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Hormone signaling in plant development

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Hormone signaling plays diverse and critical roles during plant development. In particular, hormone interactions regulate meristem function and therefore control formation of all organs in the plant. Recent advances have dissected commonalities and differences in the interaction of auxin and cytokinin in the regulation of shoot and root apical meristem function. In addition, brassinosteroid hormones have recently been discovered to regulate root apical meristem size. Further insights have also been made into our understanding of the mechanism of crosstalk among auxin, cytokinin, and strigolactone in axillary meristems.

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Introduction

Plant growth hormones, primarily auxin, cytokinin (CK), brassinosteroids (BRs), gibberellins (GA), and strigolactones (SLs), play an amazing array of roles during plant development, from embryogenesis to senescence. In this review, we focus on the role of hormones in meristems, as continuous growth of new organs throughout the plant's life cycle is achieved through the activity of these stem cell populations. The primary meristems in a plant are the shoot apical meristem (SAM), responsible for generating all aboveground organs, and the root apical meristem (RAM), responsible for producing all underground organs. Initiation and outgrowth of axillary meristems (AMs) are responsible for producing all secondary axes of growth including flowers. The last 20 years have seen remarkable advances in our understanding of hormonal regulation of meristem function and plant development. This review focuses on advances in the last two years, in particular on the molecular mechanism of interaction between hormones. Two themes emerge in the mechanisms of hormone crosstalk: first, hormones regulate biosynthesis and

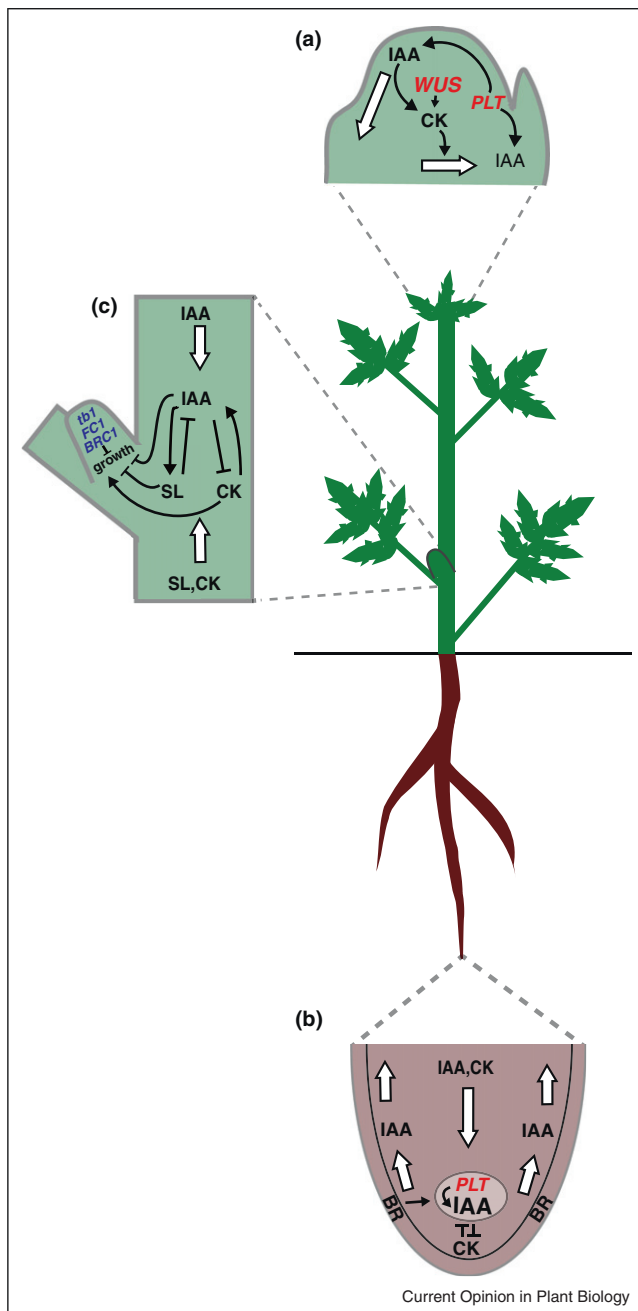
transport of other hormones, and second, hormone interactions converge on regulation of particular transcription factors which integrate and coordinate the developmental response.

Hormone signaling in the shoot apical meristem

In the SAM, several hormones, including auxin, CK, and GA, act both independently and in combination to regulate meristem function [1–3]. In *Arabidopsis*, low levels of GA and high levels of CK are known to maintain the stem cell population in the SAM center. This stem cell population is defined by the activity of the homeodomain transcription factor *WUSCHEL* (*WUS*) [4]. Previously, it was shown that high CK levels in the meristem are maintained by *WUS*-mediated repression of two negative regulators of CK signaling, *ARABIDOPSIS RESPONSE REGULATORS*, *ARR7* and *ARR15* [5]. For further information on the mechanisms of hormone signaling see the review by Shan *et al.* in this issue [6]. Recently, auxin was also discovered to play a role in maintenance of high CK levels in the meristem. The auxin-activated *AUXIN RESPONSE FACTOR/MONOPTEROUS* (*ARF5/MP*) transcriptional regulator was found to directly repress *ARR7* and *ARR15* expression [7•]. Therefore, high levels of CK in the SAM are maintained not only by *WUS*, but also by auxin signaling (Figure 1a).

Along with maintenance of SAM stem cells, auxin and CK regulate organogenesis, with auxin being required for organ initiation in the peripheral zone [8], while CK acts to modulate auxin distribution [9,10]. The site of organ initiation and outgrowth occurs in areas of high auxin, and the localization of auxin is determined by transport of auxin via the PINFORMED (PIN) family of proteins [8]. Many factors that regulate organ position or phyllotaxy in the SAM, including auxin and CK, converge on regulation of the *PIN* genes [9–11]. Studies on the maize *aberrant phyllotaxy1* (*abph1*) gene, which encodes an A-type *ARR* CK signaling regulator, show that *abph1* is required for proper *Zea mays PIN1* (*ZmPIN1*) expression and auxin localization in incipient leaf primordia in the SAM [10]. In addition, CK treatment was found to induce *ZmPIN1* expression in the SAM. In *Arabidopsis*, a recent study using a hypocotyl explant *in vitro* system as a model system for organogenesis found that high CK levels strongly induced expression of *PIN3* and *PIN6* but reduced the expression of *PIN2* [9]. CK also has differential effects on *PIN* expression in the root [9,12]. These results suggest that CK regulates auxin transport through

Figure 1



Hormonal regulation of plant development. **(a)** In the SAM, high cytokinin (CK) levels are maintained in the center of the meristem through the combined effects of auxin (IAA) and *WUS* signaling. Meanwhile, high levels of IAA are transported to the periphery of the meristem to sites of organ initiation, facilitated by upregulation of *PIN1* by *PLT*. Upon primordia initiation, IAA is immediately transported to the next site of organ initiation. CK also impacts organogenesis through modulation of auxin transport. **(b)** In the root, IAA and CK are transported basipetally through the vasculature into the meristem. High CK levels in the root tip restricts IAA signaling and allows cell differentiation, while high IAA levels above the tip leads to establishment of the QC (tan oval) and the root stem cell population through activation of *WOX5* and *PLT*. *PLT* in turn upregulates *PIN* expression, helping maintain high IAA levels in the QC. Meanwhile, brassinosteroid (BR) signaling initiated from the epidermal

transcriptional regulation of the *PIN* genes in both the root and the shoot.

Recent work has shown that *PIN1* expression is also controlled by several members of the *PLETHORA* (*PLT*) family of transcription factors (Figure 1a) [13^{*}]. Loss of *PLT* activity in the SAM periphery was found to reduce *PIN1* expression and alter auxin localization patterns, resulting in predictable changes in phyllotaxy [13^{*}]. Interestingly, *PLT* gene family members were previously shown to induce *PIN1* expression in the RAM [14] but functions in meristem maintenance in the RAM rather than organogenesis [15].

Hormone signaling in the root apical meristem

In contrast to the SAM, where auxin and CK act in conjunction to establish the stem cell population, auxin and CK act antagonistically to establish and maintain the RAM stem cell population (Figure 1b). The RAM consists of a small group of rarely dividing cells known as the quiescent center (QC), surrounded by more rapidly dividing stem cells that give rise to the various root tissue types. Similar to *WUS* in the SAM, expression of *WUSCHEL-RELATED HOMEBOX 5* (*WOX5*) is required for maintenance of the root stem cell population [16]. *WOX5* facilitates proper expression of the *PLT* genes and is restricted to the QC by auxin signaling at the root tip [15,17^{*}]. Crosstalk between auxin and CK in the RAM converges on the regulation of auxin transport and signaling. Under high auxin conditions, the *SHORT HYPOCOTYL2* (*SHY2*)/*IAA3* repressor is degraded, allowing ARF proteins to activate *PIN* expression, leading to high accumulation of auxin in the root tip [18]. In contrast, high CK levels induce expression of *ARR1* and *ARR12* genes, activating *SHY2*, which represses auxin signaling at the root tip beneath the QC [18,19].

Previously, the majority of auxin–CK interactions were found to occur at the transcriptional level. A new study has found that CKs can also directly regulate auxin transport through control of *PIN1* localization [20]. CK reduces *PIN1* levels by targeting *PIN1* proteins for lytic degradation in the vacuole [20]. In another recent study, multiple *arr* mutants, which have a reduced RAM phenotype, were found to have reduced *PIN* protein levels, but not decreased *PIN* transcript levels [21], providing

layer acts in maintenance of the root stem cell population. **(c)** IAA travels basipetally in the stem and indirectly inhibits the outgrowth of axillary buds, while CK and SL travel acropetally in the stem and directly regulate (promote and suppress, respectively) axillary bud outgrowth. Proper endogenous levels of IAA, CK, and SL may be maintained by interactions between these hormones through feedback loops. The TCP family of transcription factors, including the maize *tb1*, rice *FC1*, and *Arabidopsis* *BRC1* genes suppress bud outgrowth in response to IAA, CK, and SL. White arrows indicate direction of hormone transport. Black arrows indicate regulation. Genes in blue function in downregulation. Genes in red function in upregulation. IAA: indole-acetic acid or auxin; CK: cytokinin; BR: brassinosteroids; SL: strigolactone.

further evidence that CK-mediated regulation of PIN1 occurs at the post-transcriptional level. It would be interesting to determine if post-transcriptional regulatory mechanisms are utilized in other auxin/CK controlled developmental processes in the plant.

Although much of the hormonal regulation of the RAM occurs through auxin and CK, other hormones are known to have an effect on the RAM, especially BRs. Two recent studies have shown that mutations in the BR receptor gene *BRASSINOSTEROID INSENSITIVE 1 (BRI1)* result in aberrant cell cycle progression in the RAM [22[•],23^{••}] and that these mutants produce smaller RAMs in a BR dosage-dependent manner [22[•]]. Although auxin is known to stimulate BR biosynthesis [24], BR activity does not affect the expression of *PIN* genes [23^{••}] and BR mutants do not show the same root tip phenotypes as auxin mutants [22[•]]. These data suggest that BRs act on the meristem independently of auxin. Interestingly, the analysis of BRs on RAM function revealed that *BRI1* expression in the root epidermis was sufficient to promote root meristem expansion and cell proliferation, while expression in the inner endodermis, QC, or stele could not rescue the *bri1* mutant phenotype [23^{••}]. As the epidermal layer of the SAM has also been shown to play a critical role in the regulation of SAM size [8,25,26], this exciting result suggests that similar modes of regulation exist in the SAM and the RAM epidermis.

Hormone signaling in axillary meristems

Shoot branching is a two-step process that begins with initiation of AMs in the axils of leaves to form lateral buds followed by bud outgrowth to form branches. Auxin is critical for this process, since genes involved in auxin biosynthesis, transport, and signaling are required for AM initiation [27]. The maize *barrenstalk1 (ba1)* gene and its rice ortholog *LAX PANICLE1 (LAX1)*, encode a basic helix–loop–helix transcription factor that functions in auxin-mediated regulation of AM initiation [28,29]. Recent papers have identified several other genes that act with *ba1/LAX1* to regulate AM function. The maize *barren stalk fastigiate1 (baf1)* gene, which encodes an AT-hook transcription regulator, was found to be required for a threshold level of *ba1* expression [30]. The rice *LAX2* gene, which encodes a novel nuclear protein that physically interacts with *LAX1*, was also shown to promote AM formation [31]. As *ba1/LAX1* related genes are expressed in AMs of many plant species, these genes are likely to be also relevant to branching in dicots [32].

Hormonal regulation of lateral bud outgrowth involves antagonistic action of auxin, CK, and SL (Figure 1c) [27,33–35]. Auxin synthesized in the shoot apex moves basipetally in the polar auxin transport stream and indirectly inhibits outgrowth of axillary buds, a phenomenon known as apical dominance. On the other hand, CK travels acropetally through the xylem into the axillary

bud, directly promoting its outgrowth. SLs, a new class of hormones, are synthesized mostly in roots and transported acropetally to directly suppress axillary bud outgrowth. Recently it was shown that SL biosynthesis in *Medicago truncatula* and rice is positively regulated by the GRAS-type transcription factors *NODULATION SIGNALING PATHWAY, NSP1* and *NSP2* [36]. However, further research is required to fully elucidate the SL biosynthesis pathway and the perception of SL in axillary buds.

Auxin and CK interact antagonistically to control branching in the shoot [35,37]. Auxin inhibits the expression of *IPTs (ISOPENETENYL TRANSFERASES)* to downregulate CK biosynthesis [38]. Additionally, auxin upregulates expression of *CKX2 (CYTOKININ OXIDASE2)*, involved in the degradation of CK [37]. On the other hand, it was recently shown that increased CK levels induce auxin biosynthesis in young, developing root and shoot tissues in *Arabidopsis*, while decreased CK levels have the opposite effect [39]. These data suggest that proper endogenous auxin and CK levels are maintained by a homeostatic feedback loop.

A feedback loop may also exist between auxin and SL [33,34]. Auxin upregulates expression of the SL biosynthetic genes [40,41]. Moreover, decreased SL increases auxin levels to promote SL biosynthesis. A recent study in *Arabidopsis* showed that SLs also dampen basipetal auxin transport in the stem and reduce PIN1 accumulation in a SL-dependent manner [42^{••}]. Recently in pea (*Pisum sativum*), decapitation was shown to cause polar localization of PIN1 in the buds followed by induction of *PIN1* expression in the stem to establish directional auxin export from bud to stem [43[•]]. These results support the hypothesis that export of auxin from the bud is important for bud outgrowth.

Environmental and hormonal regulation of shoot branching is integrated by members of the TCP family of transcription factors including the maize *teosinte branched1 (tb1)*, rice *FINECULM1 (FC1)*, and the *Arabidopsis BRANCHED (BRC1)* genes, which suppress bud outgrowth [27]. *FC1* and *BRC1* have been shown to interact with auxin and SL in rice and *Arabidopsis*. Recently, negative regulation of *FC1* expression by CK was reported in rice [44]. A new gene in this pathway was recently identified in maize, the homeodomain leucine zipper gene *grassy tillers1 (gt1)*, which suppresses bud outgrowth [45]. Expression of *gt1* is upregulated by shading and is *tb1*-dependent [45]. Further study of the interactions between hormones, *tb1*, *gt1* and the environment will lead to an understanding of the characteristic plant architectures of different species.

Conclusions

Although crosstalk between hormones is incredibly complex, recent years have seen a dissection of the molecular

mechanisms of hormone interaction. This will certainly continue in the future, aided by modeling studies to dissect the complex feedback and feed forward regulatory mechanisms. It is striking that hormone interaction modules are redeployed over and over again during development. The interaction between auxin, CK and GA plays a fundamental role in SAM function. Interestingly, the auxin–CK–GA module is redeployed in the regulation of compound leaf development in tomato [46–48]. Auxin and CK have long been known to have opposite functions in the root and shoot, and the auxin–CK interaction module is deployed to different effect in the SAM and RAM. Auxin and CK also have opposing roles in the axillary bud. Is this a coincidence or accident of evolution? More likely this interaction reflects a common regulatory mechanism in meristems intersecting with different downstream transcription factors to achieve the appropriate developmental responses.

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