dominate, and enjoy sending off long notes to directors seeking updates on performance indicators, or explanations for apparent transgressions – all this, of course, 'within the next seven days'. The director must eventually learn how to vanquish these arrogant intrusions, but he must also wonder why he accepted the directorship when it involved putting up with such nonsense.

It's lonely up there: Most directors find that their job cuts them off from the rest of the lab: they have to meet a lot of strangers, travel frequently, attend far too many worthless meetings, and grapple with too many official documents and reports. They also end up spending a lot of time with the same small handful of colleagues; this is by design, not chance! The director is thus condemned to be a very lonely person, unless he makes a significant effort to break free.

Poorly paid: Finally, and this is a serious concern by itself, the director of a national lab is very poorly paid especially if you consider the nature of his responsibilities and the variety of roles that he must play. The numbers simply do not add up! Scientists who grew through the system might still covet the director's post, but for most others this is simply a very thankless job.

1. 'Usefully'? It may be easier to describe what is *not* useful. Examples: (a) sitting in a meeting for 2 h, when 15 min are sufficient, but the meeting meanders on with a lot of irrelevant talk; it is usually about rules, and what Swamy says or does not say, or some gossip about what is happening at the HQ; (b) signing at least a hundred files or notes every day, every week, every month!; (c) presiding over a farewell meeting – preceded by high tea – to eulogize the achievements of a retiring colleague; (d) declaring open the 13th annual basketball meet at the other end of the town; (e) deposing in the Sessions Court in the 'illegal' ad hoc appointments case; (f) receiving a memorandum from some aggrieved group and countering their searing hostility; or (g) travelling to Delhi for a meeting with the Minister which had to be postponed 'owing to unforeseen circumstances'.
2. I write 'he' deliberately; we have had very, very few lady directors.
3. The greatest change inhibitor is what is collectively called the 'administration': this entity is supposed to support the R&D establishment's core functions and activities; in reality, it often grievously hurts performance.

Srinivas Bhogle, Cranes Software International Limited, 4th Floor, Block 1, Shankaranarayana Building, 25 M.G. Road, Bangalore 560 001, India
e-mail: Srinivas.Bhogle@cranessoftware.com

RESEARCH NEWS

Exciting developments in plant stem cell research

Vageeshbabu S. Hanur

Continuous production of new organs and postembryonic elaboration of architecture throughout the life cycle extending often even decades, is a unique ability of higher plants. This requires the steady availability and maintenance of a reservoir of undifferentiated stem cells at the apical meristems. Along the axis, the upper shoot apical meristem (SAM) produces all the aerial organs like stem, leaves and flowers, whereas the root apical meristem below the ground level produces the primary and lateral root systems. The SAM, which acts as a self-renewing source of pluripotent stem cell populations, becomes a source of initiation of new organs. It is amazing to understand that all the parts of a plant, from the smallest plants to the giant trees, are continuously developed systematically from a few cells, i.e. stem cells residing in the meristematic region. Rate of (asymmetric) stem cell division is balanced with the rate of loss of stem cells due to consumption of cells towards differentiation, and this balance results in the maintenance of critical mass of stem cell pool. In plants, fine mechanisms exist to establish the stem cell pool immediately during embryogenesis as well as to maintain this pool throughout the life cycle. Termination of the stem cell maintenance occurs with the formation of inner whorls of the flower, particularly the carpels (gynoecium) in the inflorescence meristems. How this critical mass of stem cells is delicately maintained throughout the life cycle of a plant in SAM, has been the subject of intense research in the field of plant biology. Availability of mutants coupled with genetic, molecular and biochemical investigations has opened up this extremely interesting field of plant stem cells, with equally stimulating questions and challenges.

The establishment of stem cells and their maintenance in the SAM involves the coordinate orchestration of several genes connected by interlinked signal transduction pathways in different zones as studied mainly in *Arabidopsis*. The stem cells are maintained mainly in the central zone of the meristem dome in three layers in tunica corpus. Below the L3 layer, the organizing centre (OC) niche contains a few cells that act as the progenitors of the pluripotent daughter stem cells present in these layers. Three genes, *WUSCHEL*, *CLAVATA* and *SHOOTMERISTEMLESS*, are major regulators of stem cells[1].

The *WUSCHEL* (*WUS*, 'bushy' or 'tousled-looking' in German) gene is responsible for the continuous production of stem cells and is regarded as the master regulator. *WUS* encodes a novel subtype of homeodomain-containing nuclear transcription factor that belongs to a different class from the KNOX (KNOTTED-like HOMEOBOX) family. Expression of *WUS* starts as early as the dermatogen stage of embryogenesis. In the active SAM, *WUS* is expressed not in stem cells per se, but in a small group of cells underneath the presumed stem cell population in the OC, affecting the fate of the stem cell in a non-cell-autonomous fashion. The *CLAVATA* (*CLV*, 'club-like' in

Table 1. Some important genes that regulate SAM

Gene	Mutant phenotype	Protein	Function
WUSCHEL (*WUS*)	Reduced SAM and floral organ number	Homeodomain transcription factor	Generation of stem cell daughter cell population
CLAVATA1, 2 (*CLV1, 2*)	Excess SAM cells and enlarged meristems	LRR receptor-like proteins	Component of receptor kinase signalling complex
CLAVATA3 (*CLV3*)	Excess SAM cells and enlarged meristems	Extracellular secretary protein of CLE/ESR1 family	Negatively regulates *WUS* as a component of *CLV1–CLV2* complex
SHOOT MERISTEMLESS (*STM*)	Lacks SAM and stem cells	Homeodomain transcription factor	Prevents meristem differentiation and organ initiation at SAM
FASCIATA (*FAS*)	Enlarged and fasciated SAM	Component of chromatin assembly factor-1	Maintains *WUS* expression domain and stable *WUS* transcription
AGAMOUS (*AG*)	Defective stamens and carpels	MADS-box transcription factor	Promotes floral meristem identity
ULTRAPETALA (*ULT*)	Shoot and floral meristem enlargement	Small family of transcriptional regulator with B-box-like motif and SAND domain	Negatively regulates size of *WUS* domain
SPLAYED (*SYD*)	Altered SAM	SNF2 chromatin-remodelling ATPase	Regulation of stem cell pool maintenance by transcriptionally controlling *WUS*
POLTERGEIST and *POL-LIKE1* (*POL, PLL1*)	Suppressed *clv* mutant phenotypes	Protein phosphatase	Stem cell specification and suppression of stem cell differentiation
HAIRY MERISTEM (*HAM*)	Meristem develops as shoot axis-like tissue	GRAS family transcription factor	Maintenance of SAM
APETALA3 (*AP3*)	Affected SAM and flower development	MADS-box transcription factor	Specification of pistils and stamens; regulation of *WUS* and *CLV3*

Latin) genes, *CLV1*, *CLV2* and *CLV3* expressed as a receptor protein complex, negatively interact with the *WUS* gene in the stem cells, thereby controlling the effective stem cell population. *CLV3* positively regulates *CLV1* (coupled with *CLV2*; *WUS* is epistatic over *CLV1* and *CLV3*, which in turn are epistatic over *CLV2*). *WUS* positively regulates *CLV3*, but *CLV3* represses *WUS*. This positive–negative feedback mechanism is a delicately maintained equilibrium, where the most important regulation on stem cells is exercised. *CLV* signalling restricts the size of the OC by repressing *WUS* transcription in the neighbouring cells, whereas *WUS* induces the expression of *CLV3*, thereby dynamically adjusting the size of the stem cell population in real time. Down-regulation of *WUS* leads to down-regulation of *CLV3*; this in turn leads to up-regulation of *WUS*. Up-regulation of *WUS* leads to up-regulation of *CLV3*, and in turn leads to down-regulation of *WUS*. This system eventually reaches an equilibrium point at which the expression of *WUS* and *CLV3* would be stable. Imbalances in the expression of either of the two tend to return to equilibrium. *CLV3* expression is spatially separated from *WUS*-expressing cells in the OC, and therefore regulates *WUS* expression by *CLAVATA* complex. In tandem, the premature differentiation of the stem cells is suppressed by the gene *SHOOTMERISTEMLESS* (*STM*). *STM* encodes a homeodomain KNOX transcription factor. This gene is expressed throughout the meristematic region, except where organ initiation takes place and it promotes meristematic cell identity. The *STM* gene acts in parallel with *WUS* to prevent the stem cells from being differentiated and consumed by lateral organs in the SAM, and therefore maintains the stem cell pool and provides meristem identity.

There are other genes that profoundly interact with *WUS*, *CLV* and *STM* with additional levels of regulation (Table 1). For example, expression of *STM* requires the activity of two genes, *CUP-SHAPED COTYLEDON1* (*CUC1*) and *CUC2*, which are positive regulators of *STM* in SAM formation. STM suppresses organ initiation by inhibiting the expression of *ASYMMETRIC LEAVES1* (*AS1*) and *AS2* genes that promote organ formation. *AS1* and *AS2*, in turn, repress the expression of *KNOX* genes. Therefore, indirectly, *STM* prevents differentiation in the meristem by allowing the expression of *KNOX* genes. *STM* and *WUS* therefore encode two major regulators of meristem formation and maintenance in *Arabidopsis* and perform independent and complementary roles. In a recent study, Song *et al.*[2] demonstrated that *POLTERGEIST* (*POL*) and *POLTERGEIST-LIKE1* (*PLL1*) are integral components of the *CLV1* signalling pathway, essential for stem cell specification and suppression of stem cell differentiation, and are central players in the stem cells by regulating *WUS*. Apart from *POL* and *PLL1*, *WUS* is an important target of the SNF2-class ATPases *SPLAYED* (*SYD*) and *BRAHMA* in the *Arabidopsis* SAM[3]. SNF2 chromatin remodelling ATPases play a vital role in ensuring proper organ development in higher eukaryotes by modulating the accessibility of *cis*-regulatory DNA regions to transcription factors and to the transcriptional machinery. However, little is

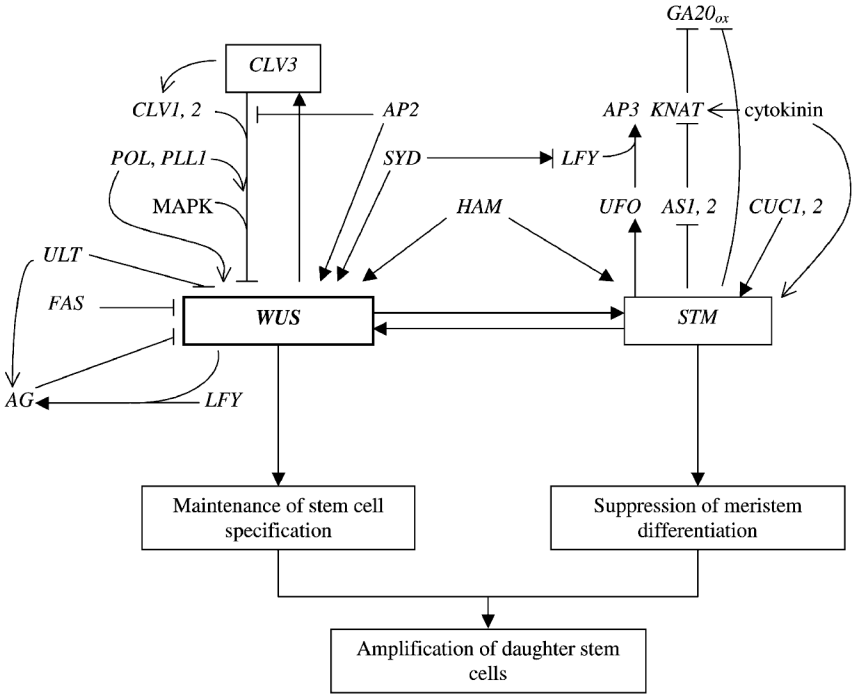

Figure 1. Simplified interaction map of genes of SAM development.

known about the biological targets of these regulatory ATPases. Similarly, chromatin assembly factor CAF-1 facilitates the formation of nucleosomes on newly replicated DNA *in vitro*. Two proteins, FASCIATA-1 (FAS-1) and FASCIATA-2 (FAS-2), which regulate genome replication and plant development, are required for the formation of CAF-1 and are implicated in maintaining *WUS* expression domain by promoting stable *WUS* transcription by facilitating the appropriate chromatin conformation[4].

In contrast to the indeterminate shoot meristem, the floral meristem terminates at the end of flower development, specifically with the formation of gynoecium where stem cell differentiation takes place. This is a result of the overcoming of the self-regulatory *WUS–CLV3* feedback loop as discussed earlier. Floral regulatory genes like *AGAMOUS* (*AG*), *LEAFY* (*LFY*), *APETALA1* (*AP1*) and *ULTRAPETALA* (*ULT*) have now been shown to regulate *WUS* expression. *AG* ensures floral meristem termination by repressing *WUS* transcription, while *WUS* activates *AG* transcription in the centre of the floral meristem[5]. *LFY* is another key floral meristem gene whose regulation is critical to the control of flower development. *AG* is directly activated by the transcription factor *LFY*. *LFY* and *WUS* act in a well-coordinated manner in regulating *AG* expression; while *LFY* provides flower specificity to *AG*, *WUS* provides regional specificity for *AG* induction in the central region of floral meristems. Another dimension of temporal specificity for *AG* induction is provided by *ULT*. Interestingly, *ULT* has a DNA-binding motif previously reported only in animal transcription factors[6]. *ULT* is a key negative regulator of cell accumulation and size of *WUS*-expressing OC in *Arabidopsis*.

Molecular genetic analysis of SAM regulation has now highlighted the complex circuitry of a plethora of genes[7]. Several genes like *CUC1*, *CUC2*, *AS1*, *AS2*, *SHOOTLESS1–4* (*SHL1–4*), *PINHEAD/ZWILLE*, *HAIRY MERISTEM* (*HAM*), *UFO*, *KNAT1*, $GA20_{ox}$ and *ENHANCER OF SHOOT REGENERATION1* (*ESR1*) are involved in different levels of SAM maintenance, differentiation and organ initiation (Figure 1). Recent finding that the floral gene, *APETALA3* (*AP3*) is involved in SAM development by regulating the *WUS–CLV* loop, has only highlighted the added complexity. What are the genes and microRNAs[8] that directly or indirectly regulate the master regulator, *WUS*? How exactly does *WUS* signal the overlying cells to establish stem cell fate? Which genes are required within stem cells per se to maintain their identity? What down-stream signal transduction pathways are involved in SAM formation? What is the exact nature of the 'stemness' signature of the stem cells? How can we select interesting QTLs and mutations through the use of sensitive genetic screens and *in vivo* biochemical experiments? What are the roles of hormones, especially auxins and cytokinins, in the SAM development both *in planta* and *in vitro*? How can we use the rich information on stem cells in plant biotechnology? These are some of the questions that emerge in the studies on plant stem cell research, particularly in the induction and maintenance of stem cells and organs. The recent deluge of publications in this field promises to be exciting and will lead to a 'picturesque denouement' of the plant stem cell research.

1. Sablowski, R., *J. Exp. Bot.*, 2007, **58**, 899–907.
2. Song, S.-K., Lee, M. M. and Clark, S. E., *Development*, 2006, **133**, 4691–4698.
3. Bezhani, S. *et al.*, *Plant Cell*, 2007, **19**, 403–416.
4. Exner, V., Taranto, P., Schonrock, N., Gruissem, W. and Hennig, L., *Development*, 2006, **133**, 4163–4172.
5. Lohmann, J. U., Hong, R. L., Hobe, M., Busch, M. A., Parcy, F., Simon, R. and Weigel, D., *Cell*, 2001, **105**, 793–803.
6. Carles, C. C., Choffnes-Inada, D., Reville, K., Lertpiriyapong, K. and Fletcher, J. C., *Development*, 2005, **132**, 897–911.
7. DeCook, R., Lall, S., Nettleton, D. and Howell, S. H., *Genetics*, 2006, **172**, 1155–1164.
8. Zhou, G.-K., Kubo, M., Zhong, R., Demura, T. and Ye, Z.-H., *Plant Cell Physiol.*, 2007, **48**, 391–404.

Vageeshbabu S. Hanur is in the Division of Biotechnology, Indian Institute of Horticultural Research, Hesaraghatta Lake Post, Bangalore 560 089, India.
e-mail: vageesh@iihr.ernet.in