The embryonic shoot: a lifeline through winter

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Received 25 July 2013; Revised 18 October 2013; Accepted 11 November 2013

Abstract

The tiny vascular axis of the embryo emerges post-embryonically as an elaborate and critical infrastructure, pervading the entire plant system. Its expansive nature is especially impressive in trees, where growth and development continue for extended periods. While the shoot apical meristem (SAM) orchestrates primary morphogenesis, the vascular system is mapped out in its wake in the provascular cylinder, situated just below the emerging leaf primordia and surrounding the rib meristem. Formation of leaf primordia and provascular tissues is incompatible with the harsh conditions of winter. Deciduous trees of boreal and temperate climates therefore enter a survival mode at the end of the season. However, to be competitive, they need to maximize their growth period while avoiding cellular frost damage. Trees achieve this by monitoring photoperiod, and by timely implementation of a survival strategy that schedules downstream events, including growth cessation, terminal bud formation, dormancy assumption, acquisition of freezing tolerance, and shedding of leaves. Of central importance are buds, which contain an embryonic shoot that allows shoot development and elongation in spring. The genetic and molecular processes that drive the cycle in synchrony with the seasons are largely elusive. Here, we review what is known about the signals and signal conduits that are involved, the processes that are initiated, and the developmental transitions that ensue in a terminal bud. We propose that addressing dormancy as a property of the SAM and the bud as a unique shoot type will facilitate our understanding of winter dormancy.

Key words: CENTRORADIALIS-LIKE1, deciduous perennial, dormancy cycle, FLOWERING LOCUS T, gibberellic acid, GH17 family proteins, lipid body, poplar, rib meristem, shoot apical meristem, terminal bud.

Introduction

Growth and development of plants are buffered against short-term fluctuations in the environment. Importantly, however, plants have evolved sensory-response mechanisms that register longer-lasting alterations in specific environmental cues to schedule developmental transitions and to reprioritize physiology in anticipation of seasonal changes. Particularly important cues are temperature and photoperiod. Of these, photoperiod provides the most reliable information, as it changes incrementally and in a completely predictable fashion. Not surprisingly, many different plant systems depend on photoperiod to schedule crucial developmental events at the apex, like the transition to flowering, and the transition to terminal bud formation and dormancy in perennials (Vince-Prue, 1994; Yanovsky and Kay, 2002; Arora et al., 2003; Cooke et al., 2012). Some developmental transitions can also be triggered by low temperatures, but the site of perception is not the same. While photoperiod is perceived at the leaves, chilling temperatures are perceived directly at the apex (Coville, 1920; Metzger, 1988; Arora et al., 2003). For example, Arabidopsis and its perennial relative Arabis alpina can flower as a result of the perception of low temperature at the shoot apical meristem (SAM), a process referred to as vernalization (Finnegan et al., 1998; Bastow et al., 2004; De Lucia et al., 2008; Wang et al., 2011).
Similarly, release from dormancy in deciduous perennials requires chilling of the SAM inside the winter bud (Vegis, 1964; Rinne et al., 2001; Arora et al., 2003; Horvath et al., 2003; Rinne and van der Schoot, 2003; Rohde and Bhalerao, 2007).

In this review, we describe what is currently known about the dormancy cycle in deciduous woody perennials, with emphasis on juvenile hybrid poplar (Rinne et al., 2010; van der Schoot and Rinne, 2011). Herein, we regard the terminal bud as a unique shoot type that can resume a normal mode of growth and development after having passed through dormancy and quiescence. This so-called dormancy cycle is triggered by photoperiod- and temperature-driven alterations in vascular leaf-to-apex signalling and results in a series of events that unfold sequentially and in parallel. Visible changes include the transformation of leaf primordia into bud scales (cataphylls), the development of an embryonic shoot (ES), the assumption of a dormant and freezing tolerant state, the abscission of leaves, the release from dormancy by chilling, the opening of bud scales in spring, and the emergence of a morphogenetically active and elongating shoot system.

To understand the complex choreography of this survival strategy, it will be necessary to identify relevant signals, assess how their production is regulated, map the production and elongating shoot system.

Photoperiod-induced floral transition

In Arabidopsis, a facultative long-day (LD) plant, the perception of LD by the leaves triggers the formation of an elongating inflorescence that produces flowers at the peripheral part of the inflorescence meristem (Yanovsky and Kay, 2002, 2003). The classic external coincidence model, attributed to Bünning (1936), proposed the existence of a circadian oscillator in the leaves with a light-insensitive day phase and a light-inducible night phase. Coincidence of an extended light period with the photosensitive part of the oscillator or clock triggers a photoperiodic response (Mouradov et al., 2002; Yanovsky and Kay, 2002, 2003; Máš, 2008). Inputs to the clock include phytochromes and cryptochromes, the effects of which are mediated by clock-regulated genes like EARLY FLOWERING 3 (McWatters et al., 2000). CONSTANS (CO) is a major output gene of the clock. CO protein is reduced in the morning of a LD by phytochrome B (PHYB), but stabilized at the end of a LD by phytochrome A (PHYA) and cryptochromes (Hayama and Coupland, 2004). As a consequence, only LDs that are sufficiently long yield enough CO to effectively upregulate the gene FLOWERING LOCUS T (FT) in the companion cells (Kardailsky et al., 1999; Kobayashi et al., 1999; Samach et al., 2000; Yanovsky and Kay, 2002; Takada and Goto, 2003; Ayre and Turgon, 2004). FT is a small (23 kDa) graft-transmissible signalling peptide that moves via plasmodesmal pore complexes into the sieve tubes, a process that requires the endoplasmic reticulum membrane protein FT-INTERACTING PROTEIN1 (FTIP1) (Liu et al., 2012). In the phloem stream, FT reaches the sinks, including the shoot apex. In Arabidopsis, as well as in rice, green fluorescent protein-tagged FT/Hd3a is delivered to the rib meristem (RM) but appears not to enter the SAM itself in this form (Corbesier et al., 2007; Tamaki et al., 2007). FT interacts with the basic leucine zipper (bZIP) protein FD in a complex with 14-3-3 proteins at the RM to promote floral transition at the SAM through transcriptional activation of the floral meristem identity gene APETALA1 (API) (Abe et al., 2005; Wigge et al., 2005). Coincident with the arrival of FT at the RM, the gene TERMINAL FLOWER 1 (TFL1) is upregulated in a patch below the SAM (Bradley et al., 1997), an area that corresponds to the RM. The TFL1 protein is very similar to FT, has shared binding motifs, and can also bind FD (Yeung et al., 1999; Banfield and Brady, 2000). Nonetheless, TFL1 is regarded as a floral suppressor, as mutants flower early (Kobayashi et al., 1999). As the TFL1 protein can bind FD in a complex with 14-3-3 receptor proteins, like FT, it may compete with FT for access to FD and delay floral transition (Bradley et al., 1997; Hanano and Goto, 2011; Jaeger et al., 2013). In inflorescence branches delay of flowering is due to the expression of the gene BRANCHED1 (BRC1), which is specific for axillary buds (Niwa et al., 2013). The BRC1 protein directly binds FT (as well as its homologue TSF) without the assistance of 14-3-3-proteins, rendering it ineffective (Niwa et al., 2013). TFL1, just like FT, moves symplasmically via plasmodesmata (PD) in the post-phloem tissues. In the inflorescence meristem, TFL1 moves from the RM into the central zone of the SAM to safeguard resident cells against specification by the floral identity genes LEAFY (LFY) and API (Conti and Bradley, 2007; Jaeger et al., 2013). The emerging picture is that, in Arabidopsis, TFL1 functions together with FT and FD in a signalling hub, integrating various signals to regulate API expression and restricting it to the peripheral SAM parts (Jaeger et al., 2013).

Although photoperiodic responses are widespread (Vince-Prue, 1994), there might be considerable variation in the precise molecular mechanisms that operate among plants, or in the way they are implemented to serve a specific developmental goal. It seems plausible, however, that photoperiod-sensitive detection and transduction mechanisms resembling those of Arabidopsis and rice might have been adopted by perennial species to regulate developmental transitions in different seasonal contexts (Horvath et al., 2003; Rinne and van der Schoot, 2003; Böhlenius et al., 2006; Chao et al., 2007; Rohde and Bhalerao, 2007; Ruonala et al., 2008; Horvath, 2009; Hsu et al., 2011; Cooke et al., 2012; Mimida et al., 2013).
Photoperiod-induced perennial bud formation

The transition to flowering in the rosette plant *Arabidopsis* and the transition to dormancy in deciduous trees are significantly different events. However, the similarity in their regulation and signalling may stem from the fact that both are survival strategies that follow the basic rules of photoperiodism. In *Arabidopsis*, the transition serves the survival in the form of seeds that are left for the next season, while for trees in temperate and boreal climates the apical transition creates a life line through an inhospitable winter. The events that prepare the perennial apex for survival are largely elusive, but significant changes take place in the various tissues that eventually constitute the terminal bud. To emphasize the importance of this, we first describe the morphogenetic events at the apex and explain why they are important for survival.

The vascular system of woody perennials, like that of herbaceous species, is initiated and mapped out at the shoot apex in a meristematic region of incipient vascular tissue just below the peripheral zone of the SAM. For descriptive reasons, this region has been called the residual meristem (Esau, 1965; Larson, 1975) or provascular tissue (Steeves and Sussex, 1989). The topographical organization of the emerging vasculature represents a small replica of the mature system (Esau, 1965). It is simply scaled up in the subapical region and elaborated further during phytomer development. Expansion, in caulescent plants, is mostly due to internode elongation, which results from cell division and cell enlargement in both the provascular tissue ring and in the enclosed, column-like area. The latter is composed of the RM and the subtending rib zone (RZ) (Sachs et al., 1960; Romberger, 1963). These primary morphogenetic processes are highly vulnerable to subzero temperatures and therefore perennials have evolved a strategy to arrest development and protect their morphogenetic tissues during overwintering.

The formation of an overwintering terminal bud is an intriguing event, as under short-day (SD) conditions, the apex ceases its normal morphogenetic behaviour and resorts to morphogenetic processes that normally occur under LDs in axillary buds. Thus, the terminal bud morphologically closely mimics the axillary buds by producing an extremely dwarfed shoot system within the confines of the bud scales (Romberger, 1963; Fig. 1). This dwarfed shoot system, also referred to as an ES, pre-formed shoot, or primordial shoot (Romberger, 1963; Steeves and Sussex, 1989; Rohde et al., 2002; Yuceer et al., 2003; Rinne et al., 2011), is an unextended and only partly developed shoot system with stipule pairs as bud scales at its base and at its summit a SAM that produced it (Romberger, 1963). Although the ES is morphologically undeveloped, the axes of the older embryonic leaves already contain axillary meristems (Romberger, 1963; Yuceer et al., 2003). The SAM forms the ES by continuing morphogenesis for a restricted time period, while internode and leaf expansion are postponed until spring. In *Populus*, the ES may produce a restricted number of embryonic leaves and leaf primordia (Rohde et al., 2002), before the SAM of the ES arrests itself in a dormant state and the bud acquires freezing tolerance (Rinne et al., 2001). Although dormancy at the SAM is incompatible with the production of new stem-leaf units (Rinne and van der Schoot, 1998; Rinne et al., 2001; Ruonala et al., 2008), existing embryonic leaves may still develop further to fill the entire bud space.

Preservation of the embryonic leaves and dwarfed vasculature within the terminal bud are necessary to allow rapid growth and development once favourable environmental conditions return. This dwarfed vasculature of the ES is of crucial importance for bridging the gap between two sequential growth seasons, as it provides the only vascular connection

![Fig. 1](image-url)  Sequence of main morphological and signalling events during the dormancy cycle. Perception of LDs is accompanied by a basic level of FT2 expression in leaves, and probably by FT2 transport to the RM subjacent to the SAM. In poplar, a symplasmic boundary separates RM and SAM. SDs rapidly downregulate FT2 to undetectable levels, resulting in the initiation of bud scales (BS), arrest of cell divisions in the RM and suppressed internode elongation. In about 6 weeks, a mature terminal bud is formed with an ES inside. The embryonic leaves (ELs) of the ES are folded or rolled up along the longitudinal axis, and the older ELs already possess an axillary meristem. Prolonged chilling (ch) hyperinduces *FT1* in the ES, presumably in the ELs, and upregulates GA<sub>3</sub>-induced LB-associated 1,3-β-glucanases (GLU; orange circle). This releases dormancy, restores PD conductivity, and allows symplasmic movement of FT1 from the ELs to the RM. Return of growth-supporting temperatures (18 °C) induces growth-related and GA<sub>3</sub>-induced glycosylphosphatidylinositol-anchored 1,3-β-glucanases (GLU; anchor symbol), upregulates *CENL1* at the RM, and promotes the production of novel (neo-) formed leaves (NFL) by the SAM. PF, leaf primordia formation; E, internode elongation; LP, leaf primordia; P, pith.
between the emerging shoot and the supply lines of the mature shoot system. In a literal sense, this little-investigated vasculature is an umbilical that is crucial for shoot emergence during bud burst.

In order to be competitive when the growing season is short, trees are faced with the challenge of maximizing the growing period and at the same time avoiding the risk of damage to their meristems by imminent freezing temperatures (Frewen et al., 2000; Rinne et al., 2010; van der Schoot and Rinne, 2011). Deciduous trees time these crucial events by monitoring the shortening of the photoperiod, the most reliable parameter for seasonal progression (Howe et al., 1995; Rinne and van der Schoot, 1998; Rinne et al., 2001, 2010; Welling et al., 2002; Böhlenius et al., 2006; Rohde and Bhalerao, 2007). Once a critical daylength is perceived at the shoot apex, the photoperiod-guided timing mechanism initiates a series of morphogenetic processes, culminating in the formation of a terminal bud (Horvath et al., 2003; Rohde and van der Schoot, 2003; Rohde and Bhalerao, 2007; Cooke et al., 2012; Figs 1 and 2). While in Arabidopsis bolting and flowering is due to a clock-regulated upregulation of FT in the leaves (see above) and is correlated with the upregulation of TFL1 in the RM zone (Bradley et al., 1997), in trees the situation is more complex. An increase in FTI expression can similarly regulate flowering in mature trees, as shown in field-grown trees, and overexpression of FTI can induce flowering even in juvenile trees (Böhlenius et al., 2006; Hsu et al., 2011). In contrast, reduced expression of FT functions in growth cessation and bud formation at the end of the growing season (Böhlenius et al., 2006). The perception of SD leads to a rapid clock-mediated downregulation of FT in the leaves (Böhlenius et al., 2006; Hsu et al., 2006; Ruonala et al., 2008). In its wake, the poplar orthologue of TFL1, CENTRORADIALIS-LIKE1 (CENL1), is upregulated in the RM (Ruonala et al., 2008), a domain comparable to that of TFL1 in Arabidopsis flowering (Conti and Bradley, 2007).

Overexpression of Avena sativa PHYA (P35S:As PHYA) in poplar results in a diminished stem elongation while the plastochron remains unchanged under LDs (Ruonala et al., 2008). As PHYA is able to protect CO from degradation (Hayama and Coupland, 2004), these overexpressors have lost the ability to respond to SDs (Olsen et al., 1997; Welling et al., 2002) and instead show an enhanced stem elongation under SDs (Ruonala et al., 2008). The loss of response may relate to the fact that FT2 expression is only transiently lowered in PHYA overexpressors under SDs and rapidly recovered to a level somewhat higher than in leaves of wild-type (wt) poplars exposed to LDs (Ruonala et al., 2008). The fact that SAM activity remains unchanged under SDs as judged from the leaf plastochron, while elongation is enhanced in PHYA overexpressors, indicates that the morphogenetic units of RM and SAM can be regulated independently (Ruonala et al., 2008; van der Schoot and Rinne, 2011).

Heterograft systems have shown that overexpression of PHYA in the stock is insufficient to prevent the formation of dormant terminal buds in the wt scion, while the reverse grafts, with a wt stock and PHYA scion, were able to form buds without being able to enter dormancy as they repeatedly flushed (Ruonala et al., 2008). This suggests that, for the production of a dormant terminal bud, SD perception may be required in the leaves as well as the apex. Indeed, literature reports have suggested that apices can respond directly to photoperiod (Wareing, 1956; Romberger, 1963), supporting the idea that not only temperature but also light responses may occur in apices.

Again, these observations indicate that the RM may respond to leaf-derived and endogenously generated signals to redirect morphogenetic events at the apex (van der Schoot and Rinne, 2011). In Arabidopsis, the RM is inactive during SDs, as reflected by a rosette form, but exposure to LDs activates the RM and initiates the formation of an elongating inflorescence stem. Similarly, in poplar, SD exposure deactivates the RM (Fig. 2), whereas under LDs the RM is active in extending the shoot. Indeed, it has been recognized in classic studies that important problems in the developmental morphology of plants are fundamentally only different aspects of the problem of how cell division and elongation are controlled in the subapical meristem (Romberger, 1963) and the area that includes the RM. Despite this, dormancy cannot be explained as resulting from deactivation of the RM alone, as axillary buds that develop under LD enter quiescence but not dormancy.

The role of the RM

Shoot-derived vascular signals destined for the apex are supplied by the source leaves via the phloem. At close proximity to the apex, they exit the sieve tubes and then travel, presumably via PD, to their destination at the RM. The RM may act as a relay station that shuttles signal or signal complexes to various destinations at the shoot apex, like leaf primordia and SAM (van der Schoot and Rinne, 2011). This might require gating of PD between the RM and the overlying SAM. Indeed, microinjection studies have shown that small fluorescent dyes do not immediately transit from the RM to the SAM (Ruonala et al., 2008), suggesting that there is a sympas- matic boundary between the RM and the SAM (Fig. 1).

The question is, what are the signals delivered to the RM that promote dormancy transition, and in what form and how are they relayed to their final destinations? Furthermore, which genes are involved in the regulation of these events? Under LDs, the leaf-born signalling peptide FT2 is likely to be delivered to the RM of poplar in a manner analogous to FT1 delivery in LD-exposed Arabidopsis (Corbesier et al., 2007). In contrast, under SDs, FT2 is completely downregulated and RM activity is arrested by either lack of FT2 import or by the arrival of as-yet-uncharacterized leaf signals (van der Schoot and Rinne, 2011).

Remarkably, the As PHYA mRNA of the PHYA-overexpressing poplar (see above) was localized among others to the RM/RZ while it was absent from the SAM, thereby strongly influencing RM activity and elongation growth (Ruonala et al., 2008). PHYA overexpression modulated the expression levels of the CENL1 gene, an orthologue of the TFL1 gene, which selectively accumulates in the RM area in both poplar and Arabidopsis (Conti and Bradley, 2007;
Ruonala et al., 2008). Elongation growth, which in poplar requires a basic level of CENL1 expression (Mohamed et al., 2010), was strongly reduced in PHYA overexpressors, and CENL1 expression levels were only half of those in wt apices (Ruonala et al., 2008). Under SDs, not only did the FT levels bounce back to wt levels, but CENL1 expression levels gradually rose to a level double that of wt poplars and, consequently, elongation growth was enhanced in these overexpressors (Ruonala et al., 2008). This implies that PHYA overexpression in the RM/RZ helped the apex to successfully resist the SD-induced inhibitory influences on elongation growth and morphogenesis. Interestingly, also in wt, CENL1 is initially upregulated during terminal bud formation, before it is completely downregulated at dormancy (Ruonala et al., 2008). We propose that lack of CENL1 function during bud formation is probably due to inhibitory influences. These could include restrictions in vascular and symplasmic connectivity, as well as BRC-like genes that are known to inhibit axillary bud activation in Arabidopsis (Niwa et al., 2013).

**The role of symplasmic signalling within the apex**

Starting with the early initiation of bud scales (cataphylls), the above events play themselves out in a timeframe of about 6 weeks, at which point the ES has entered a dormant state. So far, the sequence of these events is mapped out only roughly, while the molecular pathways that bring about these transitions are almost completely unknown. Within the confines of
the terminal bud, a developing ES emerges with a dwarfed vascular system that provides continuity with the vascular system of the main shoot (Fig. 1). *FT2* is completely downregulated within a week of SDs, while *CENL1* is initially upregulated and subsequently downregulated between week 3 and 6 (Ruonala et al., 2008). Therefore, it seems likely that *CENL1* protein liberated from competition for FD with FT, supplied by source leaves, may interact with the bZIP factor FD in a complex with 14-3-3 receptor proteins, as described for *Arabidopsis* (Bradley et al., 1997; Hanano and Goto, 2011; Taoka et al., 2011, 2013; Jaeger et al., 2013). This function could safeguard the SAM from determination during dormancy, in line with the role of *TFL1* in the inflorescence meristem in *Arabidopsis* (Conti and Bradley, 2007). In brief, it can be speculated that, in poplar, ES maturation requires *CENL1* but not *FT2*, although *FT2* downregulation might be a prerequisite.

The precise timing of bud scale formation and its regulation is not known. It is observed that shortly after the downregulation of *FT2* in the source leaves, the SAM starts to produce bud scales (Ruttink et al., 2007; Ruonala et al., 2008). Significantly, when a certain number of bud scales are produced, the developmental programme of primordia is again altered and the SAM commences production of leaves. However, these leaves are small and embryonic, and they arise on a severely dwarfed shoot that completely lacks internode elongation.

That after scale formation leaf initiation resumes suggests that scale regulation is a transient event. As basic levels of *FT2* expression in source leaves are required during normal vegetative development (Böhlenius et al., 2006; Ruonala et al., 2008), it seems possible that *FT2* is, directly or indirectly, involved in the formation of leaf primordia. Consequently, withholding the apex *FT2* would influence primordia fate and development. Alternatively, or additionally, a positive signal is generated within the source leaves to instruct remote leaf primordia to execute a transient developmental programme.

**ES emergence**

The ES inside the enlarging bud scales is formed by the activity of the SAM, which produces a restricted number of embryonic leaves with secondary axillary meristems developing in the older leaf axils (Fig. 1). The processes that regulate growth of the extremely dwarfed ES are largely unknown. Early SD-induced changes in gene expression, additional to *FT2* and *CENL1*, which potentially relate to bud scale initiation and ES formation, are: *PICKLE*, a gene that in *Arabidopsis* represses the gene *AINTEGUMENTA* (Mizukami and Fischer, 2000); *GA-INSENSITIVE* (*GAI*), which encodes a nuclear protein of the DELLA subfamily of GRAS transcription factors (Ruttink et al., 2007); genes involved in GA biosynthesis and signalling (Rinne et al., 2011; Cooke et al., 2012); genes controlling the signalling conduits (Rinne et al., 2011); a diverse cluster of MADS box genes (Bielenberg et al., 2004, 2008; Yamane et al., 2011). Interestingly, the mRNA of *GAI*, a systemic signalling molecule that requires specific RNA motifs for its trafficking through the phloem (Huang and Yu, 2009), influences leaf formation (Haywood et al., 2005) and could be involved in changing the fate of primordia. While bud scales are initiated early, they might not become consolidated as bud scales until after 2–3 weeks of SDs, as, up to that point, return to LDs will reverse lamina development, albeit incompletely (Ruonala et al., 2008). *CENL1* expression might be needed for the maturation of the dwarfed ES system, even if leaf expansion and internode elongation are prevented. In contrast, *FT2* might be necessary for normal non-dwarfed growth and development, and perhaps also for elongation, and its complete downregulation may contribute to the dwarfing of the ES. It is not known if the plastochron of the ES is different from that of the apex before SD exposure. It appears, however, that the PD that interconnect SAM cells into symplasmic fields are significantly narrowed after 10–15 d of SD exposure in poplar (Ruonala et al., 2008). It was speculated that diminished symplasmic connectivity at this point in time might contribute to a decreased sink function of apical tissues, reducing not only the intake of building materials but potentially also signalling molecules, including peptides, hormones, mRNAs, and microRNAs that are provided via the sieve tubes and the symplasmic extension network (Lough and Lucas, 2006; Kehr and Buhtz, 2008).

Somewhat later in the developmental trajectory of the terminal bud, at around SD week 3–4, major shifts occur in the expression of genes that are involved in cell division, metabolism, and acclimation (Ruttink et al., 2007). Changes also occur in the expression of genes involved in light-, ethylene-, and abscisic acid (ABA) signalling (Ruttink et al., 2007). Ethylene is thought to be involved in the timing of dormancy (Ruonala et al., 2006; Ruttink et al., 2007), while, in its wake, genes for ABA production are upregulated (Ruttink et al., 2007). ABA has various roles in the developing bud, and although its role in dormancy is not clear, it has a prominent function in facilitation acclimation and dehydration tolerance (Welling et al., 1997, 2002; Rinne et al., 1998; Welling and Palva, 2006).

During exposure to SDs, large numbers of minute lipid bodies (LBs) emerge in the cytoplasm of apex cells, mostly in the SAM and RM/RZ (Rinne et al., 2001, 2011). In terminal buds, LB accumulation is particularly high after a few weeks of SDs, coinciding with ES maturation. LBs are of universal occurrence and, although originally viewed as simple storage bags for triglycerides (TAGs), they are emerging as novel organelles with important signalling functions (Murphy, 2001). They are pinched off from specialized sites at the endoplasmic reticulum, where the ethylene receptor is also localized (Grefen et al., 2008), and possess a half-membrane that separates their lipid core of TAGs from the aqueous environment of the cytoplasm (Murphy, 2001; van der Schoot et al., 2011). A possible link exists between ethylene and LB formation, as ethylene biosynthesis genes (Ruttink et al., 2007) are co-expressed with a LB marker in birch (van der Schoot et al., 2011). The specific mechanism by which LBs form is under debate and might vary from tissue to tissue in different organisms. The LBs of seeds, called oil bodies, are decorated by a number of specific proteins, among
which are oleosins, caleosins, and sterolesins, that function to stabilize the single lipid layer, prevent fusion of individual LBs, and provide docking sites for enzymes that function in TAG hydrolysis (Murphy, 2001; van der Schoot et al., 2011). In Arabidopsis seeds, oleosins improve freezing tolerance (Shimada et al., 2008), and in their absence LBs fuse, resulting in a delay in seed germination (Siloto et al., 2006). In the Populus trichocarpa genome, eight oleosins have been identified (Huang et al., 2009), and three of them are differentially regulated during the dormancy cycle in the poplar apex (P.H. Rinne, L.K. Paul and C. van der Schoot, unpublished results). The presence of oleosins in Arabidopsis seeds and in the buds of trees suggests that they are intimately related to survival strategies in plants (van der Schoot et al., 2011).

ABA might play a role in LB production and LB maintenance by promoting oleosin production, as abi3-4 mutants in Arabidopsis have delayed oleosin expression (Parcy et al., 1994) and fused LBs. In addition to their role in freezing tolerance, as in Arabidopsis seeds (Shimada et al., 2008), LBs may be involved in the chilling-induced release from dormancy at the SAM by virtue of the presence of enzymes associated with the LB protein coat. Although many proteins may associate with LBs (Murphy, 2001; van der Schoot et al., 2011), an important group of proteins are the 1,3-β-glucanases (Rinne et al., 2011). These enzymes [glycosyl-hydrolase17 (GH17) family proteins; Fig. 1] are of interest as they are regulated by ABA (Leubner-Metzger et al., 1998; Leubner-Metzger and Meins, 2000), the biosynthesis of which increases during the development of dormancy and the production of 1,3-β-glucanase-decorated LBs.

**Cessation and self-arrest of the SAM**

As bud development proceeds in a precisely scheduled fashion, it is clear that the completion of the ES is mainly regulated by physiological and genetic factors. However, it is plausible that additional mechanisms, such as physical constraints imposed by closed hardy bud scales, play a role in halting ES development during bud development (Couturier et al., 2011). Mechanical forces might directly influence gene expression, as illustrated by for example the expression of so-called touch genes (Lee et al., 2005). Regardless of the precise mechanism, it is true to say that the differentiation of leaves in the terminal buds under SD ceases when the available space inside the bud is filled. Unlike the axillary buds, which may be subjected to similar ‘filling laws’ (Couturier et al., 2011) under LD conditions, the SD-induced terminal buds (winter buds) are subjected to additional self-imposed constraints. The end station of the SD-induced train of events is the self-arrest of the SAM in a state of dormancy (van der Schoot and Rinne, 2011). This is achieved via an intrinsic mechanism that obstructs return of the SAM to a morphogenetically active state. Although axillary buds form under LDs in the axis of leaves, these buds are merely paradormant, a condition of inhibition imposed by a proliferating apex, in which polar auxin transport and/or the subtending leaves play a major role (Crawford et al., 2010; Kohlen et al., 2011). Removal of the sources of suppression, such as an auxin-producing shoot apex, will release paradormancy and result in bud burst and branch formation, while dormant buds will remain in a dormant state even when the apex is removed (van der Schoot and Rinne, 2011).

The SD-induced dormant state is a transient affair that serves to arrest all morphogenetic patterning at the SAM. In both poplar and birch, SAM cells assume this state of self-arrest by shutting down all forms of intercellular communication (Rinne and van der Schoot, 1998; Rinne et al., 2001; Ruonala et al., 2008). Symplasmic signalling is prevented by the production of dormancy sphincter complexes (DSCs) at PD entrances. DSCs are composed of a callose-containing ring external to the PD neck and a callosic plug inside the PD channel (Rinne and van der Schoot, 1998; Rinne et al., 2001; Ruonala et al., 2008). Callose deposition results from a shift in balance of two enzymes, 1,3-β-glucanase and 1,3-β-glucansynthase, also called callose synthase (Rinne et al., 2001, 2005; Levy et al., 2007a,b; Levy and Eipel, 2009; Xu and Jackson, 2010; Maule et al., 2011). DSCs function as circuit breakers in the symplasmic circuitry of the SAM (van der Schoot and Rinne, 2011), the installation of which ensures that SAM cells can no longer exchange the morphogens, signalling molecules and transcription factors that drive and coordinate primary morphogenesis (Rinne and van der Schoot, 1998; Rinne et al., 2001; Ruonala et al., 2008). As a direct consequence, the symplasmically integrated SAM (Rinne and van der Schoot, 1998; Rinne et al., 2001) becomes a mere collection of disconnected cells where communication lines are silenced and all cells are ‘off-line’ (Rinne et al., 2001; van der Schoot and Rinne, 2011; Fig. 2). This state of isolation effectively prevents the ES from resuming morphogenesis. Disconnected from their shared signalling network, and deprived from the stabilizing condition of electric and metabolic coupling, individual cells may rely exclusively on cell autonomous processes and may reprioritize metabolism in order to enhance their freezing tolerance (Rinne et al., 2001). Cut off from the supply routes of the stem, the heterotrophic SAM strongly reduces its metabolism. The membrane potentials of individual cells are reduced to values below the diffusion potential, indicating absence of ATP-driven proton-mediated uptake processes and lack of substrate availability (Rinne and van der Schoot, 1998; Rinne et al., 2001; Ruonala et al., 2008). Reserve stores in the young stem subtending the terminal bud are filled with materials that are retrieved from the senescent leaves before they are abscised (Fracheboud et al., 2009), to proactively support the fast growth of the young shoot during bud break in spring.

**Temperature effects on vegetative and floral meristems**

The arrested dormant state of the SAM is both the end point of the SD-initiated trajectory as well as the turning point and the start for regrowth in spring. The first requirement for regrowth is that the SAM is released from dormancy. The universal mechanism for this is a sufficiently long exposure to...
low chilling temperatures (Coville, 1920; Chouard, 1960; Vegis, 1964; Fig. 2) that by convention is expressed as a chilling requirement, which can be species and ecotype specific. Nonetheless, a 6–8-week exposure to a temperature of approximately 5 °C is adequate for most species (Rinne et al., 2001, 2011). In addition to its indispensable role in dormancy release, chilling is vital for the development of freezing tolerance (Weiser, 1970; Welling et al., 1997; Rinne et al., 2001). In juvenile trees, development of freezing tolerance is a two-step process, the first level of which is initiated by SD exposure, whereas the second, deeper level requires chilling but not light (Rinne et al., 2001; Welling et al., 2002). For example, in juvenile birch, SDS at 18 °C bring freezing tolerance to a level of approximately –20 °C, but subsequent additional and prolonged chilling releases the SAM from dormancy and deepens freezing tolerance of the quiescent ‘stand-by’ state to –70 °C (Rinne et al., 2001; Fig. 2).

The effects of chilling are cell autonomous. They cannot be imported from other parts of the plant and the SAM itself has to perceive chilling (Vegis, 1964; Rinne et al., 2001). Import is also physically impossible, as both the phloem supply routes and the PD of the SAM are dysfunctional and physically obstructed by callose deposits (Aloni et al., 1991; Aloni and Peterson, 1991, 1997; Rinne and van der Schoot, 1998; Rinne et al., 2001; Ruonala et al., 2008). In addition, however, a substantial part of the effect of SDS and chilling might be at the level of chromatin modifications, a situation reminiscent of vernalization (Chouard, 1960; Rinne and van der Schoot, 2003; Horvath et al., 2003; Horvath, 2009; Cooke et al., 2012). Both chilling-induced dormancy release and vernalization have a quantitative aspect, and in both cases the chilling requirements are only slowly fulfilled. In both cases, it is also the SAM itself that has to perceive the chilling. It remains to be seen whether there are any commonalities at the molecular level. In vernalization of Arabidopsis winter annuals, chilling epigenetically silences FLOWERING LOCUS C (FLC), thereby releasing the repression of flowering (Gendall et al., 2001; Bastow et al., 2004; De Luca et al., 2008). This FLC-based mechanism is not operating in dormancy release.

Chromatin modifications might also underlie the chilling-induced hyperinduction of FT1 in poplar buds (Hsu et al., 2011), up to a level 800–900 times compared with non-chilled bud (Rinne et al., 2011). Such chilling-induced modifications also occur in gibberellin (GA) biosynthesis genes, the upregulation of which has been related to gene methylation (Finnegan et al., 1996, 1998). Our unpublished results show that applied GA3 could also upregulate FT in LD apices of juvenile poplar but not in dormant buds (L. K. Paul and C. van der Schoot, unpublished results). Thus, it seems plausible that chilling-induced changes in FT1 methylation are a prerequisite for GA-enhanced FT1 expression (Rinne et al., 2011). It is noteworthy that CENL1 did not undergo such modifications and was responsive to applied GA also under SDS. The effect of chilling on FT1 expression might not be mediated by a functional circadian clock, as it tends to be disrupted by chilling, as shown in chestnut (Ramos et al., 2005). This direct effect of chilling on FT1 expression is not dissimilar to the situation in vernalization, where H3K4 demethylation and H3K27 trimethylation of FT repressors advance flowering in Arabidopsis (Jiang et al., 2008). However, whether the molecular mechanism of FT1 hyperinduction in Populus involves histone modifications like H3K4 trimethylation in FT chromatin remains to be established.

Dormancy release by GA-recruited GH17 proteins

How does chilling release the SAM from dormancy? It is known that application of GA can often release dormancy without chilling, suggesting that chilling might result in accumulation of GA. The literature is somewhat ambiguous about this capacity of GA, and it was suggested that this might be due to the fact that different GA species might have been applied (Rinne et al., 2011). It appears that applied GA4, which is the GA that functions in shoot elongation in poplar (Eriksson, 2000; Eriksson and Moritz, 2002; Israelsen et al., 2004), results in canonical bud burst, i.e. bud opening and the emergence of a morphogenetically active and elongating shoot (Rinne et al., 2011). In contrast, low concentrations of GA3 only resulted in bud opening and the protrusion of a few embryonic leaves, a non-canonical form of bud burst, whereas higher concentrations induced cellular proliferation at the bud base and subsequent abscission (Rinne et al., 2011). It is tempting to speculate that this resembles the little-investigated process of terminal bud abscission that takes place in many trees species beyond the juvenile stage (Junttila, 1976; Cooke et al., 2012).

As in many dormant systems callose obstructs sieve tubes (Aloni et al., 1991; Aloni and Peterson, 1991, 1997) as well as PD in the SAM (Rinne et al., 2001; Rinne and van der Schoot, 2003; Mazzitelli et al., 2007), chilling and GA4 application, which release dormancy, must be able to reconstitute these symplasmic connections through hydrolysis of callose. In birch, extended chilling promotes the production of 1,3-β-glucanases in the dormant SAM. These enzymes (GH17 family proteins) regulate the turnover of callose (Iglesias and Meins, 2000; Rinne et al., 2005; Levy et al., 2007a,b; Epel, 2009; Chen and Kim, 2009) and are targeted to the PD during chilling, resulting in the restoration of PD conductivity (Rinne et al., 2001; Rinne and van der Schoot, 2003). Localization experiments showed that the LBs that are produced under SDS (see above) in the SAM and RM/RZ of the ES are decorated with 1,3-β-glucanases, while some 1,3-β-glucanase is present in the cytoplasm (Rinne et al., 2001). During chilling, the randomly distributed cytoplasmic LBs become displaced towards the cell wall where they appear to associate with PD, resulting in hydrolysis of PD callose and restoration of PD conductivity (Rinne et al., 2001; Rinne and van der Schoot, 2003) and conversion of the off-line dormant state into a stand-by quiescent state (Fig. 2).

In Arabidopsis, the GH17 family is subdivided into three clades (Doxey et al., 2007). To determine which genes are involved in the release from dormancy, 10 orthologues of poplar genes belonging to two of these clades were identified.
(Rinne et al., 2011). They included homologues encoding 1,3-β-glucanases, detected in isolated LBs of birch (Rinne et al., 2001), and genes that encode cell-wall 1,3-β-glucanases with a glycosylphosphatidylinositol (GPI) anchor (Bayer et al., 2006; Rinne et al., 2011). One of them lacks the catalytic site of GH17 but it has a C-terminal domain that is similar to that of the other GH17 proteins, and a CBM43 carbohydrate-binding module that targets PD callose (Simpson et al., 2009). Similar modules were present in the two poplar GH17 members that were identified as orthologues of the Arabidopsis BG_ppap (Rinne et al., 2011), which also has a GPI anchor, and localizes at PD to modify its conductance (Levy et al., 2007a).

Transcript profiling revealed that the poplar GH17 genes were differentially regulated by SDs, chilling, and application of GA3 and GA4, showing that they are regulated in different phases of the dormancy cycle (Rinne et al., 2011; Figs 1 and 2). Remarkably, expression analysis showed that their responses to these different treatments could be clustered into groups that correspond to their specific protein domain architecture. For example, the four genes encoding LB-GH17 proteins lacking a GPI anchor are upregulated by GA1 (Fig. 1) but downregulated by GA4, and are mostly upregulated towards the end of the dormancy induction period, corresponding to the peak in ethylene, ABA, and LB production, and during chilling-induced release from dormancy (Rinne et al., 2011). In contrast, five genes encoding GH17 proteins that possess a GPI anchor were downregulated by GA3 but upregulated by GA4, while two of them were initially upregulated but then downregulated towards the end of the dormancy induction period. Only one of the selected members with a GPI anchor was unaffected by both GA3 and GA4, and showed only a slight upregulation by SDs and chilling (Rinne et al., 2011).

Although GA4 can release dormancy and induce canonical bud burst when applied to a dormant and non-chilled bud, it was concluded that it cannot be responsible for dormancy release in the natural situation, as judged from the gene expression data. In contrast, in case of GA3, which cannot induce release from dormancy when applied, the transcript pattern was highly similar to the pattern induced by natural chilling during release from dormancy (Rinne et al., 2011). That applied GA3 could not induce canonical bud burst is thought to be due to the fact that it upregulates genes that encode LB-associated GH17 enzymes (Rinne et al., 2011). These reside on LBs that are randomly scattered in the cytoplasm and can only hydrolyse callose at PD after chilling has displaced them to the plasma membrane, from where they diffuse to the PD entrances (see below). Thus, it is expected that GA3, together with chilling, might advance natural bud burst. This hypothesis could be tested by analysing the actual GA forms during dormancy cycling.

Another noteworthy difference between GA4 and GA3 action is that, when applied to dormant non-chilled buds, GA4 transiently upregulates CENLI while GA3 upregulates it more constitutively (Rinne et al., 2011). This transient upregulation of CENLI by GA4 is followed by canonical bud burst (Fig. 1), whereas applied GA3 fails to induce canonical bud burst, possibly because it cannot promote opening of PD with LB-associated GH17s.

GA biosynthesis genes have non-redundant functions as they are differentially expressed during the dormancy cycle. In poplar, chilling specifically upregulated certain members of the GA3 oxidase and GA20 oxidase families, which have very low abundance during growth under LDs, while other members of the same families showed the opposite pattern (Rinne et al., 2011). The GA-catabolizing genes from the GA2 oxidase family, for example GAox1 (Thomas et al., 1999), were also upregulated towards the end of the chilling period, possibly to counteract increased GA biosynthesis and maintain homeostatic control. The two putative poplar orthologues of the GA receptor GIBBERELLIN INSENSITIVE DWARF (GID) were upregulated during SD exposure, showing sensitization of the dormant system to GA, while DELLA-like, a negative regulator of growth, was downregulated.

Our studies suggest that chilling-induced release from dormancy is mediated predominantly by LB-associated GH17 enzymes (Figs 1 and 2). Nonetheless, two GH17 enzymes with a GPI anchor are upregulated in the first few weeks of chilling exposure (Rinne et al., 2011). Thus, LB GH17 proteins may act in concert with some GH17 proteins with a GPI-lipid anchor that are regulatable by GA as well as by chilling. The LB delivery system is an ingenious solution for the problem that metabolic activity in the partially dehydrated system might be challenging under low temperatures. The machinery for dormancy release appears to be pre-installed during SD exposure at a time when temperatures still support normal cellular activities. This dormancy-release function is not incompatible with the fact that the multifunctional LB-associated oleosins may facilitate freezing tolerance, as in Arabidopsis seeds (Siloto et al., 2006; Shimada et al., 2008), and provide TAGs for membrane restoration in spring. Delivery of the GH17 proteins to the target sites at the plasma membrane and PD takes place in a relatively small window of opportunity, which is during chilling but prior to the dehydration of the system by freezing conditions. By the end of the chilling period dormancy is released, after having primed the bud for a further increase in freezing tolerance (Welling et al., 2002; Rinne et al., 2010).

It is not known precisely how LBs deliver their cargo to the PD, but it appears to involve components of the cytoskeleton (L.K. Paul and C. van der Schoot, unpublished results). Transient expression studies with enhanced green fluorescent protein-labelled GH17 proteins in Nicotiana benthamiana showed that LBs deliver the fluorescent fusion protein to the plasma membrane where they localize as distinct sandwich-like patches at both ends of the PD channels, which were indicated by a fluorescent PD marker (movement protein of tobacco mosaic virus conjugated to red fluorescent protein; Rinne et al., 2011). In contrast, protein fusions of GH17 proteins with a GPI anchor localize in a punctate pattern at the PD or inside the PD channel. A model depicts delivery of LB-associated GH17 proteins resulting from fusion of the single lipid layer of the LB with the cytoplasmic leaflet of the plasma membrane (van der Schoot et al., 2011). GH17 enzymes may be recruited by membrane rafts.
and laterally transferred to the intracellular callose plug of the DSC at the PD entrance (Rinne et al., 2011; van der Schoot et al., 2011). GH17 proteins with a GPI anchor are likely to be transferred via the Golgi excretion pathway to the cell membrane, where they are moved to the extracellular space to be collected by membrane rafts at the extra-cellular leaflet of the plasma membrane and transported to the extracellular sphincter ring of the DSCs (Simpson et al., 2009; Rinne et al., 2011).

The release from dormancy of non-chilled buds by GA₄ application does not utilize the LB delivery system, and GA₄ actually inhibits transcription of LB-associated GH17 genes. In addition, application of GA₄ prevents alignment of LBs with the plasma membrane and instead may ‘dissolve’ the LBs, as apparent from transmission electron microscopy investigations (Rinne et al., 2011). Nonetheless, the DSCs at the PD disappear, indicating that applied GA₄ induces hydrolysis of callose in DSCs (Rinne et al., 2011).

**Bud break: a time to grow up**

The genes FT2, FT1, and CENLI are under complex regulation during the dormancy cycle (Fig. 2). For example, FT1 in embryonic leaves is hyperinduced by prolonged chilling (Fig. 2), and independently of CO (Rinne et al., 2011), but the situation is reversed when, after sufficient chilling, the temperatures rise in spring. At about 18 °C, the expression of CO was upregulated while that of FT1 transcripts was reduced (Rinne et al., 2011). In plants growing in LDs, CENLI is expressed at modest levels in the RM, whereas, coinciding with ES development, CENLI is transiently upregulated during the first 3–4 weeks of SDs (Ruonala et al., 2008). Throughout the chilling phase, CENLI transcripts are at a very low level, but once dormancy is released, the elevation of the ambient temperature to 18 °C upregulates its expression (Figs 1 and 2). Just prior to canonical bud burst CENLI expression peaks, suggesting that in mature buds it is a marker for bud burst (Mohamed et al., 2010; Rinne et al., 2011; Fig. 1). The expression of GA biosynthesis and signalling genes is also under complex regulation. Considering how they regulate FT1, FT2, and CENLI, they are likely to have a significant role in the development of the ES and its activation in spring.

To sustain and fuel the initiation of morphogenetic activity of the SAM and the RM/RZ may require a combination of import via the restored symplasmic connections as well as substrate uptake from the apoplasmic space in the ES. The latter requires substrate-specific carriers and proton-extrusion pumps. Plasma membrane-localized H⁺-extrusion pumps (H⁺-ATPases) are encoded by a small family of genes (Palmgren, 2001) that are upregulated just prior to bud break, as shown in raspberry and peach (Gévaudant et al., 2001; Mazzitelli et al., 2007). As light stimulates substrate uptake by increasing plasma membrane H⁺-ATPase activity (van Bel and van der Schoot, 1981; van Bel et al., 1981), this may drive cellular division and growth in both the bud scale bases and the ES (van der Schoot and Rinne, 2011). The initiation of internode elongation, leaf enlargement, and leaf production at the activated SAM subsequently results in bud break and shoot formation. Bud scales have their own dynamics and, although they develop in synchrony with the ES, growth of the scales can be localized and independent of ES activity, as demonstrated by the fact that some bud scales open exposing a dead shoot that did not survive winter (Romberger, 1963). In *Populus*, GA₃ application to dormant buds induces non-canonical bud burst, in which the buds open and a few small leaves may protrude without any signs of internode elongation and new formation of leaves. Although these unexpanded ES are not dead, applied GA₃ may only override constraints on the bud scales and older embryonic leaves but not those of the entire ES. In the natural situation, chilling differentially affects the various parts of the dormant bud. Bud scales and embryonic leaves respond much earlier than the RM and SAM, and only sufficient chilling leads to canonical bud burst (Rinne et al., 2011), which requires collaboration, synchrony, and control of the various parts of this unique shoot system.

**Acknowledgements**

This work was supported by the Norwegian Research Council (grant numbers 171970 and 192013). We thank the reviewers for helpful comments.

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