constraints (stresses) are combined.

### References

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# INDEX

# PROGRAM

## Monday 28 November

14h — Welcome speeches
by the President of the Urban Community of Grand Poitiers,
the President of Xavier Bernard Foundation,
the Deputy Director General of Science and Innovation at INRAE,
the President of the INRAE Nouvelle-Aquitaine-Poitiers research centre

### Opening Keynote

14h30 — Jan Traas
Morphogenesis at the shoot meristem: a challenging problem

15h30 — Coffee Break

### Session 1: The functioning of SAM

16h — Keynote by Henrik Jönsson
On the initiation and maintenance of shoot meristems

#### Short communications

16h30 — SC1. Magalie Uyttewaal
Tight control of division plane orientation is necessary
to optimize the growth capacity of tissues and organs in *Arabidopsis thaliana*

16h45 — SC2. Patrick Laufs
De novo stem cell establishment in meristems
requires repression of organ boundary cell fate

17h — SC3. Marianne Lang
How mechanical signals contribute to plant resilience
after drastic pruning: the case of pollard trees

17h15 — SC4. Jean-Christophe Palauqui
Analysis of natural variation in meristematic conversion

17h30 — SC5. Juan Alonso Serra
Hydraulic stress at the meristem-organ boundaries

17h45 — SC6. Philippe Andrey
Computational analysis of cell division patterns in the shoot apical meristem

18h — Break

19h30 — Dinning cocktail.

## Tuesday 29 november

### Session 1 (continued)

9h Keynote by Dorota Kwiatkowska
Changing SAM geometry and generation of phyllotactic patterns

9h30 Keynote by Alexis Peaucelle
From phyllotaxis to Homogalacturonan and back:
exploring the origins of plant growth

10h Keynote by Robert Sablowski
How meristem cells measure themselves and why it matters

10h30 Keynote by Sylvie Dinant
The distribution of sugars and amino acids between source and sink organs:
more than just a transporter's game

11h Coffee Break

**Short communications**

11h30 SC7. Jasmine Burguet
Model-based reconstruction of whole organ growth dynamics
reveals invariant patterns in leaf morphogenesis

11h45 SC8. Nicolas Arnaud
Statistical spatio-temporal atlasing of gene expression patterns
during organ growth

12h SC9. Sana Dieudonné
Bract inhibition at floral transition in *Arabidopsis thaliana*

### Session 2: Determination and regulation of SAM fate in the plant

12h15 Keynote by Yoan Coudert
Off with their head: a tale of decapitation and auxin

12h45 Keynote by Romain Barillot
Representation and functions of shoot apical meristems in FSPMs

13h15 Lunch

14h30 Keynote by Evelyne Costes
What did we learn on meristem fates by modelling fruit tree development?

**Short communications**

15h SC10. Guillaume Charrier
Detecting dormancy dynamics in woody plants
by characterizing hydraulic connectivity between stem and bud

15h15 SC11. Nicolas Dusart
Temperature heterogeneity at crown scale possible impact
on tree architecture after late spring frost

15h30 SC12. Amélia Gaston
Axillary meristem is central to the trade-off between flowering and runnering in strawberry

15h45 Coffee Break

16h15 Keynote by Jessica Bertheloot
Control of lateral meristems: how is sugar availability involved in the environmental control of axillary bud outgrowth?

**Short communications**

16h45 SC13. Filipa Lara Lopez
Sugar signaling modulates SHOOT MERISTEMLESS expression and meristem function in *Arabidopsis*

17h SC14. Tom de Swaef
A hydraulically based model framework for the grass leaf meristem

## Session 3: Toward FSPM integrating SAM functions

17h15 Keynote by Christophe Godin
Cauliflowers and the genetic origin of fractals in plants

17h45 Break

19h30 Dinning cocktail

## Wednesday 30 November

## Session 3 (continued)

9h SC15. Jean-Louis Durand
The SAM and the leaf series in grasses: a new model

9h15 SC 16. Bruno Moulia
Linking genes to plant global morphogenesis: the role of tropisms just beyond the SAM

9h30 Keynote by Anne Goelzer
Towards the integration of cellular scales in individual plant models

10h Coffee Break

10h30 General discussion
What is the next step to integrating SAM biology to the plant level?
Animation Robert Faivre

12h30 **END OF CONFERENCE**

**Posters** (during all the conference):

P1 Eric Biot *et al.*
BIP, a new software design for batch analysis of biological images

P2 Anthony Scriven *et al*.
Can U-Net replace CLV3? Machine learning for the identification of biological landmarks in shoot apical meristem images

P3 Landry Duguet *et al*.
Revisiting PIN1 polarity interpretation at the SAM
based on automated PIN1 map reconstruction

## NOTES

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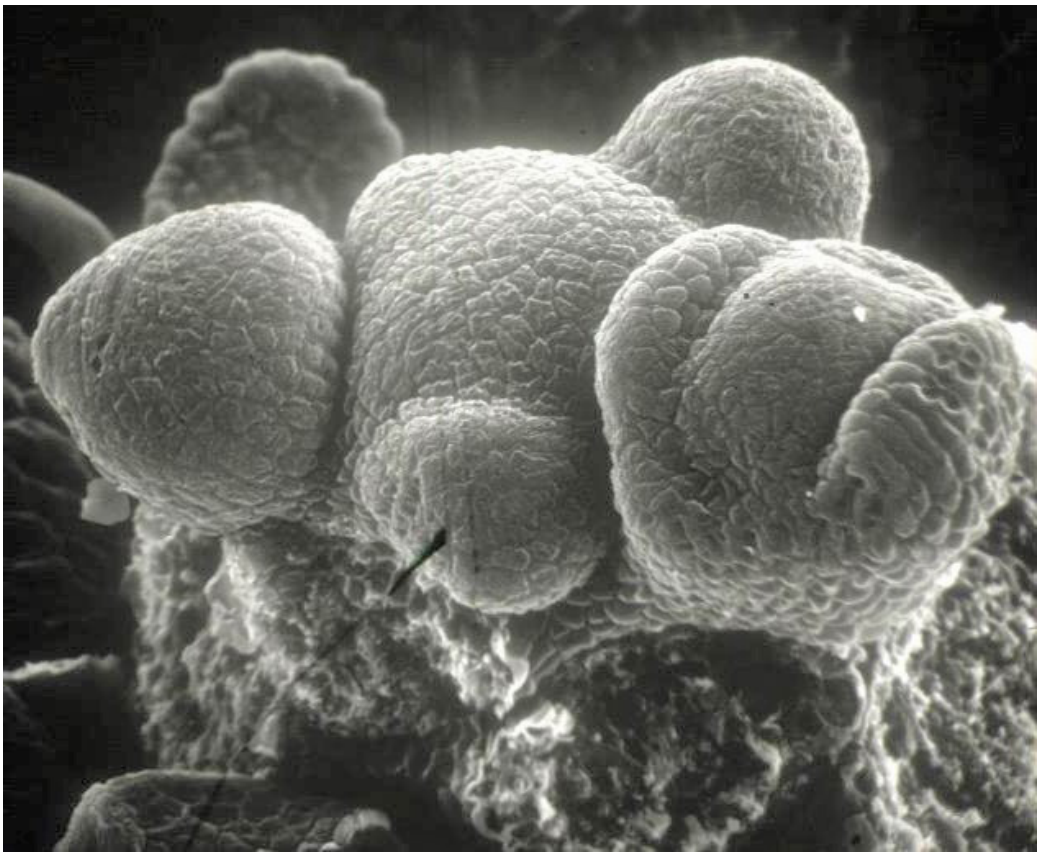
**Abstracts**

# FROM GENES TO PLANT ARCHITECTURE THE SHOOT APICAL MERISTEM IN ALL ITS STATES

Coordinators: Jessica Bertheloot, Jean-Louis Durand, Christophe Godin



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