Available online at www.sciencedirect.com

ScienceDirect

Current Opinion in Plant Biology

The growth of a stable stationary structure: coordinating cell behavior and patterning at the shoot apical meristem

Jekaterina Truskina[1,2] and Teva Vernoux[1]

Plants are characterized by their ability to produce new organs post-embryonically throughout their entire life cycle. In particular development of all above-ground organs relies almost entirely on the function of the shoot apical meristem (SAM). The SAM performs a dual role by maintaining a pool of undifferentiated cells and simultaneously driving cell differentiation to initiate organogenesis. Both processes require strict coordination between individual cells which leads to formation of reproducible morphological and molecular patterns within SAM. The patterns are formed and maintained in large part due to spatio-temporal variation in signaling of plant hormones auxin and cytokinin resulting in tissue-specific transcriptional regulation. Integration of these mechanisms into computational models further identifies the key regulatory interactions involved in SAM function.

Addresses
[1] Laboratoire Reproduction et Développement des Plantes, Univ Lyon, ENS de Lyon, UCB Lyon 1, CNRS, INRA, F-69342 Lyon, France
[2] Centre for Plant Integrative Biology, School of Biosciences, University of Nottingham, Loughborough LE12 5RD, UK

Corresponding author: Vernoux, Teva (teva.vernoux@ens-lyon.fr)

Current Opinion in Plant Biology 2018, **41**:83–88

This review comes from a themed issue on **Growth and development**

Edited by **Gwyneth Ingram** and **Ari Pekka Mähönen**

http://dx.doi.org/10.1016/j.pbi.2017.09.011

Introduction

Multicellular organisms are characterized by the presence of recognizable patterns shaping their body structures. These patterns are produced from complex distributions of cell fates in space and time. In higher plants the shoot apical meristem (SAM) is a dynamic structure with undifferentiated stem cells in its center and differentiated organ primordia at its periphery (reviewed in [1,2]). Two opposite processes occur in the SAM: the stem cell pool is constantly maintained and renewed whereas some cells accelerate their growth and division rate and eventually differentiate to become part of the newly forming organs (the leaves and flowers). The balance between these two processes is strictly controlled over the life of the plant and the location and timing of new organ emergence appears to be tightly regulated. This regulation can be first seen from the organization of the SAM which is divided into functional zones with distinct cellular behaviors (division and expansion) and distinct cellular identities. In *Arabidopsis thaliana* the dome-shaped structure of the SAM is divided into the central, peripheral and rib zones. The central zone is found at the summit and contains undifferentiated stem cells. The laterally located peripheral zone is the site of organ primordia initiation. The rib zone, situated below central and peripheral zones, produces the internal tissues of the stem. The SAM can be further divided into individual cell layers. In the center of the SAM the top two layers (L1 and L2; collectively referred as tunica) are able to divide only in one direction (anticlinally) whereas the deeper layers (L3 and further; collectively referred as corpus) are able to divide in any direction. This organization is largely similar in other higher plants with some variations in the number of tunica layers. The molecular patterns associated with the functional zones of the SAM are established by tissue-specific expression of key regulatory genes as well as mobile signals such as proteins and hormones, which move between cells in the different SAM zones. In this review, we summarize recent findings on the mechanisms controlling and coordinating cell behavior and pattern formation at the shoot apical meristem.

Setting the geometry of the SAM: coordinating growth and cell division

Pattern formation at the SAM begins at the cellular level. The cells in the central zone where the stem cells are located divide slower than the cells in the peripheral zone [3,4]. The cells in the central zone of the SAM have overall similar cell size despite frequently observed asymmetric cell divisions [5•,6•]. A few recent studies have started to elucidate how the balance between cells division and cell expansion is maintained [5•,6•,7]. In particular, the cell divisions appear to be triggered by a combination of factors including reaching a critical size and adding a critical cell volume increment instead of a single decisive event [5•]. Moreover, the cell cycle length [6•] and the cell growth rate [5•,7] are adjusted to the variable initial cell size acquired after geometrically asymmetric cell division illustrating the presence of a compensatory mechanism that allows the meristem to maintain the

desired overall uniform structure. Indeed, the local variability of cell growth rates in the meristem plays a key role in setting the geometry of the meristem [8], highlighting the importance of cell behavior in generating a specific shape.

The occurrence of both geometrically symmetric and asymmetric cell divisions in the SAM questions not only the long-standing debate of how cells determine where to build a new cell wall but also whether this might play a role in the function of the SAM. A few recent publications discuss the rules behind positioning of new cell walls [9,10••]. The assumption that the cells divide along local minima of plane area [11] was challenged by providing evidence that the new division planes orient along the maxima of mechanical tensions in cell walls induced by local heterogeneous growth which can differ from the plane area minimum [10••].

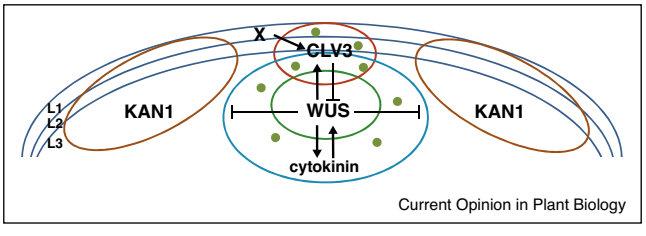
Several recent publications are further highlighting the importance of mechanical signals in the SAM. The division of the SAM into the central and peripheral zones indeed correlates with differences in mechanical properties: the central zone of the SAM is characterized by increased stiffness of the tissue compared to more peripheral regions [12–14] or organ primordia [15,16]. These mechanical properties appear to be genetically controlled [12] and caused by differences in auxin content [15]. However how the spatio-temporal distribution of the mechanical properties affects cell behavior and SAM function still remains to be clearly established.

Setting the organization of the SAM: the gene network controlling cell identities

The functional zones of the SAM are characterized by specific expression of master regulatory genes with CLV3 in the central zone [17], WUS in the organizing center [18] and KAN1 in the boundary domain [19•] amongst many others. Several recent publications have attempted to model SAM maintenance based on expression patterns and interactions of these regulatory genes [19•,20••,21,22,23••]. Computer simulations attempted to define the minimal regulatory networks required for functioning of the SAM (Figure 1). The models always include the well-described WUS-CLV3 feedback loop, which dynamically maintains the size of stem cell niche [24–27]. Repression of the differentiation-promoting genes such as KAN1 by WUS contributes to the entry into differentiation [19•,20••]. Furthermore, this modeling work emphasizes the importance of cytokinin signaling in SAM maintenance by showing that regulation of WUS expression by cytokinin [28,29] and activation of cytokinin signaling by WUS [30] are fundamental for correct positioning of WUS in the SAM [20••,21]. Recently an additional signaling network was identified which includes putative movement of a CLE peptide produced in organ primordia to the center of the SAM where it regulates stem cell activity [23••] thus providing an extra feedback regulation from developing organs on the stem cell niche and providing an interesting mechanisms for integrating stem cell maintenance and organogenesis.

The maintenance of the stem cell niche though WUS continues to be the subject of extensive research. WUS was shown to be a mobile protein which moves from the WUS expression domain into L1 and L2 layers of the SAM [25]. Lately, plasmodesmata were confirmed to mediate this movement [31]. Structural domains responsible for the spatial distribution and subcellular localization of WUS protein were identified with partially contradicting results in two independent studies [31,32]. Homodimerization appears to play a crucial role in restricting WUS protein movement [31,32], in control of CLV3 expression [33•] and in regulation of SAM growth [31,32]. Surprisingly, WUS was shown to activate CLV3 at low concentrations and repress at high concentrations, which accounts for the restriction of CLV3 expression to the upper layers of the central zone [33•]. Interestingly, misexpression of WUS reduced its protein stability leading to degradation [32] which sheds a new light on the previously described influence of WUS misexpression on SAM size and cell division rates in the peripheral zone [34,35]. These molecular details would need to be considered in future models as they modify significantly our understanding of the molecular regulations at play. The WUS-mediated control of the stem cell niche involves direct regulation of multiple genes [19•,36] but only WUS-CLV3 interaction has been characterized in details [24–27,33•]. A recent publication focuses on HEC1, a direct target of WUS, which influences stem cell activity and controls expression of a subset of WUS target genes in a manner antagonistic to WUS [37]. This illustrates the need for broadening the analysis of the different targets of WUS.

Figure 1



Minimal gene interaction network controlling SAM maintenance. CLV3 (red circle) and WUS (green circle) regulate each other expression though the movement of WUS protein (green dots). The expression of the cell differentiation-promoting genes such as KAN1 (brown circle) is limited to the periphery of the SAM through direct repression by WUS protein. WUS is activated by cytokinin signaling (light blue circle) and in turn activates cytokinin signaling by itself. CLV3 is activated by a hypothetical L1-derived signal (X).
Adapted from [19–21].

The well-studied WUS-CLV3 interaction module was long believed to govern the shape and size of the meristematic region in the SAM. New evidence suggest that the apical-basal and lateral symmetries of the meristematic SAM region appear to be controlled by fundamentally different pathways with CLV3-WUS pathway being more involved in the establishment of the apical-basal axis whereas the HD-ZIPIII family transcription factors and ERECTA predominantly influence the central-to-peripheral axis [38–40]. CLV3, HD-ZIPIII transcription factors and ERECTA appear to act in three different pathways which regulate the shape and size of the meristem [39,40]. Interestingly, the HD-ZIPIII transcription factors act independently of WUS in the maintenance of the stem cell pool [38].

The size and shape of the SAM can vary depending on the ecotype [3,20••,41] or on environmental conditions [20••,41]. The plants were shown to be able to adapt to these individual variations by positively scaling both the size and the shape of CLV3 and WUS expression domains in correlation with increased meristem size and changes in the geometry of the SAM [20••]. This study identifies a plausible feedback from the geometry on the expression of the WUS gene and thus on the size of the stem cell niche, giving a hint on how cellular patterns may adapt to the size and shape of plant tissues.

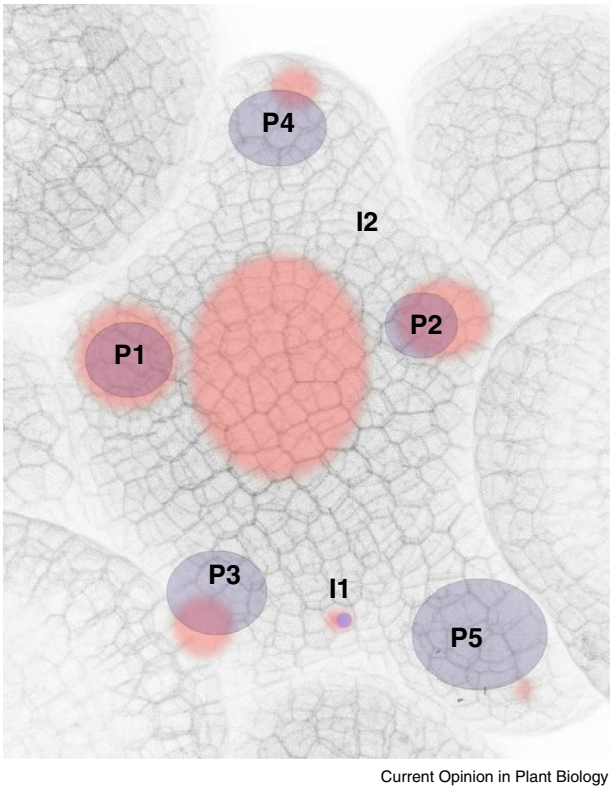
A few recent publications started to unravel gene regulatory networks involved in adaptation of the SAM to environmental conditions. In particular, the SAM stem cell niche was regulated in response to light and metabolic signals with both pathways independently activating WUS expression though the TOR kinase [42••].

Setting the location and timing of organ initiation: the role of hormone signals

At the periphery of the SAM, new leaf or flower primordia are initiated at predictable positions and with regular time intervals between initiation events (reviewed in [43–46]). A long-standing theory postulates that the positioning and timing of organs at the growing shoot apex is determined by the presence of inhibitory signals around developing organ primordia, these inhibitory fields preventing initiation of new primordia. The current understanding of the molecular mechanisms behind organ initiation suggests that this inhibition results from auxin depletion in the regions surrounding a local auxin accumulation that drives organ primordia, a pattern created through self-organization of polar auxin transport as a result of a feedback regulation between auxin and its transport [47–50]. Interestingly, the creation of local auxin maxima requires to some degree the auxin response factor MONOPTEROS that orients auxin transport towards the sites of the developing organ primordia [51]. This suggests that MONOPTEROS is required for the feedback between auxin and its transport. Recent findings indicate that the timing of primordia initiation is also regulated by an interplay between auxin and cytokinin signaling [52••] (Figure 2). This study focuses on the role of the AHP6 protein which production is induced by auxin and enriched in organ primordia and developing flowers. The AHP6 protein produced in the primordia is then able to move to the neighboring cells where it acts as an inhibitor of cytokinin signaling. The movement of AHP6 creates a differential in cytokinin signaling activity between sites of successive organ initiation that facilitates sequential initiation of organs and thus provides robustness to the timing of organ initiation.

In addition to auxin and cytokinin, the establishment of accurate organogenesis patterns at the shoot apex may also requires reduced brassinosteroid (BR) hormone accumulation at the boundary region between the meristem and organ primordia [53,54]. The depletion of BR at the boundary domain is achieved by the domain-specific regulatory transcription factor LOB which induces

Figure 2



The initiation of organ primordia is regulated by auxin and cytokinin. The developing organ primordia are characterized by high auxin signaling (blue) in primordia of all stages (P1–P5). Cytokinin signaling (red) is the highest in the young primodia (P1 and P2) but decreases rapidly in the older primordia (P3–P5). Auxin and cytokinin signaling is first switched on at the site of the next primordia initiation (I1) but absent from I2 site where primordia is predicted to initiate after I1. Adapted from [52].

expression of BR-inactivating enzyme BAS1 [53] and at the same time though reduced expression of brassinosteroid-activated transcription factor BZR1 specifically at the boundary region [54].

The analysis of the role of AHP6 discussed above also led to discover the existence of noise on the timing of organ initiation leading to specific phyllotactic defects. This stimulated a new modeling attempt which integrated random fluctuations in local perception of inhibitory signals [55••]. The model is able to account for the deviations from the expected organ initiation pattern which is occasionally observed in various plant species.

Differential auxin patterns continue to regulate development following the initiation of the shoot organs. In particular, the developing leaf primordia require transient low auxin zone at the adaxial (upper) side for successful establishment of leaf polarity [56]. The auxin depletion at the adaxial site is achieved by PIN1 auxin efflux transporter which moves auxin away from the adaxial site of the developing leaf primordia towards the meristem. The same mechanisms that pattern the meristem are thus also key in establishing the symmetry of the organs.

Axillary meristem initiation and formation is regulated by pulses of auxin and cytokinin

In many seed plant species, new leaves are formed at the shoot apical meristem during vegetative growth phase. At the upper (adaxial) side of the newly formed leaf an axillary meristem (AM) can be initiated. The AM serves as a small stem cell niche and gives rise to axillary buds which are able to remain dormant or eventually produce an axillary shoot [57,58].

The formation of the axillary meristem appears to be tightly controlled by patterns of hormone signaling levels which presents a remarkable similarity to the mechanisms behind the pattern formation in the SAM proper. The process requires initial auxin depletion at the future AM initiation site in the leaf axil [59•,60] closely followed by a pulse of cytokinin signaling [59•]. This auxin depletion in the leaf axil is achieved well before AM initiation at the early stages of leaf primordia formation due to directed polar auxin transport mediated by PIN1 localization [59•,60].

Lately, the axillary meristem was shown to be regulated by the same key genes as the main SAM. Specifically, the regulators of the shoot stem-cell niche WUS and CLV3 were dynamically induced one after another during initiation of the AM creating a two-step pattern of expression [61]. Interestingly, CLV3 was initially induced in the WUS-specific central domain before the expression shifted to the expected L1 and L2 layers at the later stages of AM formation [61]. Two recent studies also reveal the importance of the mobile stem-cell specific gene STM for AM initiation [62•,63•].

The organ development at the SAM in maize is characterized by complicated transitions from indeterminate inflorescence meristem to determinate axillary meristems [64]. A recent study elucidates molecular mechanisms and gene modules which regulate switches between different meristem types using a systematic approach [65••]. The spatio-temporal transcriptional profiling lead to identification of distinctive gene clusters which function in modules during meristem maintenance and development.

Conclusions

The remarkable ability of plants to continually produce new aerial organs results mainly from the activity of the shoot apical meristem. The symmetries of the future organs are laid out early during development in the SAM and this process is controlled by specific molecular patterns. A key mechanism appears to be contrasting hormone signaling between different regions in the SAM which results in tissue-specific gene expression patterns. In turn, the differentially expressed regulatory genes trigger cell-specific programs promoting cell fate determination. A strong emerging trend in recent research is that a similar set of signals and genes define a patterning module that is used in the SAM, the developing organs and to establish new meristems such as the AM. How this module is reused and how this allows to link organ and tissue development to the SAM activity is yet to be fully characterized but some of the key mechanisms have clearly been identified.

References and recommended reading

Papers of particular interest, published within the period of review, have been highlighted as:

- • of special interest
- •• of outstanding interest

1. Barton MK: **Twenty years on: the inner workings of the shoot apical meristem, a developmental dynamo**. *Dev Biol* 2010, **341**:95-113.

2. Murray JAH, Jones A, Godin C, Traas J: **Systems analysis of shoot apical meristem growth and development: integrating hormonal and mechanical signaling**. *Plant Cell* 2012, **24**:3907-3919.

3. Laufs P, Grandjean O, Jonak C, Kiêu K, Traas J: **Cellular parameters of the shoot apical meristem in Arabidopsis**. *Plant Cell* 1998, **10**:1375-1390.

4. Reddy GV, Heisler MG, Ehrhardt DW, Meyerowitz EM: **Real-time lineage analysis reveals oriented cell divisions associated with morphogenesis at the shoot apex of *Arabidopsis thaliana***. *Development* 2004, **131**:4225-4237.

5. • Willis L, Refahi Y, Wightman R, Landrein B, Teles J, Huang KC, Meyerowitz EM, Jönsson H: **Cell size and growth regulation in the *Arabidopsis thaliana* apical stem cell niche**. *Proc Natl Acad Sci U S A* 2016, **113**:E8238-E8246.

Live shoot apices were imaged over 3–4 days following the cell cycle of individual cells in the central zone of the SAM. The results indicated that single trigger events such as reaching a certain cell size, acquiring a critical increment in cell size or reaching a specific time point since birth

did not induce cell division. The study also highlights the inverse correlation between the birth cell size and the cell growth rate in cells produced though asymmetric cell divisions.

6. • Jones RA, Forero-Vargas M, Withers SP, Smith RS, Traas J, Dewitte W, Murray JAH: **Cell-size dependent progression of the cell cycle creates homeostasis and flexibility of plant cell size**. *Nat Commun* 2017, **8**:15060.
The cell cycle dynamics were measured in living SAMs in both central zone and organ primordia. The cells divided cell-autonomously at individual time points depending on their size at birth. The division events were triggered by reaching threshold activity levels of the CYCLIN DEPENDENT KINASES (CDKs) and these levels was shown to be modulated by the cell size.

7. Serrano-Mislata A, Schiessl K, Sablowski R: **Active control of cell size generates spatial detail during plant organogenesis**. *Curr Biol* 2015, **25**:2991-2996.

8. Uyttewaal M, Burian A, Alim K, Landrein B, Borowska-Wykre?t D, Dedieu A, Peaucelle A, Ludynia M, Traas J, Boudaoud A *et al.*: **Mechanical stress acts via katanin to amplify differences in growth rate between adjacent cells in Arabidopsis**. *Cell* 2012, **149**:439-451.

9. Shapiro BE, Tobin C, Mjolsness E, Meyerowitz EM: **Analysis of cell division patterns in the Arabidopsis shoot apical meristem**. *Proc Natl Acad Sci U S A* 2015, **112**:4815-4820.

10. •• Louveaux M, Julien J-D, Mirabet V, Boudaoud A, Hamant O: **Cell division plane orientation based on tensile stress in *Arabidopsis thaliana***. *Proc Natl Acad Sci U S A* 2016, **113**:E4294-E4303.
The positioning of new cell walls during division in L1 layer of the whole SAM was examined and compared to theoretical predictions from the recently formulated Besson–Dumais rule. When the Besson–Dumais rule failed to explain the cell wall positions particularly in the boundary domain of the SAM, a new model based on mechanical tension was developed which was able to predict cell wall positioning in various zones of the SAM.

11. Besson S, Dumais J: **Universal rule for the symmetric division of plant cells**. *Proc Natl Acad Sci U S A* 2011, **108**:6294-6299.

12. Milani P, Mirabet V, Cellier C, Rozier F, Hamant O, Das P, Boudaoud A: **Matching patterns of gene expression to mechanical stiffness at cell resolution through quantitative tandem epifluorescence and nanoindentation**. *Plant Physiol* 2014, **165**:1399-1408.

13. Milani P, Gholamirad M, Traas J, Arnéodo A, Boudaoud A, Argoul F, Hamant O: **In vivo analysis of local wall stiffness at the shoot apical meristem in Arabidopsis using atomic force microscopy**. *Plant J* 2011, **67**:1116-1123.

14. Kierzkowski D, Nakayama N, Routier-Kierzkowska A-L, Weber A, Bayer E, Schorderet M, Reinhardt D, Kuhlemeier C, Smith RS: **Elastic domains regulate growth and organogenesis in the plant shoot apical meristem**. *Science* 2012, **335**:1096-1099.

15. Braybrook SA, Peaucelle A: **Mechano-chemical aspects of organ formation in *Arabidopsis thaliana*: the relationship between auxin and pectin**. *PLoS ONE* 2013, **8**:e57813.

16. Peaucelle A, Braybrook SA, Le Guillou L, Bron E, Kuhlemeier C, Höfte H: **Pectin-induced changes in cell wall mechanics underlie organ initiation in Arabidopsis**. *Curr Biol* 2011, **21**:1720-1726.

17. Fletcher JC, Brand U, Running MP, Simon R, Meyerowitz EM: **Signaling of cell fate decisions by CLAVATA3 in Arabidopsis shoot meristems**. *Science* 1999, **283**:1911-1914.

18. Mayer KF, Schoof H, Haecker A, Lenhard M, Jürgens G, Laux T: **Role of WUSCHEL in regulating stem cell fate in the Arabidopsis shoot meristem**. *Cell* 1998, **95**:805-815.

19. • Yadav RK, Perales M, Gruel J, Ohno C, Heisler M, Girke T, Jönsson H, Reddy GV: **Plant stem cell maintenance involves direct transcriptional repression of differentiation program**. *Mol Syst Biol* 2013, **9**:654.
The direct targets of WUS were identified including differentiation-promoting transcription factors such as KAN1. The WUS-CLV3 and WUS-KAN1 genetic interactions provided a basis for a computational model of SAM maintenance.

20. •• Gruel J, Landrein B, Tarr P, Schuster C, Refahi Y, Sampathkumar A, Hamant O, Meyerowitz EM, Jönsson H: **An epidermis-driven mechanism positions and scales stem cell niches in plants**. *Sci Adv* 2016, **2**:e1500989.
The maintenance of the SAM structure and function was modeled using known genetic interactions. In particular, the importance of the L1-derived signals was emphasized. Additionally, the study showed that the variations in SAM size are accompanied by variations in WUS and CLV3 gene expression domains.

21. Adibi M, Yoshida S, Weijers D, Fleck C: **Centering the organizing center in the *Arabidopsis thaliana* shoot apical meristem by a combination of cytokinin signaling and self-organization**. *PLOS ONE* 2016, **11**:e0147830.

22. Fujita H, Toyokura K, Okada K, Kawaguchi M: **Reaction-diffusion pattern in shoot apical meristem of plants**. *PLoS ONE* 2011, **6**:e18243.

23. •• Je BI, Gruel J, Lee YK, Bommert P, Arevalo ED, Eveland AL, Wu Q, Goldshmidt A, Meeley R, Bartlett M *et al.*: **Signaling from maize organ primordia via FASCIATED EAR3 regulates stem cell proliferation and yield traits**. *Nat Genet* 2016, **48**:785-791.
The authors identified genetical network which provides feedback regulation from forming organ primordia to the center of the SAM. The network is based on a ligand-receptor interaction with the transmembrane receptor FEA3 expressed in the SAM and a CLE peptide which is expressed in organ primordia.

24. Schoof H, Lenhard M, Haecker A, Mayer KF, Jürgens G, Laux T: **The stem cell population of Arabidopsis shoot meristems in maintained by a regulatory loop between the CLAVATA and WUSCHEL genes**. *Cell* 2000, **100**:635-644.

25. Yadav RK, Perales M, Gruel J, Girke T, Jönsson H, Reddy GV: **WUSCHEL protein movement mediates stem cell homeostasis in the Arabidopsis shoot apex**. *Genes Dev* 2011, **25**:2025-2030.

26. Lenhard M, Laux T: **Stem cell homeostasis in the Arabidopsis shoot meristem is regulated by intercellular movement of CLAVATA3 and its sequestration by CLAVATA1**. *Development* 2003, **130**:3163-3173.

27. Brand U, Fletcher JC, Hobe M, Meyerowitz EM, Simon R: **Dependence of stem cell fate in Arabidopsis on a feedback loop regulated by CLV3 activity**. *Science* 2000, **289**:617-619.

28. Chickarmane VS, Gordon SP, Tarr PT, Heisler MG, Meyerowitz EM: **Cytokinin signaling as a positional cue for patterning the apical-basal axis of the growing Arabidopsis shoot meristem**. *Proc Natl Acad Sci U S A* 2012, **109**:4002-4007.

29. Gordon SP, Chickarmane VS, Ohno C, Meyerowitz EM: **Multiple feedback loops through cytokinin signaling control stem cell number within the Arabidopsis shoot meristem**. *Proc Natl Acad Sci U S A* 2009, **106**:16529-16534.

30. Leibfried A, To JPC, Busch W, Stehling S, Kehle A, Demar M, Kieber JJ, Lohmann JU: **WUSCHEL controls meristem function by direct regulation of cytokinin-inducible response regulators**. *Nature* 2005, **438**:1172-1175.

31. Daum G, Medzihradszky A, Suzaki T, Lohmann JU: **A mechanistic framework for noncell autonomous stem cell induction in Arabidopsis**. *Proc Natl Acad Sci U S A* 2014, **111**:14619-14624.

32. Rodriguez K, Perales M, Snipes S, Yadav RK, Diaz-Mendoza M, Reddy GV: **DNA-dependent homodimerization, sub-cellular partitioning, and protein destabilization control WUSCHEL levels and spatial patterning**. *Proc Natl Acad Sci U S A* 2016, **113**:E6307-E6315.

33. • Perales M, Rodriguez K, Snipes S, Yadav RK, Diaz-Mendoza M, Reddy GV: **Threshold-dependent transcriptional discrimination underlies stem cell homeostasis**. *Proc Natl Acad Sci U S A* 2016, **113**:E6298-E6306.
The authors have analyzed the WUS binding sites in CLV3 with an unprecedented level of details. WUS was shown to act as both an activator and a repressor of CLV3 in a concentration-dependant manner by directly binding a group of *cis*-elements within CLV3 sequence with various affinities.

34. Brand U, Grünewald M, Hobe M, Simon R: **Regulation of CLV3 expression by two homeobox genes in Arabidopsis**. *Plant Physiol* 2002, **129**:565-575.

35. Yadav RK, Tavakkoli M, Reddy GV: **WUSCHEL mediates stem cell homeostasis by regulating stem cell number and patterns of cell division and differentiation of stem cell progenitors**. *Development* 2010, **137**:3581-3589.

36. Busch W, Miotk A, Ariel FD, Zhao Z, Forner J, Daum G, Suzaki T, Schuster C, Schultheiss SJ, Leibfried A *et al.*: **Transcriptional control of a plant stem cell niche**. *Dev Cell* 2010, **18**:849-861.

37. Schuster C, Gaillochet C, Medzihradszky A, Busch W, Daum G, Krebs M, Kehle A, Lohmann JU: **A regulatory framework for shoot stem cell control integrating metabolic, transcriptional, and phytohormone signals**. *Dev Cell* 2014, **28**:438-449.

38. Lee C, Clark SE: **A WUSCHEL-independent stem cell specification pathway is repressed by PHB, PHV and CNA in Arabidopsis**. *PLOS ONE* 2015, **10**:e0126006.

39. Mandel T, Candela H, Landau U, Asis L, Zelinger E, Carles CC, Williams LE: **Differential regulation of meristem size, morphology and organization by the ERECTA, CLAVATA and class III HD-ZIP pathways**. *Development* 2016, **143**:1612-1622.

40. Landau U, Asis L, Eshed Williams L: **The ERECTA, CLAVATA and class III HD-ZIP pathways display synergistic interactions in regulating floral meristem activities**. *PLOS ONE* 2015, **10**: e0125408.

41. Landrein B, Refahi Y, Besnard F, Hervieux N, Mirabet V, Boudaoud A, Vernoux T, Hamant O: **Meristem size contributes to the robustness of phyllotaxis in Arabidopsis**. *J Exp Bot* 2015, **66**:1317-1324.

42. •• Pfeiffer A, Janocha D, Dong Y, Medzihradszky A, Schöne S, Daum G, Suzaki T, Forner J, Langenecker T, Rempel E *et al.*: **Integration of light and metabolic signals for stem cell activation at the shoot apical meristem**. *Elife* 2016:5.
Expression of the stem cell niche gene WUS was induced by light or by sugar in young seedlings. These environmental signals were shown to act though independent signaling pathways converging on the common regulator the TOR kinase.

43. Kuhlemeier C: **Phyllotaxis**. *Trends Plant Sci* 2007, **12**:143-150.

44. Bartlett ME, Thompson B: **Meristem identity and phyllotaxis in inflorescence development**. *Front Plant Sci* 2014:5.

45. Traas J: **Phyllotaxis**. *Development* 2013, **140**:249-253.

46. Galvan-Ampudia CS, Chaumeret AM, Godin C, Vernoux T: **Phyllotaxis: from patterns of organogenesis at the meristem to shoot architecture**. *Wiley Interdiscip Rev Dev Biol* 2016, **5**:460-473.

47. Jönsson H, Heisler MG, Shapiro BE, Meyerowitz EM, Mjolsness E: **An auxin-driven polarized transport model for phyllotaxis**. *Proc Natl Acad Sci U S A* 2006, **103**:1633-1638.

48. Smith RS, Guyomarc'h S, Mandel T, Reinhardt D, Kuhlemeier C, Prusinkiewicz P: **A plausible model of phyllotaxis**. *Proc Natl Acad Sci U S A* 2006, **103**:1301-1306.

49. Stoma S, Lucas M, Chopard J, Schaedel M, Traas J, Godin C: **Flux-based transport enhancement as a plausible unifying mechanism for auxin transport in meristem development**. *PLOS Comput Biol* 2008, **4**:e1000207.

50. Reinhardt D, Pesce E-R, Stieger P, Mandel T, Baltensperger K, Bennett M, Traas J, Friml J, Kuhlemeier C: **Regulation of phyllotaxis by polar auxin transport**. *Nature* 2003, **426**:255-260.

51. Bhatia N, Bozorg B, Larsson A, Ohno C, Jönsson H, Heisler MG: **Auxin acts through MONOPTEROS to regulate plant cell polarity and pattern phyllotaxis**. *Curr Biol* 2016, **26**:3202-3208.

52. •• Besnard F, Refahi Y, Morin V, Marteaux B, Brunoud G, Chambrier P, Rozier F, Mirabet V, Legrand J, Lainé S *et al.*: **Cytokinin signalling inhibitory fields provide robustness to phyllotaxis**. *Nature* 2014, **505**:417-421.
The authors supplemented and expanded the long-standing theory of inhibitory fields generated by differential auxin concentrations which control organogenesis at the shoot apical meristem by providing evidence for the essential role of cytokinin signaling patterns in this process. The distribution of cytokinin restricted by the cytokinin inhibitor AHP6 was shown to be decisive for the timing of organ initiation.

53. Bell EM, Lin W, Husbands AY, Yu L, Jaganatha V, Jablonska B, Mangeon A, Neff MM, Girke T, Springer PS: **Arabidopsis lateral organ boundaries negatively regulates brassinosteroid accumulation to limit growth in organ boundaries**. *Proc Natl Acad Sci U S A* 2012, **109**:21146-21151.

54. Gendron JM, Liu J-S, Fan M, Bai M-Y, Wenkel S, Springer PS, Barton MK, Wang Z-Y: **Brassinosteroids regulate organ boundary formation in the shoot apical meristem of Arabidopsis**. *Proc Natl Acad Sci U S A* 2012, **109**:21152-21157.

55. •• Refahi Y, Brunoud G, Farcot E, Jean-Marie A, Pulkkinen M, Vernoux T, Godin C:, Refahi Y, Brunoud G, Farcot E, Jean-Marie A, Pulkkinen M, Vernoux T, Godin C: **A stochastic multicellular model identifies biological watermarks from disorders in self-organized patterns of phyllotaxis**. *eLife* 2016, **5**.
This work provided a computational model of organ initiation at the SAM which takes into account a degree of randomness in perception of inhibitory signals coming from the developing primordia. The model is able to explain disruptions in organ arrangement which are occasionally observed even in wild type plants.

56. Qi J, Wang Y, Yu T, Cunha A, Wu B, Vernoux T, Meyerowitz E, Jiao Y: **Auxin depletion from leaf primordia contributes to organ patterning**. *Proc Natl Acad Sci U S A* 2014, **111**: 18769-18774.

57. Bennett T, Leyser O: **Something on the side: axillary meristems and plant development**. *Plant Mol Biol* 2006, **60**:843-854.

58. Yang M, Jiao Y: **Regulation of axillary meristem initiation by transcription factors and plant hormones**. *Front Plant Sci* 2016, **7**:183.

59. • Wang Y, Wang J, Shi B, Yu T, Qi J, Meyerowitz EM, Jiao Y: **The stem cell niche in leaf axils is established by auxin and cytokinin in Arabidopsis**. *Plant Cell* 2014, **26**:2055-2067.
The study illustrated the importance of differential hormone signaling at various stages during initiation of axillary meristems. The boundary region near the leaf primordia at the site of the future axillary meristem was characterized by low levels of auxin signaling. The substantial development required a strong transient pulse of cytokinin signaling.

60. Wang Q, Kohlen W, Rossmann S, Vernoux T, Theres K: **Auxin depletion from the leaf axil conditions competence for axillary meristem formation in Arabidopsis and tomato**. *Plant Cell* 2014, **26**:2068-2079.

61. Xin W, Wang Z, Liang Y, Wang Y, Hu Y: **Dynamic expression reveals a two-step patterning of WUS and CLV3 during axillary shoot meristem formation in Arabidopsis**. *J Plant Physiol* 2017, **214**:1-6.

62. • Balkunde R, Kitagawa M, Xu XM, Wang J, Jackson D: **SHOOT MERISTEMLESS trafficking controls axillary meristem formation, meristem size and organ boundaries in Arabidopsis**. *Plant J* 2017, **90**:435-446.
The functionality behind the movement of the mobile transcription factor STM was revealed. STM movement was shown to be required to prevent formation of auxiliary meristems during embryogenesis and for boundary specification at the SAM.

63. • Shi B, Zhang C, Tian C, Wang J, Wang Q, Xu T, Xu Y, Ohno C, Sablowski R, Heisler MG *et al.*: **Two-step regulation of a meristematic cell population acting in shoot branching in Arabidopsis**. *PLoS Genet* 2016, **12**:e1006168.
The authors demonstrate that initiation of auxiliary meristems requires upregulation of STM expression which is accomplished through direct activation by the transcription factor REVOLUTA.

64. Thompson BE, Hake S: **Translational biology: from Arabidopsis flowers to grass inflorescence architecture**. *Plant Physiol* 2009, **149**:38-45.

65. •• Eveland AL, Goldshmidt A, Pautler M, Morohashi K, Liseron-Monfils C, Lewis MW, Kumari S, Hiraga S, Yang F, Unger-Wallace E *et al.*: **Regulatory modules controlling maize inflorescence architecture**. *Genome Res* 2014, **24**:431-443.
This work identified genetical networks which regulate maize shoot organ development. The transcriptional profiling of various stages of inflorescence development prompted identification of gene modules that control transition between different meristem types.