



Update on Developmental Plasticity at High Temperature

Developmental Plasticity at High Temperature^{1[OPEN]}

Lam Dai Vu,^{a,b,c,d} Xiangyu Xu,^{a,b} Kris Gevaert,^{c,d,2} and Ive De Smet^{a,b,2,3,4}

^aDepartment of Plant Biotechnology and Bioinformatics, Ghent University, B-9052 Ghent, Belgium

^bVIB Center for Plant Systems Biology, B-9052 Ghent, Belgium

^cDepartment of Biomolecular Medicine, Ghent University, B-9000 Ghent, Belgium

^dVIB Center for Medical Biotechnology, B-9000 Ghent, Belgium

ORCID IDs: 0000-0001-5078-7532 (L.D.V.); 0000-0002-4237-0283 (K.G.); 0000-0003-4607-8893 (I.D.S.).

A severe consequence of climate change is global warming with heat waves occurring across the world, including in many important agricultural production areas (Lobell et al., 2011; Sun et al., 2014; Christidis et al., 2015; Lesk et al., 2016). This phenomenon leads to a significant drop in crop yield and quality and to a shift in the distribution of native and invasive plant species (Challinor et al., 2014; Merow et al., 2017).

As sessile organisms, plants possess complex mechanisms that help them cope with even the slightest increase in temperature. A large number of studies explored the response and acclimation to heat shock that occurs at, for plants, potentially lethal high temperatures (Driedonks et al., 2015; Bäurle, 2016; Ohama et al., 2017). For *Arabidopsis* (*Arabidopsis thaliana*), a sudden heat shock for a short time without previous heat acclimation at temperatures higher than 40°C may lead to plant death (Yeh et al., 2012). However, acquired thermotolerance from a previous exposure to moderate heat (less than 37°C) can increase the chance to survive (Larkindale and Vierling, 2008; Finka et al., 2012; Yeh et al., 2012; Sedaghatmehr et al., 2016; Ling et al., 2018). In contrast, a mildly increased ambient temperature, typically up to 27°C to 32°C (referred to as high [ambient] temperature in the context of this review) for *Arabidopsis*, causes numerous significant changes in plant architecture and the transition between developmental stages without resulting in plant death (Fig. 1; Quint et al., 2016; Casal and Balasubramanian, 2019; Jin and Zhu, 2019). The response to high ambient temperature is controlled by distinct mechanisms with limited overlap in response to extreme heat (Quint et al., 2016).

In this review, we assess thermal responses during plant growth at different developmental stages, including seed germination, root and shoot thermomorphogenesis (the effect of high ambient temperature on

the organization and shape of the plant body; Quint et al., 2016; Casal and Balasubramanian, 2019), floral transition, and fruit dehiscence, and the underlying molecular mechanisms (e.g. transcriptional, posttranscriptional, and protein levels), mainly focusing on knowledge gained from the model plant *Arabidopsis*. High-temperature effects on other processes, such as metabolic pathways and redox homeostasis, have been reviewed elsewhere (Salvucci and Crafts-Brandner, 2004; de Pinto et al., 2015; Suzuki and Katano, 2018; Wang et al., 2018).

HIGH TEMPERATURE INHIBITS SEED GERMINATION

Germinating under favorable seasonal conditions can increase the survival chance and the fitness of young seedlings (Finch-Savage and Leubner-Metzger, 2006). Temperature is an important factor, and high temperature has an inhibitory effect on seed germination, which is termed thermoinhibition (Hills et al., 2003; Fig. 1). For *Arabidopsis*, seed germination is reduced

ADVANCES

- Auxin produced in the leaf upon a high temperature trigger acts as a mobile signal that controls hypocotyl elongation.
- Distinct high temperature signalling mechanisms exist in the root versus the shoot.
- Light, circadian clock, and high temperature signalling are intertwined.
- Multiple thermosensors exist, which are distributed throughout various regulatory networks that control growth and development.
- Immune responses at high temperature converge on PIF4.

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²These authors contributed equally to the article.

³Author for contact: ive.desmet@psb.vib-ugent.be.

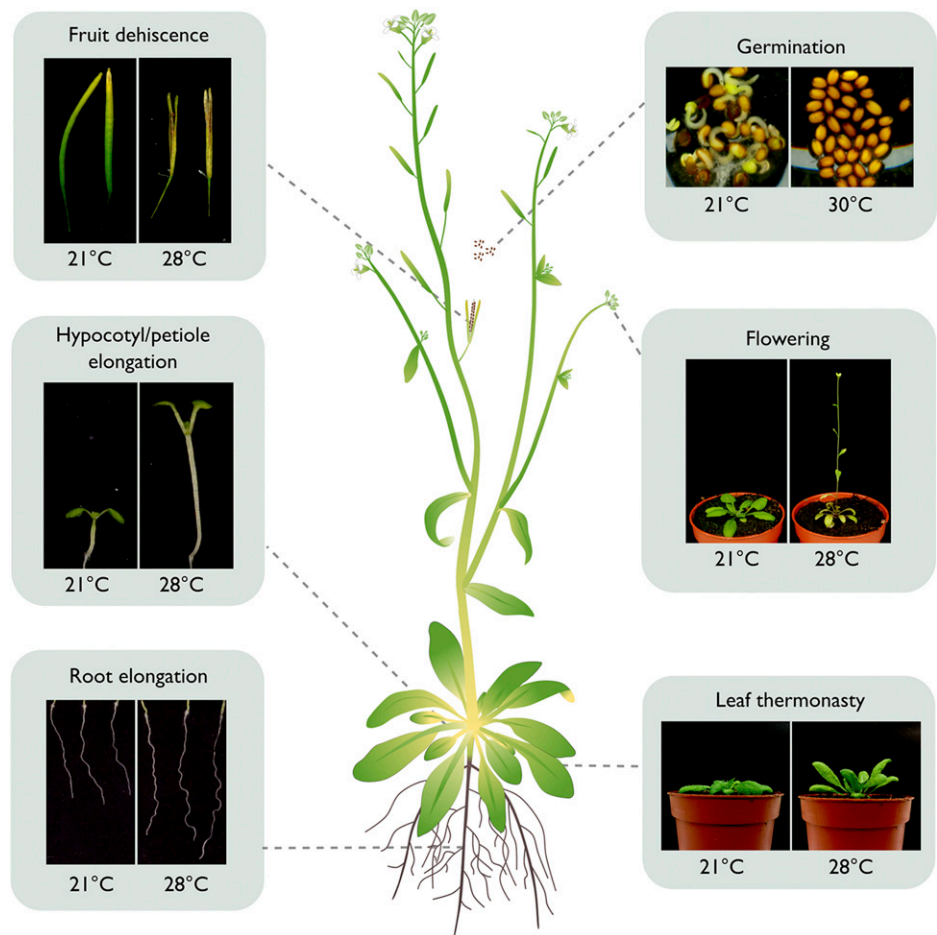
⁴Senior author

L.D.V., X.X., K.G., and I.D.S. wrote the article.

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Figure 1. High ambient temperature has effects on plant architecture and development. Representative images are shown for the indicated phenotypes of organs and processes at optimal (21°C) and high (28°C and 30°C) temperatures.



by ~40% at 32°C compared with 21°C (Chiu et al., 2016). Abscisic acid (ABA) and gibberellic acid (GA) act antagonistically to regulate seed germination, in which GAs are promoting factors (Debeaujon and Koornneef, 2000). High temperature promotes ABA biosynthesis (Toh et al., 2008). Increased ABA levels dampen protein ubiquitination and proteasome activity, which is required to degrade seed dormancy-promoting proteins, such as DELLA proteins (negative regulators of GA signaling), ABA INSENSITIVE3 (ABI3), and ABI5 (Chiu et al., 2016). ABI3, ABI5, and DELLAs induce the expression of high temperature-responsive genes in the seeds, such as *SOMNUS* (*SOM*; Lim et al., 2013). Subsequently, *SOM* promotes the expression of ABA biosynthesis genes and decreases the expression GA biosynthesis genes (Toh et al., 2008; Lim et al., 2013; Chiu et al., 2016). However, the epigenetic factor *POWERDRESS* (*PWR*) interacts with ABI3 and negatively controls *SOM* expression to control seed germination at high temperature (Yang et al., 2019). Another thermoinhibitory pathway is regulated by *DELAY OF GERMINATION1* (*DOG1*). *DOG1* inhibits GA metabolism in seeds in a temperature-dependent manner (Graeber et al., 2014), and inhibition of *DOG1* expression allows seeds to germinate at 32°C (Huo et al., 2016).

After a period of exposure to high temperature, the accumulation of *PHYTOCHROME INTERACTING*

FACTOR3-LIKE5 (*PIL5*)/*PHYTOCHROME-INTERACTING FACTOR1* (*PIF1*), a negative regulator of seed germination, leads to a secondary dormancy at conditions that are normally permissive for germination (Martel et al., 2018). Interestingly, when seeds are transferred back to light and 22°C after a preincubation at 32°C in the dark, *PIL5* accumulation is reduced by an increased expression of *PHYTOCHROME D* (*PHYD*). *phyD*, together with other phytochromes, marks *PIL5* for degradation via phosphorylation and relieves the repression of seed germination.

In summary, high ambient temperature inhibits seed germination mainly by up-regulating ABA signaling and reducing GA signaling. Furthermore, high temperature-induced reactive oxygen species generation by mitochondrial small heat shock proteins also plays a role (Ma et al., 2019).

PHYTOHORMONES REGULATE THERMOMORPHOGENIC GROWTH OF SEEDLINGS AT HIGH TEMPERATURE

At high temperature, the elongation of the hypocotyl and the upward bending of the leaves in seedlings (or thermonastic movement) gives plants an advantage to

maximize cooling capacity by moving away from heat-absorbing soil and having better access to cooling air streams (Fig. 1; Gray et al., 1998; Crawford et al., 2012; Bridge et al., 2013; Quint et al., 2016; Park et al., 2019). The phytohormone auxin contributes to this response by inducing the expression of *AUXIN RESPONSE FACTORS*, which activate cell expansion-promoting genes in the hypocotyl epidermis (Reed et al., 2018). In addition, auxin signaling is enhanced by stabilization of the major auxin receptor *TRANSPORT INHIBITOR RESPONSE1* (*TIR1*) at increased temperature (Wang et al., 2016) and by alterations in the auxin transport system (Hanzawa et al., 2013).

The transcription factor *PIF4*, a central regulator of many high temperature-related responses in *Arabidopsis*, promotes auxin biosynthesis in cotyledons and leaf blades at high temperature (Franklin et al., 2011; Sun et al., 2012; Bellstaedt et al., 2019). Auxin then travels from cotyledons to the hypocotyl, where it induces growth-promoting brassinosteroid (BR) biosynthesis and signaling (Fig. 2; Ibañez et al., 2018; Bellstaedt et al., 2019). Furthermore, auxin biosynthesis and redistribution play similar roles in the regulation of thermonastic leaf movement (Park

et al., 2019). Excision of cotyledon or leaf blades abolishes thermoresponsive cell elongation in the abaxial petiole zone. Indeed, inhibiting *PIN-FORMED* (*PIN*)-mediated auxin redistribution leads to a significant reduction in thermonastic petiole movement. In addition, the expression of *PINOID* (*PID*), encoding a protein kinase that controls phosphorylation-mediated *PIN* polarization to regulate polar auxin transport, is promoted by *PIF4* at high temperature (Fig. 2; Park et al., 2019).

The cross talk of auxin and BR signaling plays an important role in the regulation of plant growth and development (Tian et al., 2018). The transcription factor *BZR1* (*BRASSINAZOLE RESISTANT1*), a positive regulator of BR signaling, *AUXIN RESPONSE FACTOR6*, and *PIF4* interact with each other and compose the "BAP" module that promotes hypocotyl elongation in response to diverse environmental stimuli (Oh et al., 2014). Especially, *PIF4* and *BZR1* form a complex and regulate the expression of common target genes interdependently, including those required for thermomorphogenesis (Oh et al., 2012). High temperature promotes this interaction by translocating *BZR1* to the

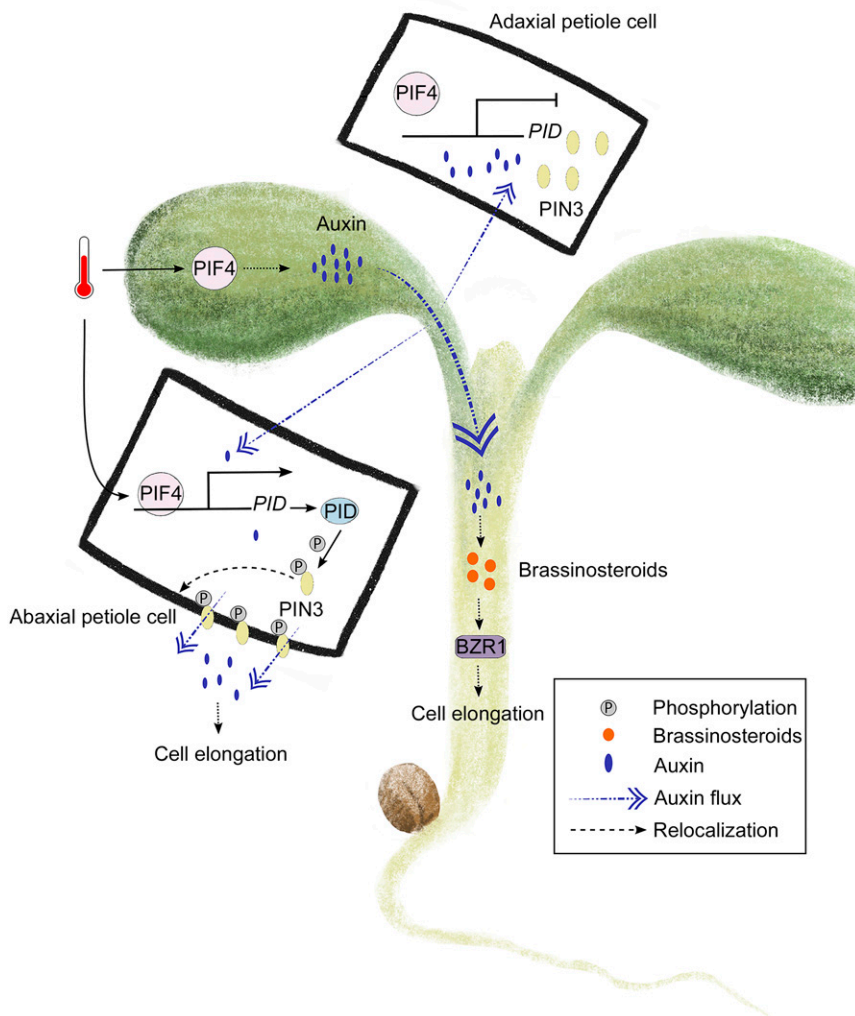


Figure 2. Organ-specific perception of high temperature and subsequent auxin distribution and downstream signaling. At high temperature, auxin moves from the leaf blade through the petiole toward the hypocotyl. In the latter organ, auxin promotes BR-mediated growth. In the petiole, *PIF4* controls *PID* expression, which impacts phosphorylation-mediated *PIN3* localization to control auxin efflux and cell elongation.

nucleus in a BR-dependent manner (Ibañez et al., 2018). Besides, at high temperature, BR also promotes *PIF4* expression via *BZR1* activation (Ibañez et al., 2018). Remarkably, in plants lacking auxin biosynthesis and signaling components, a defect in thermomorphogenic elongation growth can be rescued by exogenous BR treatment (Ibañez et al., 2018). However, this defect cannot be rescued by auxin treatment if the plants lack BR biosynthesis and signaling components. This indicates that BR acts downstream of auxin and promotes *PIF4* expression via *BZR1* to generate a signaling amplification loop to promote hypocotyl growth under extended exposure to high temperature (Fig. 2). In contrast, *FLOWERING CONTROL LOCUS A* attenuates *PIF4* activity by triggering the dissociation with, for example, the *YUCCA8* promoter, especially under long-term exposure to high temperature (Lee et al., 2014).

PIF4 also binds to the BR-responsive transcription factor *BRI1-EMS-SUPPRESSOR1* (*BES1*) and modifies the DNA-binding specificity and transcriptional activity of *BES1* (Martínez et al., 2018). The *BES1* homodimer represses the expression of BR biosynthesis genes, while the *PIF4-BES1* complex coactivates BR biosynthesis, which is essential for thermomorphogenic growth. The formation of this complex depends on the availability of *PIF4* and *BES1* (Martínez et al., 2018). Furthermore, *PIF4* has been shown to be phosphorylated by the BR signaling repressor *BRASSINOSTEROID-INSENSITIVE2* to control its stability and repress diurnal hypocotyl growth (Bernardo-García et al., 2014). It would be interesting to investigate whether thermomorphogenesis is also regulated by phytohormone-controlled posttranslational modifications of *PIF4*.

In *Arabidopsis*, expression of the GA oxidases *GA20ox1* and *GA3ox1*, major GA biosynthetic genes, is highly up-regulated in plants grown at 29°C compared with plants grown at 20°C, whereas the GA catabolism gene *GA2ox1* is down-regulated (Stavang et al., 2009). The resulting increased level of GA induces the degradation of DELLA proteins, such as *REPRESSOR OF GA*, which inhibits the transcriptional activity of "BAP" module components and mediates proteasomal degradation of *PIF4* to suppress elongation growth (de Lucas et al., 2008; Feng et al., 2008; Li et al., 2012, 2016; Oh et al., 2014). Furthermore, the reduction of temperature-induced hypocotyl elongation in the GA biosynthesis mutant *gai-1D* can be rescued by treatment with the bioactive BR epibrassinolide, indicating that GA also regulates thermomorphogenesis via BR signaling pathways (Ibañez et al., 2018).

THERMOMORPHOGENIC GROWTH INTERSECTS WITH LIGHT SIGNALING

Light and temperature share a large set of common regulators, including PIF proteins, and likely act interdependently to control plant growth (Legris et al., 2017). Induction of hypocotyl elongation by PIFs is antagonized by red light-sensing phytochromes, which

promote photomorphogenesis (Zhu et al., 2000; Shen et al., 2008). High temperature spontaneously reverts the light-activated Pfr form of phytochrome B (*phyB*) to the inactive Pr form in a light-independent process called thermal reversion or dark reversion (Fig. 3C; Sweere, 2001; Klose et al., 2015; Legris et al., 2016). Alteration in the activity of phytochromes affects thermoresponsive elongation growth in *Arabidopsis* (Jung et al., 2016). Therefore, *phyB*, and conceivably other phytochromes, have been put forward as major sensors in *Arabidopsis* that integrate both light and temperature cues (Jung et al., 2016; Legris et al., 2016; Vu et al., 2019).

Similar to *phyB*, in *Marchantia polymorpha*, high temperature shortens the lifetime of photoactivated *PHOTOTROPIN* (*PHOT*), a homolog of the *Arabidopsis* blue light receptors *phot1* and *phot2* (Fujii et al., 2017). This leads to inactivation of the *PHOT* kinase domain and repositioning of the chloroplasts, establishing its role as a thermosensor in *M. polymorpha* (Fujii et al., 2017; Vu et al., 2019). However, as of yet, there is no evidence showing whether phototropins also play a role in thermosensing and thermomorphogenesis in *Arabidopsis*. In addition, blue light represses thermomorphogenesis via its receptor *CRYPTOCHROME1* (*CRY1*; Ma et al., 2016). *CRY1* interacts physically with *PIF4* and binds to the promoter of *PIF4* targets to repress *PIF4* transcriptional activity without affecting *PIF4* affinity to DNA. The repressive activity of *CRY1* is enhanced by both blue light and high temperature. Similarly, temperature-dependent *PIF4* activity is also repressed by *UVB-RESISTANCE8* (*UVR8*) under UV light (Hayes et al., 2017). However, unlike *CRY1*, *UVR8* does not interact directly with *PIF4*. It was proposed that UVB-dependent inhibition of thermomorphogenesis might be mediated by the *UVR8*-promoted stabilization of *LONG HYPOCOTYL IN FAR-RED1*, which represses *PIF4* activity via heterodimer formation (Hornitschek et al., 2009; Hayes et al., 2017). Between 20°C and 30°C, the inversion of the active *UVR8* monomer to the inactive homodimer is more rapid than at lower temperature (5°C–10°C; Findlay and Jenkins, 2016). It remains to be investigated how thermosensing information is transduced to the dimerization of cryptochromes and *UVR8* or whether temperature modulates their activity via an alternative pathway.

In addition to photoreceptors, other key components of light signaling pathways, such as *DE-ETIOLATED1* (*DET1*) and the E3 ubiquitin ligase *CONSTITUTIVE PHOTOMORPHOGENESIS1* (*COP1*), also play important roles in thermomorphogenesis, possibly by promoting *PIF4* expression and stabilizing the *PIF4* protein via yet unknown mechanisms (Delker et al., 2014; Gangappa and Kumar, 2017). Upon light perception, *phyB* and *CRY1* suppress *COP1* activity to promote photomorphogenesis (Sheerin et al., 2015; Holtkotte et al., 2017). The transcriptional repressor *LONG HYPOCOTYL5*, which is a downstream target of *DET1* and *COP1*, modulates *PIF4* transcriptional activity, not by repressing *PIF4* expression but rather by competitive binding to the promoter of common downstream

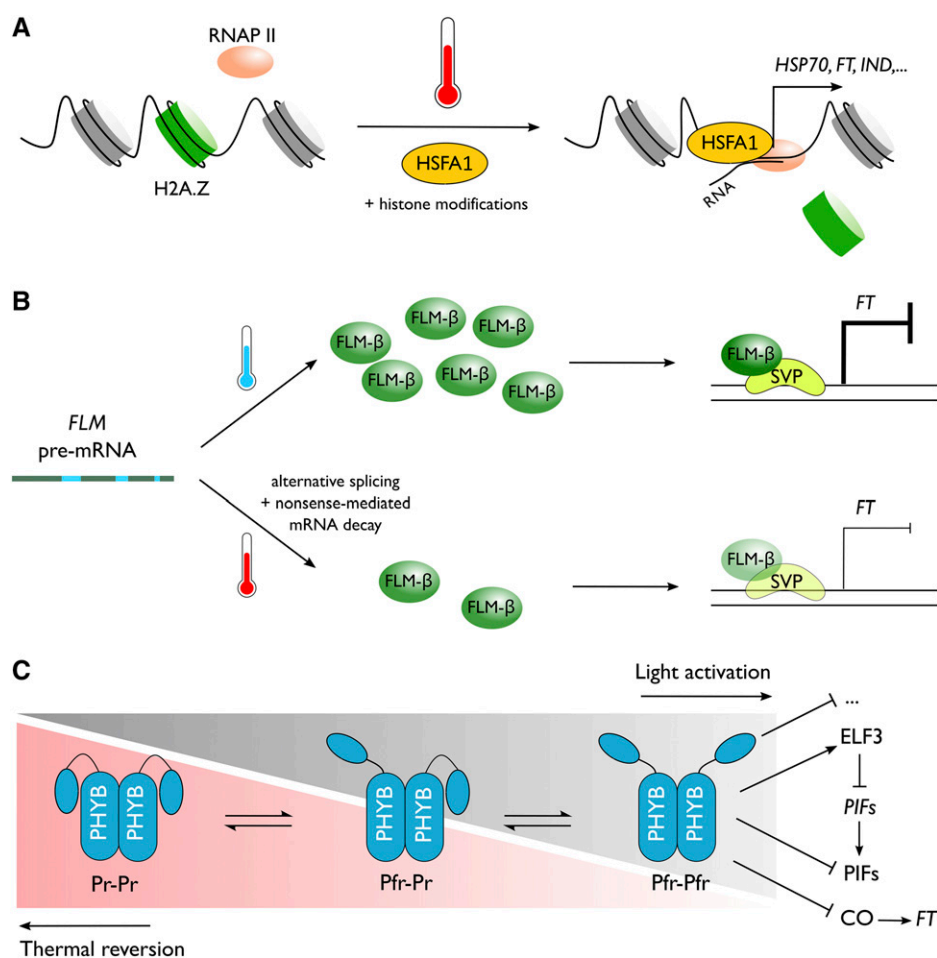


Figure 3. Molecular regulation of thermomorphogenesis. A, Transcriptional regulation by chromatin remodeling. B, Posttranscriptional regulation by alternative splicing. C, Posttranslational regulation by thermal reversion of photoreceptors.

targets (Fig. 4; Gangappa and Kumar, 2017; Park et al., 2017).

The CULLIN3-BLADE-ON-PETIOLE1 (BOP1)/BOP2 E3 ligase complex acts in the phyB signaling pathway to suppress elongation growth under red light by decreasing PIF4 levels following polyubiquitination (Zhang et al., 2017). Loss-of-function mutants of *BOP2* and its homolog *BOP1* show no difference in elongation growth at 22°C but display a significantly longer hypocotyl at 28°C, indicating their role in modulating thermomorphogenesis. Astoundingly, while light enhances BOP2 activity, BOP2 can still ubiquitinate PIF4 in the dark (Zhang et al., 2017). This suggests that phyB-mediated phosphorylation of PIF4 is not required for its ubiquitination by BOP2. Whether BOP2 modulates PIF4 during thermomorphogenesis by a phyB-independent mechanism or phyB controls BOP2 activity in an alternative pathway remains to be investigated.

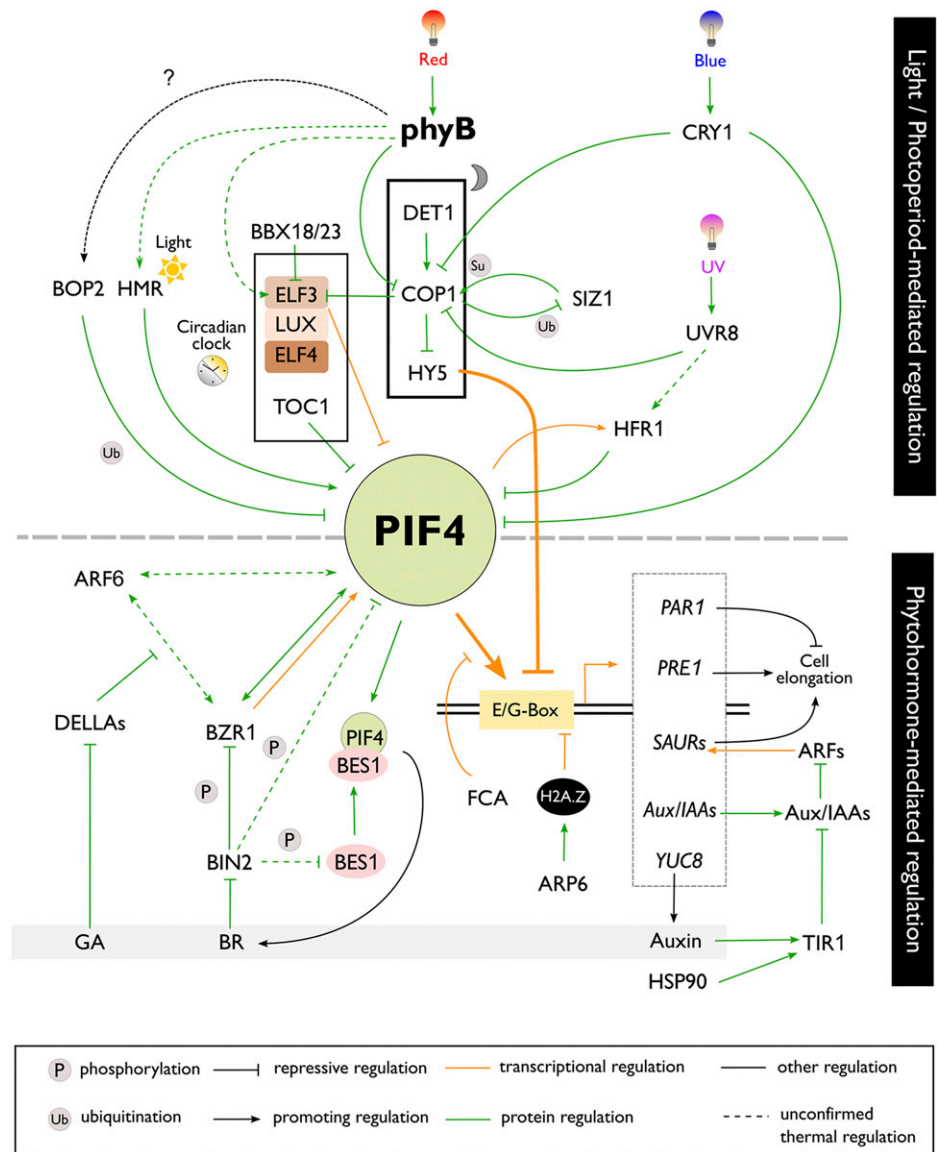
LIGHT SIGNALING AND CIRCADIAN COMPONENTS COORDINATE TO CONTROL THERMOMORPHOGENIC GROWTH

Physiological and morphological responses to external stimuli are often the result of the interaction

between the circadian clock components and the environmental input (Hotta et al., 2007). Overexpression of the circadian clock gene *TIMING OF CAB EXPRESSION1* suppresses thermomorphogenic growth (Zhu et al., 2016). Conversely, the loss-of-function *toc1-2* mutant shows hypersensitivity to high temperature, which can be suppressed in the presence of the *pif4* mutation. Indeed, *TIMING OF CAB EXPRESSION1* functions upstream of PIF4 and transmits circadian information into PIF4-mediated thermal responses by binding to PIF4 and inhibiting PIF4 transcriptional activity.

Another clock component, EARLY FLOWERING3 (ELF3), a subunit of the clock-regulating Evening Complex (EC; Fig. 4), also regulates thermomorphogenesis via PIF4 (Box et al., 2015; Raschke et al., 2015). At 22°C, ELF3 directly binds to the *PIF4* promoter and represses *PIF4* transcription. This repression can be reversed when the temperature increases to 27°C. Furthermore, ELF3 can bind directly to the PIF4 protein independently from the EC to suppress PIF4 activity (Nieto et al., 2015). During thermomorphogenesis, ELF3 accumulation is partially negatively regulated by COP1 and by its interaction with two B-box domain (BBX) proteins, BBX18 and BBX23 (Ding et al., 2018). Overexpression of *BBX18* increases thermomorphogenic

Figure 4. Light/photoperiod- and phytohormone-dependent thermoresponsive pathways converge at PIF4. Here, light and circadian clock components are integrated with temperature information to mediate thermoresponsive growth, which is controlled by phytohormone signaling. The thermosensory machinery is mainly controlled by phyB, while the roles of other light receptors are still largely elusive. PIF4 mainly mediates thermomorphogenesis by promoting auxin biosynthesis and signaling, while BR signaling plays an important downstream function. For further details on the components of these pathways, see the main text.



response in the wild type but not in *pif4*. Transcriptional targets of BBX18, BBX23, and PIF4 show a large overlap, further demonstrating the role of BBX18 and BBX23 in thermomorphogenesis. Altogether, this indicates that BBX18 and BBX23 mediate thermomorphogenesis via the ELF3-PIF4 pathway.

Transcriptomic and chromatin immunoprecipitation data indicate that the EC can directly bind to promoters and regulate the expression of a number of target genes at night in a thermoresponsive manner independently from PIF4 and phyB (Ezer et al., 2017). Conversely, phyB and the EC also share a significant overlap of thermoresponsive binding loci. Furthermore, hypocotyl elongation caused by loss of functional ELF3 is completely abolished by overexpression of *PHYB*. These observations indicate that a large portion of light and temperature information may be transmitted to the circadian EC via phyB. Indeed, ELF3 interacts with phyB-Pfr directly, and this leads to the accumulation of

ELF3 in the light (Liu et al., 2001; Nieto et al., 2015). Under short-day conditions, a large portion of mis-regulated thermoresponsive transcripts in phytochrome mutants occurs at night, leading to the previous belief that phyB mainly regulates thermal response during the night (Jung et al., 2016). However, phyB also senses temperature and controls thermomorphogenesis during the daytime via a distinct pathway composed of HEMERA (HMR) and PIF4 (Fig. 4; Qiu et al., 2019). In the light, HMR interacts with photoactivated phyB and mediates the formation of phyB nuclear bodies to initiate photomorphogenesis (Chen et al., 2010). Under long-day or continuous red light conditions, HMR interacts with PIF4 to activate thermoresponsive genes by increasing PIF4 protein accumulation in warm temperatures (Qiu et al., 2019). In contrast, HMR function only plays a minor role under short-day conditions. Interestingly, during photomorphogenesis, HMR accumulates by interacting with the Pfr form of phyB

(Galvão et al., 2012). Since high temperature decreases Pfr abundance, phyB should regulate the HMR-PIF4 interaction via an unknown mechanism during thermomorphogenesis in the light.

CHROMATIN REMODELING REGULATES THERMOMORPHOGENIC GROWTH

Dynamic nucleosome positioning is an important regulatory mechanism of gene transcription (Bai and Morozov, 2010). At low temperature, the H2A histone variant H2A.Z is found to be enriched at many heat-inducible genes (Kumar and Wigge, 2010; Cortijo et al., 2017; Kumar, 2018). At temperatures higher than 22°C, H2A.Z occupation is reduced and chromatin accessibility for RNA polymerase II is increased, which allows higher transcription of thermoresponsive genes (Fig. 3A; Kumar and Wigge, 2010). Expectedly, loss-of-function mutants in *ACTIN-RELATED PROTEIN6* (*ARP6*), which is required for proper H2A.Z deposition, display a constitutive high-temperature phenotype, including a long hypocotyl (Choi et al., 2005; Deal et al., 2005, 2007; Kumar and Wigge, 2010). However, the depletion of H2A.Z is not directly affected by high temperature but is rather mediated by the recruitment of transcription factors, such as those of the HEAT SHOCK FACTOR A1 family (Cortijo et al., 2017). Furthermore, H3 deacetylation, which is controlled by PWR and HISTONE DEACETYLASE9, regulates genes that are also regulated by H2A.Z dynamics (Tasset et al., 2018). Loss-of-function *pwr* mutants are suppressed in hypocotyl growth, largely by attenuating the expression of *PIF4* and auxin biosynthesis.

HIGH TEMPERATURE AFFECTS FLORAL TRANSITION

Seasonal cues such as daylength, light quality, and temperature control the transition from vegetative to reproductive growth (Amasino, 2010; Capovilla et al., 2015; Song et al., 2015). A mild increase in temperature can trigger floral transition in Arabidopsis under non-inductive short-day conditions (Fig. 1; Balasubramanian et al., 2006). This is mainly attributed to an increase in expression of the major flowering-promoting genes *FLOWERING LOCUS T* (*FT*), *TWIN SISTER OF FT*, and *SUPPRESSOR OF OVEREXPRESSION OF CO1* (Blázquez et al., 2003; Balasubramanian et al., 2006; Seo et al., 2009; Lee et al., 2013).

Similar to thermomorphogenic elongation growth, light receptors also play an important role in thermoresponsive flowering. In Arabidopsis, phyB and CRY2 negatively and positively regulate thermal flower transition, respectively (Blázquez et al., 2003; Halliday et al., 2003). Under long-day conditions, phyB destabilizes CONSTANS (CO), which induces *FT* expression to promote photoperiodic flowering, while cryptochromes and phyA enhance CO stability (Valverde et al., 2004). It

will be interesting to investigate whether light receptors couple photoperiodic flowering with thermoresponsive flowering via known photoperiodic pathways (Kaiserli et al., 2015; Zhang et al., 2018).

Chromatin remodeling at H2A.Z also plays a role in the regulation of temperature-dependent flowering (Kumar et al., 2012; Tasset et al., 2018). It was previously suggested that an increase in temperature would reduce the occupancy of H2A.Z at the *FT* locus, leading to a higher enrichment of PIF4 at the *FT* locus and promoting *FT* expression (Kumar et al., 2012). However, in more recent studies, the difference in the flowering phenotype of *pif4* plants and the wild type at high temperature appeared negligible in both short- and long-day conditions (Galvão et al., 2015; Fernández et al., 2016). Conversely, *arp6* and *pwr* mutants show early- and late-flowering phenotypes, respectively, constitutively at both low and high temperature (Kumar and Wigge, 2010; Tasset et al., 2018). Therefore, in contrast to hypocotyl growth, thermal induction of flowering mediated by H2A.Z depletion requires an unknown transcriptional regulator independent from PIF4. For example, GA-regulated temperature-mediated flowering independently of FT and PIFs might play a crucial role (Galvão et al., 2015).

Another important regulator of gene expression in response to environmental stimuli is alternative splicing that results in different protein isoforms (Syed et al., 2012). For example, thermally primed splicing memory can lead to a higher survival chance in Arabidopsis during heat stress (Ling et al., 2018). It was previously suggested that the flowering regulator *FLOWERING LOCUS M* (*FLM*) is targeted by temperature-dependent alternative splicing, which results in two main spliced forms, *FLM-β* and *FLM-δ*, that control flowering (Posé et al., 2013). However, in many Arabidopsis accessions, temperature-sensitive flowering can be largely explained by altered accumulation of the flowering-repressive *FLM-β* isoform, whereas *FLM-δ* does not play a significant role (Fig. 3B; Lutz et al., 2015, 2017). The level of nonsense *FLM* transcripts is increased at high temperature and leads to nonsense-mediated mRNA decay of *FLM*, which also compromises the level of the functional *FLM-β* transcripts (Sureshkumar et al., 2016). Furthermore, *SHORT VEGETATIVE PHASE*, which promotes *FT* expression and is inhibited by interaction with *FLM-β*, is itself destabilized at high temperature (Lee et al., 2013). The expression of other related flowering genes in the *FLM* clade is also affected by temperature-controlled splicing (Airoldi et al., 2015; Verhage et al., 2017). Surprisingly, the splicing machineries themselves are targeted by temperature-induced alternative splicing. Hence, it is suggested that this may serve as the earlier step of a temperature-dependent mechanism that mediates altered splicing of other downstream thermoresponsive genes (Verhage et al., 2017). Furthermore, similar to light-responsive alternative splicing (Shikata et al., 2014) and alternative promoter selection (Ushijima et al., 2017), it is likely that phytochromes also affect high temperature-dependent generation of protein isoforms.

MicroRNAs serve as another regulatory checkpoint of transcriptional machineries controlling *FT* expression at high temperature (Lee et al., 2010). High temperature induces the expression of *miR172*, which targets the mRNA of a subset of APETALA2 flowering repressors (Lee et al., 2010; Zhu and Helliwell, 2011). Conversely, an increased temperature from 15°C to 21°C to 27°C reduces the level of *miR169*, which targets the mRNAs of *JASMONATE-ZIM-DOMAIN PROTEIN4* and the gene encoding NF-YA2, a subunit of the transcriptional complex Nuclear Factor Y (NF-Y), which both positively affect the expression of *FT* (Gyula et al., 2018). In addition to microRNAs, thermoregulation of floral transition by long noncoding RNAs also occurs. For example, *FLOWERING LONG INTERGENIC NON CODING RNA (FLINC)*, a long intergenic noncoding RNA, is down-regulated at 25°C compared with 16°C (Severing et al., 2018). Knockout mutants of *FLINC* have higher *FT* expression and flower earlier than wild-type plants, while overexpression of *FLINC* delays flowering. However, the molecular mechanisms underlying *FLINC* activity remain unexplored.

It is clear that Arabidopsis flowering is regulated by temperature at multiple checkpoints. In agreement with this, a recent mathematical model has predicted multiple thermosensing inputs for *FLC* expression during vernalization, and they highly depend on the cold duration as well as spikes of warm temperature (Antoniou-Kourouniotti et al., 2018). Similarly, in silico simulations also show different thermosensitivities for *FT* expression (Kinmonth-Schultz et al., 2019). This suggests that thermosensory information controlling a specific thermal response is highly variable and depends largely on growth conditions and length of thermal exposure, instead of being generated by only a few core thermosensors (Antoniou-Kourouniotti et al., 2018; Vu et al., 2019).

FRUIT DEHISCENCE IS PROMOTED BY HIGH TEMPERATURE

In several plant species, including Brassicaceae species, hydrolytic enzymes decompose the cell wall during ripening, promoting cell separation precisely at an abscission cell layer between the fruit valve and the replum (called fruit dehiscence) and leading to the release and dispersal of the fruit content (Spence et al., 1996). In agriculture, however, early seed dispersal by fruit dehiscence is an undesirable trait that significantly reduces crop yield (Price et al., 1996).

In Arabidopsis, fruit dehiscence is accelerated by high ambient temperature (Fig. 1; Li et al., 2018). *INDEHISCENT (IND)*, a transcription factor specifically expressed at the fruit valve-replum junction, positively regulates fruit opening (Liljegren et al., 2004; Ogawa et al., 2009). Expression of *IND* is significantly increased at 27°C compared with 17°C, seemingly independently from its upstream transcriptional regulators (Li et al., 2018). Intriguingly, the thermal induction of

IND expression is promoted by the eviction of histone H2A.Z from its promoter (Li et al., 2018). As expected, early dehiscence could also be observed in the loss-of-function *arp6* mutants (Li et al., 2018). This also suggests that transcriptional regulation by chromatin dynamics is conserved across different processes and developmental stages, from general thermal responsive factors (such as *HEAT SHOCK PROTEIN70*; Kumar and Wigge, 2010) to flowering genes (such as *FT*; Kumar et al., 2012) and fruit dehiscence regulators (such as *IND*; Li et al., 2018).

FEELING THE HEAT UNDERGROUND: ROOT THERMOMORPHOGENESIS

Increased temperature can affect root growth, either directly or indirectly via signaling of the shoot for water and nutrient demand or via carbon supply from the shoot to the root (Heckathorn et al., 2013). However, it was recently shown that the primary root can autonomously sense and respond to high temperature (Bellstaedt et al., 2019). While the associated molecular mechanism is largely unknown, the stability of the auxin receptor TIR1, for example, is positively regulated by the heat shock protein HEAT SHOCK PROTEIN 90 at high temperature (29°C; Fig. 4). This boosts auxin signaling at high temperature and enhances primary root growth and lateral root formation (Wang et al., 2016). Furthermore, temperature-dependent root growth is regulated by intracellular distribution of auxin (Feraru et al., 2019). At high temperature (29°C), the intracellular auxin carrier PIN-LIKES6 is less stable in the root meristem (Feraru et al., 2019). This increases nuclear distribution of auxin and auxin signaling in the root meristem, which contributes to promotion of root growth at high temperature.

BRs also play a role in root responses to high temperature, but independently of auxin or players that regulate the shoot thermomorphogenesis response. Elevated ambient temperature reduces the level of the BR receptor BRI1, likely by controlling BRI1 ubiquitination status, to negatively regulate BR signaling and root growth (Martins et al., 2017).

Of note, while root growth is unquestionably affected by increased temperature (Fig. 1), root thermomorphogenesis is not consistently observed in different species or experimental setups (Gladish and Rost, 1993; Seiler, 1998; Martins et al., 2017). For example, in contrast to the observations mentioned above in Arabidopsis, both lateral and primary root growth of garden pea (*Pisum sativum*) are inhibited by 32°C (Gladish and Rost, 1993).

TEMPERATURE COORDINATES THE THERMOMORPHOGENIC GROWTH AND PLANT IMMUNITY TRADEOFF

Plants have developed two different lines of defense against pathogen infection (Bigeard et al., 2015). First,

plants can perceive pathogens by recognition of microbe-associated molecular patterns by pattern-recognition receptors, inducing pattern-triggered immunity. Second, effector molecules synthesized by pathogens can be injected into the plant cells to weaken the cell for further infection and induce effector-triggered immunity (ETI). Elevated temperature increases susceptibility toward infection in Arabidopsis and other plant species, mainly via inhibition of ETI (Cheng et al., 2013). The reduced ETI response is also observed for the constitutively thermoresponsive *arp6* mutants. Furthermore, the biosynthesis and accumulation of salicylic acid, which is pivotal for defense against pathogens, are suppressed at high temperature, enhancing pathogenesis (Huot et al., 2017).

As a result of infection, at optimal growth temperature, plant growth is repressed in favor of defense against pathogens (Alcázar and Parker, 2011; Wang and Wang, 2014). However, high temperature is inhibitory to immunity and promotes growth (Alcázar and Parker, 2011). For example, growth defects and autoimmunity in *snc1-1*, a gain-of-function mutant in *SUPPRESSOR OF npr1-1*, *CONSTITUTIVE1* (*SNC1*), are abolished at 28°C (Zhu et al., 2010). Temperature induces the expression of *HOPZ-ETI-DEFICIENT1* (*ZED1*)-RELATED KINASES and *TEOSINTE BRANCHED1*, *CYCLOIDEA*, AND *PROLIFERATING CELL FACTOR* transcription factors (Wang et al., 2017, 2019). *ZED1* and *ZED1-RELATED KINASES* interact with *TEOSINTE BRANCHED1*, *CYCLOIDEA*, AND *PROLIFERATING CELL FACTORS* and repress *SNC1* expression to inhibit immunity at high temperature (Wang et al., 2017, 2019).

Interestingly, the DET1-COP1-PIF4 module integrates seasonal cues, such as light and temperature, to coordinate immunity and growth (Gangappa et al., 2017; Gangappa and Kumar, 2018). The loss-of-function *pif4* mutant shows an increase in transcription of pathogenesis-related genes. Expectedly, enhancing PIF4 signaling via DET1 and COP1 activity increased susceptibility to infection even at low temperature (Gangappa et al., 2017; Gangappa and Kumar, 2018). In addition, by physically connecting COP1 and small ubiquitin-related modifier (SUMO) conjugation activity in nuclear bodies, the SUMO E3 ligase SAP and Miz1 (*SIZ1*) acts as a positive regulator of thermomorphogenesis (Hammoudi et al., 2018; Mazur et al., 2019). At the same time, *SIZ1* negatively regulates the immune response at high temperature. Hereby, *SIZ1* acts upstream of PIF4 and BZR1 via enhancement of COP1 activity by sumoylation. Therefore, *SIZ1* is another hub for the temperature-dependent tradeoff between growth and immunity.

CONCLUDING REMARKS AND FUTURE PERSPECTIVES

Molecular mechanisms that control a multitude of high temperature-mediated effects on plant growth and development are complex, including extensive cross talk with other pathways, such as hormone regulation

OUTSTANDING QUESTIONS

- Given that the phyabcde mutant transcriptome does not fully overlap with the high temperature - regulated transcriptome, it is likely that other thermosensors exist. What are these?
- What are the organ-specific high temperature sensing and signaling mechanisms?
- What is the identity of membrane-associated high temperature sensors, if any?
- Are the Arabidopsis-centered high temperature sensing and signaling mechanisms conserved in all plants, including crops?

and light signaling. PIF4 is considered as the central regulator of thermal response, with the majority of described thermoresponsive pathways converging at PIF4 (Fig. 4). Hereby, the effects of auxin, BRs, and GAs have been extensively explored (Stavang et al., 2009; Galvão et al., 2015; Martins et al., 2017; Ibañez et al., 2018; Martínez et al., 2018), and links between the phyB-PIF4 module with ABA, ethylene, and jasmonate have emerged in other biological contexts (Sakuraba et al., 2014; Song et al., 2014; Campos et al., 2016; Jin et al., 2018). It is furthermore important to note that depending on the developmental process, plant organ, or tissue, high temperature can lead, for example, to increased auxin levels, such as during hypocotyl elongation (Franklin et al., 2011; Sun et al., 2012), or decreased auxin levels, such as in Arabidopsis anthers resulting in male sterility or during apical hook opening in the dark (Sakata et al., 2010; Jin et al., 2018). This suggests that high-temperature responses are highly regulated, even on the level of the same set of temperature signaling molecules. There are thus many open questions that need to be tackled in the future (see “Outstanding Questions”).

Since a change in temperature can be detected at any location in the cell, we suspect that there are still other thermoresponsive pathways, which can act independently of phyB-PIF4, to be discovered. Nearly all analyses described above are performed in laboratory conditions, but diurnal and seasonal temperature fluctuations display specific magnitudes, rhythms, and durations, making it important to study plant developmental plasticity and the underlying molecular mechanisms in more natural conditions or even in the field (Song et al., 2018).

Here, we have mainly discussed the molecular regulation of developmental plasticity at high temperature in the dicot model plant Arabidopsis. Thus, a big remaining question is: is all of this relevant in other species, including crops? For example, high temperature-induced

hypocotyl elongation seems conserved among dicot crop species, such as cabbage (*Brassica oleracea*) and tomato (*Solanum lycopersicum*; Quint et al., 2016). However, in contrast to Arabidopsis (Capovilla et al., 2017), species such as *Chrysanthemum morifolium*, *Populus* spp., or *Boechea stricta* (the perennial relative of Arabidopsis) are delayed in flowering when the ambient temperature increases (Anderson et al., 2011; Hsu et al., 2011; Nakano et al., 2013). Therefore, it is important for future molecular studies to focus on specific and relevant high temperature-associated phenotypes in the crop of interest. In this context, some components associated with high temperature were already studied in other species, including monocot crops, such as the effect of high temperature on yield and the role of H2A.Z in *Brachypodium distachyon* (Boden et al., 2013), the role of phyB in rice (*Oryza sativa*) anther development and pollen viability (Sun et al., 2017), or the role of auxin in male sterility in wheat (*Triticum aestivum*) caused by high temperature (Sakata et al., 2010). Nevertheless, investigating whether central high-temperature sensing and response regulators are functionally conserved in crop plants is very much needed.

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