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MOTHER-OF-FT-AND-TFL1* represses seed germination under far-red light by modulating phytohormone responses in *Arabidopsis thaliana

SHORT TITLE: MFT represses germination under FR-light

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ABSTRACT

Seed germination in many plant species is triggered by sunlight, which is rich in the red (R) wavelength and repressed by under-the-canopy light rich in far-red (FR). R:FR ratios are sensed by phytochromes to regulate levels of gibberellins (GA) and abscisic acid (ABA), which induce and inhibit germination respectively. In this study we have discovered that, under FR light conditions, germination is repressed by MOTHER-OF-FT-AND-TFL1 (MFT) through the regulation of the ABA and GA signalling pathways. We also show that *MFT* gene expression is tightly regulated by light quality. Previous work has shown that under FR light conditions the transcription factor PHYTOCHROME-INTERACTING-FACTOR1 (PIF1) accumulates and promotes expression of *SOMNUS* (*SOM*) that, in turn, leads to increased ABA and decreased GA levels. PIF1 also promotes expression of genes encoding ABA-INSENSITIVE5 (*ABI5*) and DELLA growth-repressor proteins, which act in the ABA and GA signalling pathways respectively. Here we show that *MFT* gene expression is promoted by FR light through the PIF1/*SOM*/*ABI5*/DELLA pathway and is repressed by R light via the transcription factor SPATULA (*SPT*). Consistent with this, we also show that *SPT* gene expression is repressed under FR light in a PIF1 dependent manner. Furthermore, transcriptomic analyses presented in this study indicate that MFT exerts its function by promoting expression of known ABA induced genes and repressing cell wall expansion related genes.

SIGNIFICANCE STATEMENT

Seeds sense environmental conditions, such as light quality, to regulate their germination. Light enriched in the far-red wavelength, such as under-the-canopy light (shade), increases ABA and decreases GA levels, the phytohormones repressing and promoting germination respectively. We have discovered that *MFT* functions as a key repressor of germination under far-red light conditions by modulating ABA and GA responses.

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INTRODUCTION

The timing of seed germination is critical for the survival of plants and the completion of their life cycle. Environmental conditions regulate accumulation and perception of the gibberellins (GA) and abscisic acid (ABA) phytohormones, which promote and repress seed

germination respectively. GA triggers degradation of the growth-repressing DELLA proteins (1, 2), whereas ABA acts through ABA-response transcription factors such as ABA-INSENSITIVE3 (ABI3), ABI4 and ABI5 (3-5). ABA and GA do not exert their effects independently of each other, but rather interact in a complex crosstalk (6-9). During development on the mother plant, seeds acquire an ABA-dependent dormant state (primary dormancy), which prevents germination even under favourable environmental conditions and contributes to seed dispersal (10). Once developed, seeds undergo an after-ripening process resulting in a gradual loss of dormancy and increased ability to germinate when exposed to the right environmental conditions such as the appropriate quality of light.

Sunlight is enriched in the red (R) wavelength, whereas under-the-canopy light (shade) is rich in far-red (FR). *Arabidopsis thaliana* (*Arabidopsis*) has five phytochrome photoreceptors that perceive R and FR light and two of them, PHYA and PHYB, are essential in promoting seed germination (11, 12). Phytochromes are synthesized as inactive forms and become active in a light-quality dependent manner. Excess of R and FR light activates and inactivates PHYB, respectively (13). In the dark, the active PHYB also reverts to its inactive form through a phosphorylation-dependent process (14). Unlike PHYB, PHYA is irreversibly activated by both R and FR light and then subjected to proteasome-mediated degradation (13). Hence, FR light has opposite effects in PHYA and PHYB (*i.e.* while it activates PHYA, it deactivates PHYB). Also, the timing and length of FR light exposure affects PHYA and PHYB differently and, as a consequence, influences the germination response. Compared to PHYB, PHYA accumulates at high levels only after relatively long periods of seed imbibition and needs high levels of FR light to respond (8). Thus, under controlled experimental conditions, a pulse of FR light relatively early during seed imbibition (when PHYA is absent) is sufficient to deactivate PHYB, which leads to repression of germination; whereas a long FR-light pulse later in imbibition still deactivates PHYB while activates PHYA to induce germination. Upon activation, both PHYA and PHYB are translocated into the nucleus to induce proteasome-directed degradation of PHYTOCHROME-INTERACTING-FACTORS (PIFs), which are a sub-family of basic helix-loop-helix (bHLH) transcription factors possessing an active phytochrome binding (APB) domain (15). In *Arabidopsis*, PIF1 (previously known as PIL5) plays a major role in the repression of seed germination (16, 17). PIF1 directly promotes expression of *ABI5* and the DELLA-encoding *GA-INSENSITIVE* (*GAI*) and *REPRESSOR-OF-GAI* (*RGA*) genes (18). PIF1 also promotes expression of *SOMNUS*

(*SOM*), which encodes a CCH-type zinc finger protein that regulates expression of genes leading to increased and decreased accumulation of ABA and GA, respectively (19).

SPATULA (SPT) is another bHLH transcription factor closely related to the PIFs, but it lacks the APB domain (20). SPT was originally described as a regulator of gynoecium development (21) and is also involved in regulating vegetative growth and seed dormancy (22-24). SPT regulation of seed dormancy involves the direct repression of *MOTHER-OF-FT-AND-TFL1* (*MFT*) (25). *MFT* is a member of the phosphatidyl ethanolamine-binding protein (PEBP) family, which is involved in diverse growth and differentiation signalling pathways in bacteria, animals and plants. In *Arabidopsis* there are six PEBP proteins and extensive analyses of two of them, *FLOWERING-LOCUS-T* (FT) and *TERMINAL-FLower1* (TFL1), have demonstrated that they antagonistically regulate flowering time and seed dormancy (26-29). In wheat it has been established that up-regulation of *MFT* expression by cold during seed development or by a mutation in its promoter leads to strong seed dormancy (30, 31). In *Arabidopsis* *MFT* is also a strong promoter of seed dormancy (25), but its expression is only weakly promoted by low temperature during seed development (32). However, *MFT* expression in the soil seed bank is seasonally regulated and correlates with low temperatures and high levels of cycling secondary dormancy (33). Furthermore, expression of *MFT* has also been shown to be promoted by ABA and DELLA proteins (34). Intriguingly, we and others have found that while freshly-matured *MFT* deficient seeds are less dormant than wild-type seeds, after-ripened (non-dormant) seeds are, counter-intuitively, more sensitive to ABA treatments (25, 34). This raised the possibility that *MFT* has opposite roles in regulating seed dormancy and non-dormant seed germination.

In the present study, we investigate the role of the *MFT* gene in regulating germination of after-ripened seeds under R and FR light. We demonstrate that *MFT* is a key component of the PIF1-dependent pathway of repression of germination and acts by integrating ABA and GA signals. Furthermore, we show that expression of the *MFT* gene is regulated by light quality: While it is promoted by the PIF1/*SOM*/DELLA-pathway under FR light, it is repressed by SPT under R light. Consistent with this, we also show that FR light represses *SPT* gene expression also in a PIF1-dependent manner. Our genetic, physiological and transcriptomic analyses reveal that *MFT* plays a major role in repressing seed germination by integrating the ABA and GA signalling pathways.

RESULTS AND DISCUSSION

MFT represses germination under FR light. We reported previously that freshly-matured *Arabidopsis* loss-of-function *mft-2* mutant seeds are less dormant than wild-type seeds, which led us to conclude that MFT promotes dormancy (25). However, ABA treatments of *mft-2* non-dormant seeds indicated that MFT promotes germination of after-ripened seeds (25, 34). This prompted us to investigate the role of MFT in regulating germination of non-dormant seeds under shade light conditions, which repress germination by inducing accumulation of endogenous ABA. In order to do this, germination assays were performed on control and *mft-2* after-ripened seeds (in the Col and *Ler* backgrounds) under different light treatments (*SI Appendix*, Fig. S1). Seeds were imbibed for three hours under white light, then treated with: (i) Two consecutive short (5 minutes) pulses of FR and R light (FR/R) to activate PHYB; (ii) a single FR light pulse (FR) to deactivate PHYB; and (iii) an initial short FR pulse followed (46-hours-after-imbition; hai) by a long (120 minutes) FR light exposure (FR-FR) to activate PHYA while also deactivating PHYB. We found that under FR/R light conditions wild-type and *mft-2* seeds germinate at similar high levels (80 %) (Fig. 1A-B). Upon FR treatments germination of wild-type seeds was, as expected, severely repressed (less than 5 %), whereas *mft-2* seeds germinated at higher rates (30-70 %) (Fig. 1A-B). We used an *mft-2* complemented line (33) to confirm that this mutant phenotype is due to a mutation in the *MFT* gene (*SI Appendix*, Fig. S2). Under FR-FR conditions germination rates of control seeds were, as expected, approximately intermediate (40 %) to those of FR/R and FR treated seeds; and *mft-2* seeds germinated at higher rates (70 %) than the controls (Fig. 1A-B). Taken together these observations demonstrate that MFT is required to repress germination under FR light conditions.

MFT promotes hypocotyl elongation in the dark. In addition to their role in seed germination, phytochromes and the PIF1-dependent pathway also control seedling hypocotyl elongation (35, 36). Thus, we investigated whether MFT also regulates seedling development and measured wild-type and *mft-2* hypocotyls of seedlings grown under dark conditions, which are known to trigger PHYB inactivation (14). We found that *mft-2* hypocotyls were significantly shorter than the wild-type controls (*SI Appendix*, Fig. S3) supporting the hypothesis that MFT promotes seedling hypocotyl elongation. These roles for MFT in repressing seed germination and promoting seedling hypocotyl elongation

parallel the established roles of the phytochrome interacting factor PIF1 (16, 17, 37, 38) and further indicates that MFT operates in the PIF1 pathway.

MFT is a positive regulator of ABA signalling. To investigate how MFT inhibits germination, we measured phytohormone levels in after-ripened seeds under FR light conditions (24 hai). ABA levels were actually elevated in FR-treated *mft-2* seeds compared to the wild-type (Fig. 2A) even though germination is higher in the mutant (Fig. 1A-B). This suggests that the inhibitory effect of MFT on germination of FR-treated seeds acts downstream of ABA. In order to test this hypothesis, we analysed triple *mft-2 cyp707a1-1 cyp707a2-1* mutant and control seeds. Both CYP707A1 and CYP707A2 are involved in ABA degradation, and double *cyp707a1-1 cyp707a2-1 (a1a2)* mutant seeds germinate poorly due to their elevated levels of endogenous ABA (39). Under FR-FR light conditions we found that the almost zero percentage germination phenotype of the *a1a2* double mutant is rescued by *mft-2* to levels that are intermediate between the wild type and the *mft-2* single mutant (Fig. 2B). We also performed germination assays of the after-ripened seeds under white light, and observed that whereas *a1a2* seed germination was impaired, *mft-2 a1a2* seed germination was almost as high as *mft-2* and wild-type control seeds (Fig. 3C). Considering that ABA induces *MFT* expression (34), these observations indicate that MFT is involved in the transduction of the ABA signal that results in germination inhibition. However, since the repression of germination in *a1a2* seeds is not completely removed in the *mft-2* background we conclude that not all of the ABA repression of germination is due to its effect on MFT. We and others have previously shown that *mft-2* seeds are hypersensitive to exogenous ABA treatment (25, 34). This contrasts with our present observation, which indicates *mft-2* to be hypo- rather than hypersensitive to elevated endogenous ABA in *a1a2* seeds (Fig. 2B-C). The hypersensitivity of *mft-2* to exogenous ABA also contrasts with studies analysing sensitivity of *mft-2* seeds to exogenous ABA during dormancy cycling (40). Thus, care needs to be taken when interpreting results from experiments using exogenous ABA.

We also measured GA accumulation in FR-treated seeds and observed no difference between *mft-2* and control seeds (Fig. 2D). However, we found that, under FR light, germination of *mft-2* seeds treated with the GA biosynthesis inhibitor paclobutrazol (PAC) was strongly inhibited (Fig. 2E), which shows that GA is required for *mft-2* seeds to germinate. We also compared the response to PAC of wild-type and *mft-2* non-dormant

seeds under white light. We found that both sets of seeds were equally affected by PAC treatments (Fig. 2F), demonstrating that high *mft-2* germination is not due to increased GA sensitivity.

***MFT* expression is promoted by FR light in a PIF1 pathway dependent manner.** Publically available transcriptomic data indicate that *MFT* gene expression is high during seed development when primary dormancy is set and, conversely, low in imbibed seeds when germination is triggered (vseed.nottingham.ac.uk). This prompted us to investigate whether light quality plays a role in regulating *MFT* expression in imbibed seeds. To test this we quantified *MFT* transcript accumulation in FR/R and FR light treated after-ripened seeds 12 and 24 hai. We observed that, compared to FR/R, *MFT* transcript accumulation is strongly induced under FR light conditions (Fig. 3A). Moreover, we established that this FR-triggered increase of *MFT* expression is strongly compromised (over 20 fold) in *pif1-1* mutant seeds (Fig. 3B), which are impaired in the FR-dependent repression of germination (18). Since active PHYA represses PIF1 accumulation, we also analysed *phyA-211* mutant seeds under FR-FR light conditions and found increased *MFT* transcript accumulation (*SI Appendix*, Fig. S4). This is consistent with our finding that *MFT* expression is positively regulated by PIF1 (Fig. 3B).

As a member of the bHLH-family of transcription factors, PIF1 preferentially binds to G-box motifs (41). Since the *MFT* promoter harbours three G-box motifs (25), we investigated by chromatin immuno-precipitation (ChIP) followed by quantitative PCR (qPCR) whether PIF1 binds the *MFT* promoter in FR-treated seeds but we found no evidence of such an interaction (*SI appendix*, Fig. S5). This indicates that the PIF1 involvement in promoting *MFT* expression under FR conditions is likely to be indirect. It is known that PIF1 does interact directly with the promoters of *SOM* and *ABI5* as well as the DELLA-encoding *RGA* and *GAI* genes (18, 19). It was previously shown in imbibed seeds under white light that *MFT* expression is promoted by ABA and repressed by GA in an *ABI5* and DELLA dependent manner, respectively (34). This prompted us to test whether this regulation also occurs under FR light conditions. We analysed *som-3*, *abi5-7* and quadruple *rgl1-1 rgl2-2 gai-6 rga-2* (hereafter referred to as *della4*) mutant seeds and found that *MFT* expression is decreased in all three mutant backgrounds (Fig. 3C-E), which indicates that *MFT* expression is promoted by these factors acting downstream of PIF1.

It is worth noting that the decrease of *MFT* transcript accumulation in *pif1-1*, *som-3* and *della4* seeds is much more pronounced (15 to 20-fold) than its decrease in *abi5-7* seeds (3-fold) (see Fig. 3B-E). This shows that, relative to PIF1/SOM/DELLA, ABI5 is a weak promoter of *MFT* expression. Interestingly, while *pif1-1*, *som-3* and multiple combinations of *della* mutant seeds germinate under FR light (17, 19, 42), *abi5* mutant seeds do not (8). This suggests that the relatively high levels of residual *MFT* transcript in *abi5* mutant seeds may be sufficient to repress germination under FR light conditions.

SPT represses both *MFT* and *ABI5* gene expression in imbibed seeds. We showed previously that freshly-matured *spt-2* mutant seeds (in the *Ler* background) are extremely dormant, but their dormancy is lost over dry storage, and after-ripened *spt-2* seeds germinate as much as *Ler* control seeds (22). In freshly-matured dry seeds, SPT binds to the *MFT* and *ABI5* promoters to repress and promote their expression respectively. However, at least in the case of SPT-*MFT*, this direct interaction is lost in imbibed seeds (25). We therefore reassessed the role of SPT in regulating these genes in developing and imbibed seeds. As previously reported in dry seeds, *MFT* transcript accumulation is increased in both developing and imbibed *spt-2* seeds (Fig. 4A); which indicates that SPT represses *MFT* expression in seeds irrespective of their developmental stage. Regarding *ABI5*, we found that its expression is decreased in developing *spt-2* seeds, which is consistent with our previous finding for dry seeds. However, *ABI5* expression is increased in imbibed *spt-2* seeds (Fig. 4B). Thus, SPT promotes *ABI5* expression in developing seeds and represses it in imbibed seeds. Using ChIP-qPCR assays, we found no evidence for direct interaction of SPT with *MFT* or *ABI5* in imbibed seeds (*SI Appendix*, Fig. S5).

SPT expression is repressed by FR light in a PIF1 pathway dependent manner. We next investigated whether *SPT* expression is regulated by light quality. We established that, compared to FR/R conditions, *SPT* transcript accumulation is inhibited by FR light in a PIF1 pathway dependent manner (Fig. 4C-D). Consistent with this, we also established that PHYA promotes *SPT* expression (*SI Appendix*, Fig. S4). ChIP-qPCR assays established that repression of *SPT* by PIF1 is likely to be indirect (*SI Appendix*, Fig. S5). Furthermore, genetic analysis revealed that *SPT* gene expression is repressed by SOM and DELLA proteins, although the repressing effect of the latter appears to be weaker (Fig. 4E-F). Finally, we also

assessed germination under FR-FR light conditions of *spt-2 mft-2* double mutant and *Ler* and parental control seeds. We found that *spt-2* seeds germinate at a lower rate than *Ler* control seeds and, importantly, *spt-2 mft-2* seeds germinate as much as the single *mft-2* mutant seeds (Fig. 4G), which is consistent with our previous observation in freshly-harvested seeds, and shows that MFT acts downstream of SPT in the light quality regulation of germination.

MFT regulates expression of growth related genes. It has been established that MFT localises in the nucleus and interacts indirectly with DNA to regulate gene expression (34, 43). In order to gain insight into the MFT mode of action, we performed RNA-sequencing based transcriptomic analyses to identify genes regulated by MFT. We analysed wild-type (*Col*) and *mft-2* after-ripened seeds under FR/R and FR light conditions (24 hai). We made two sets of gene expression profile comparisons from three transcriptomic datasets: (i) FR vs FR/R treated *Col* seeds (*Col_{FR}* vs *Col_{FR/R}*), and (ii) FR treated *Col* seeds vs FR treated *mft-2* seeds (*Col_{FR}* vs *mft-2_{FR}*). We reasoned that genes that are up-regulated by the MFT mediated FR light response will show increased expression in *Col_{FR}* compared to *Col_{FR/R}* and *mft-2_{FR}*. Similarly, genes that are down-regulated by MFT will have decreased expression in *Col_{FR}*. Using at least a two-fold difference threshold in each comparison, we found 175 MFT up-regulated genes and 74 MFT down-regulated genes (Dataset S1 and S2).

Among the MFT up-regulated group are *MFT* itself and genes known to be induced by ABA and involved in ABA signalling such as *ABI2*, *PYL13/RCAR7* and *GCR2/GPCR*, although the role of the latter in this pathway has been controversial (44-46). The gene most strongly up-regulated by MFT is *PLP1/PLAVIA*, which encodes a phospholipase known to promote hypocotyl elongation (47). Also among this group of MFT up-regulated genes are *CAT1*, which is known to act downstream of *ABI5* to regulate reactive oxygen species (ROS) homeostasis in germinating seeds (48); and *DOGL1*, *DOGL2* and *DOGL3*, which are closely related to the strong dormancy promoter DELAY-OF-GERMINATION1 (*DOG1*) (49). Notably, another of the genes up-regulated by MFT, *NCED4/CCD4*, encodes a negative regulator of β -carotene, a biosynthetic precursor of ABA (50, 51). Thus, it is possible that the higher-than-normal ABA levels found in *mft-2* seeds is a consequence of the decreased *NCED4/CCD4* transcript abundance and a concomitant increase of β -carotene. MFT also promotes expression of genes involved in seed development and seed storage, as well as in lipid metabolism including oxylipin biosynthesis. *AOS/CYP74A*, which is involved in an early step

in the biosynthesis of the oxylipin 12-oxo-phytodienoic acid (OPDA) (52), is up-regulated by MFT. We reported previously that OPDA is a potent repressor of germination that interacts with MFT and ABA in a complex network of feedback interactions (53, 54). We are currently investigating the role of OPDA in the repression of germination by FR light.

SPT gene expression is 11-fold decreased by FR light and MFT partially contributes to this repression, highlighting the complex feedback interactions between these two key players. Many of the other MFT down-regulated genes are predicted to be involved in cell wall metabolism, response to GA and root growth. The *DVL19/RTFL10* gene, belonging to the *DEVIL/ROTUNDIFOLIA* family, is the most strongly down-regulated by FR light and this appears to be completely dependent on MFT. Little is known about the function of this gene; however, overexpression of other members of this gene family results in elongated cells at the base of trichomes (55). Many genes involved in auxin signalling (for example *AUX1*, *HLS1/COP3*, *GH3.1/WES1*, *WOX11*, *SAUR77*, *PAP1/IAA26*) are also repressed by MFT, as well as *CYP90A1* involved in brassinosteroid biosynthesis. Both auxin and brassinosteroid phytohormones regulate a wide range of plant development and physiological processes and are recognised as positive growth regulators of root and shoot development (56). *GASA6*, *GASA14* and *EXPA1* are also repressed by MFT and are known to be promoted by GA and repressed by ABA and DELLA proteins. It has been reported that *GASA6* and *GASA14* promote cell elongation and leaf expansion, as well as seed germination (57, 58). *GASA6* requires the cell wall loosening function of *EXPA1* (59) and it is expressed in the hypocotyl-radical transition zone of the embryonic axis (58). This is consistent with the reported tissue specificity of *MFT* gene promoter activity in ABA treated seeds (34).

Conclusion. The integration of the data presented in this study with current knowledge of FR-light signalling allows us to propose a model (Fig. 5) in which MFT plays a key role in the integration of signals downstream of core signalling components and the antagonistically acting phytohormones ABA and GA. Previous reports have established that light activated phytochromes lead to PIF1 degradation (17) and, when phytochromes are deactivated, PIF1 accumulates and induces *SOM* expression. *SOM*, in turn, promotes and represses ABA and GA accumulation respectively (19). This then leads to repression of seed germination through a mechanism involving ABI5 and DELLA proteins (2, 4). In the present work, we have shown that *SOM* also represses germination through the promotion of the germination

inhibitor MFT. We show that this effect of SOM on MFT is due to SOM repressing SPT, which is a negative regulator of *MFT* expression. Our data also demonstrate that the growth repressing DELLA proteins inhibit and promote *SPT* and *MFT* expression respectively, which is entirely consistent with the fact that DELLAs accumulate under light conditions that repress germination. Furthermore, MFT is also promoted, albeit weakly, by ABI5 which itself is repressed by SPT. Our data also highlight that as well as acting downstream of ABA, MFT represses its accumulation. Thus, MFT counteracts the effect of SOM on ABA accumulation. Finally, while we show that MFT plays a key role in the integration of signalling downstream of ABA and GA, both phytohormones can still affect germination independently of MFT.

In summary, our findings establish that shade (FR light) promotes expression of *MFT*, which in turn represses germination by up and down regulating expression of genes involved in ABA signalling and cell wall expansion respectively. Moreover, we show that this MFT-dependent mechanism of germination inhibition is actively repressed by SPT under R light conditions that induce germination. Publically available data indicate that *MFT* is strongly expressed in the endosperm during the late stages of seed development (vseed.nottingham.ac.uk). It has been established that the endosperm plays a crucial role in promoting dormancy and repressing germination of non-dormant seeds under FR light conditions (7, 8). Whether MFT plays a role in this endosperm-based pathway leading to repression of germination remains to be established.

EXPERIMENTAL PROCEDURES

Growth conditions and biological materials. Plants were grown in a greenhouse supplemented with artificial light to give a photoperiod of 16 h light at a temperature of 20–22 °C. Seeds were harvested and after-ripened for at least 8 weeks before analyses. Original mutant and transgenic lines were described previously: *mft-2* (Col/Ler) and gMFT (34); *cyp707a1-1 cyp707a2-1 (a1a2)* (39); *pif1-1/pil5-1* (16); *som-3* (19), *rgl1-1 rgl2-2 gai-6 rga-2 (della4)* (2); *abi5-7* (60); *spt-2* (61); 35S:PIF1myc (18); 35S:SPTmyc (25).

Germination assays. Sterilized seeds were plated on water agar (0.9 % w/v) and allowed to imbibe under dim light for 3 hours and then LED-irradiated with FR ($4.5 \mu\text{mol m}^{-2} \text{s}^{-1}$) and R ($20 \mu\text{mol.m}^{-2} \text{s}^{-1}$) as indicated in Figure 1A. After FR/R, FR and FR-FR treatments plates were wrapped in foil and kept at 20 °C. Germination was scored on the basis of radical emergence

of 50-100 seeds *per* replica. Paclobutrazol (Sigma-Aldrich) was included in the water agar medium where indicated.

Phytohormone analyses. Phytohormones were extracted and quantified from four biological replicates of 100 mg of treated seeds according to the protocol described previously (53).

Molecular biology techniques. RNA extractions were performed as described previously (25). Standard protocols were used for RQ1 RNase-Free DNase treatments (Promega), cDNA synthesis (SuperScript®II, Invitrogen) and qPCRs (iTaQ™ Universal Syber® Green, Bio-Rad). Expression of *UBQ11* was used for normalization and gene expression was expressed as a fold change relative to the control sample. ChIP assays were performed as described previously (18) followed by qPCR and DNA amplification normalized to the amplification of *UBQ11* and expressed relative to the negative control (-Ab). Relative qPCR amplifications were calculated following the Delta-Delta Ct method ($2^{-\Delta\Delta Ct}$). Primer sequences for the qPCRs are described in *SI Appendix*, Table S1.

Transcriptomic analyses. RNA yield from three independent biological samples was quantified and quality checked using a Nanodrop spectrophotometer and Agilent bioanalyser RNA nano chip. 500 ng of total RNA was used for library preparation using the NEBNext RNA Ultra Library preparation kit for Illumina in conjunction with the NEBNext Poly(A) mRNA Magnetic Isolation Module (New England BioLabs Inc.), and NEBNext single 6bp indexing primers, according to the manufacturer's instructions. Libraries were pooled at equimolar ratios, and the pool was sent for 2 x 150 base paired end sequencing on a HiSeq 3000 at the University of Leeds Next Generation Sequencing Facility. Ribosomal RNA was filtered with mapping to rRNA_115_tax_silva_v1.0 downloaded from SILVA database (<https://www.arb-silva.de/>). The remaining RNAseq reads were mapped to the cDNA reference sequence from TAIR10. BWA (62) was used with default parameters for mapping. Samtools (63) was used for read quantification (*SI Appendix*, Table S2). The methods in Bioconductor package EdgeR (64) were used to identify the differential expressed genes from comparisons described in the main text. Only genes with at least a two-fold change in each of the two comparisons, and a minimum of 5 RPKM in Col_{FR} (for MFR promotion) or Col_{FR/R} and *mft-2_{FR}* (for MFT repression), were considered in the analyses. Raw RNAseq data has been deposited at the NCBI (ID PRJNA471797).

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FIGURE LEGENDS

Fig. 1. Germination of *mft-2* seeds under different light quality treatments. (-B) Control and *mft-2* after-ripened seeds (in Col and Ler backgrounds) upon FR/R, FR and FR-FR light treatments as indicated in *SI Appendix*, Fig. S1. Data are means of four biological replicates and error bars represent standard deviation. Different lower case letters indicate statistically significant differences (*t*-test, $p < 0.01$).

Fig. 2. Phytohormone and germination analyses of *mft-2* seeds. (A) ABA accumulation in FR-treated wild-type (Col) and *mft-2* seeds (24 hai). (B-C) Germination assays of Col, single *mft-2*, double *cyp707a1-1 cyp707a2-1* (*a1a2*) and triple *mft-2 a1a2* mutant non-dormant seeds upon FR-FR (B) and white light (WL; C) conditions. (D) GA (GA_4) accumulation in FR-treated wild-type (Col) and *mft-2* seeds (24 hai). (E-F) Germination assays of Col and *mft-2* seeds on control (-PAC) and paclobutrazol supplemented plates under FR (+PAC, 10 μ M; E) and WL light conditions (+PAC, 5 and 10 μ M; F). Phytohormone and germination data are means of four biological replicas and error bars represent standard deviation. Different lower case letters indicate statistically significant differences (*t*-test, $p < 0.01$).

Fig. 3. Characterisation of *MFT* gene expression. (A) Relative *MFT* expression in FR/R and FR-treated wild-type (Col) seeds (12 and 24 hai). (B-E) Relative *MFT* expression in FR-treated *pif1-1*, *som-3*, *della4* (*rgl1-1*, *rgl2-2*, *gai-6* and *rga-2*) and *abi5-7* mutant seeds and their respective Col/Ler controls (24 hai). Data are means of three biological replicates and error bars represent standard deviation. Different lower case letters indicate statistically significant differences (*t*-test, $p < 0.01$).

Fig. 4. The role of *SPT* in light-quality dependent germination. (A-B) Relative *MFT* and *ABI5* expression in developing (Dev) and stratified imbibed (Imb) control (Ler) and *spt-2* seeds. (C) Relative *SPT* expression in FR/R and FR-treated wild-type (Col) seeds (12 and 24 hai). (D-F) Relative *SPT* expression in FR-treated *pif1-1*, *som-3* and *della4* (*rgl1-1*, *rgl2-2*, *gai-6*, *rga-2*) mutant seeds and their respective Col/Ler controls (24 hai). (G) Germination assays of Ler, *spt-2*, *mft-2* and *spt-2 mft-2* after-ripened seeds under FR-FR light conditions. Error bars represent standard deviation of at least three biological replicates. Different lower case letters indicate statistically significant differences (*t*-test, $p < 0.05$).

Fig. 5. The role of *MFT* and *SPT* in the light-quality dependent regulation of seed germination. PHYB, which is present at the onset of imbibition, is activated and deactivated by R and FR light respectively (a). PHYA, which accumulates a few hours after imbibition, is activated by FR light (b). Active phytochromes (PHYA*, PHYB*) trigger PIF1 degradation (c). In the absence of PHYA* and PHYB* PIF1 accumulates to promote *SOM* expression (d). *SOM* induces ABA and inhibits GA accumulation (e, f), as well as repressing *SPT* expression (g). *SPT* represses *MFT* expression (h) and *MFT* partially contributes to *SPT* repression under FR light (i). ABA acts, at least partially, through *ABI5* (j), whereas GA triggers degradation of the DELLA proteins (k). The growth repressing DELLA proteins inhibit, albeit weakly, *SPT* expression (l) and promote *MFT* expression (m). *SPT* represses *ABI5* expression (n) and *ABI5* is a weak promoter of *MFT* expression (o). *MFT* inhibits seed germination (p) through regulation of growth related genes (not depicted in the model). *MFT* also represses ABA accumulation (q). Both ABA and GA have *MFT*-independent effects on germination (r, s).