Circadian and environmental signal transduction in a natural population of *Arabidopsis*

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Abstract

Plants sense and respond to environmental cues during 24 h fluctuations in their environment. This requires the integration of internal cues such as circadian timing with environmental cues such as light and temperature to elicit cellular responses through signal transduction. The integration and transduction of circadian and environmental signals within plants growing in natural environments remain poorly understood. To gain insights into the 24 h dynamics of environmental signalling in nature, we performed a field study of cell signalling in a natural population of *Arabidopsis halleri.* As a representative model signalling pathway, we exploited the transduction of circadian and environmental signals from the nucleus to chloroplasts, by a sigma factor, to study diel cycles of environmental signalling under natural conditions. Using dynamic linear models to interpret the data, we identified that circadian regulation and temperature are key regulators of this pathway under natural conditions. We identified potential time-delay steps between pathway components, and diel fluctuations in the response of the pathway to temperature cues that are reminiscent of the process of circadian gating. This approach allowed us to identify dynamic integration and transduction of environmental cues, in the cells of plants, under naturally fluctuating diel cycles.

Introduction

Plants have sophisticated environmental sensing and signalling mechanisms that underpin their responses to the fluctuating environment. Under naturally fluctuating conditions, this requires signalling pathways that integrate dynamic, overlapping and complex environmental stimuli [1, 2]. These environmental fluctuations include the 24 h changes in environmental conditions that arise from the cycle of day and night. The 24 h environmental fluctuations have selected for the evolution of circadian clocks, which are endogenous biological oscillators that produce a cellular estimate of the time of day. Over each day, circadian rhythms structure the responses of plants to environmental fluctuations by aligning transcription, metabolism and development with the daily fluctuating environment [3-8]. In plants, environmental information including the light and temperature conditions is used to adjust the phase of the circadian oscillator, through the process of entrainment, so that the phase is aligned with the 24 h environmental cycle. This alignment between the circadian oscillator and the 24 fluctuating environment contributes to the fitness of plants [5].

Under natural conditions, circadian timing information is combined with environmental cues to establish a temporal program of gene expression [9]. For example, 97% of diel transcript profiles in field-grown rice can be predicted from meteorological data [9], and temperature cues regulate the alternative splicing of transcripts encoding circadian oscillator components in field-grown sugarcane [10]. Recent studies have provided insights into the diel organization of the transcriptome and metabolism, under field conditions, for several crops and natural plant populations [9-17]. However, the diel dynamics of environmental signalling pathways, with defined inputs and outputs, are less well understood under natural conditions. Understanding signal transduction in plants under natural conditions is a valuable part of translating laboratory studies into crop improvement. For example, this could contribute to forecasting the responses of ecosystems and crops to increasingly unpredictable climates [18]. Experiments conducted in controlled conditions that mimic components of field conditions remain unable to replicate all aspects of plant gene regulation

under natural conditions [17], so field experiments provide valuable insights into plant environmental responses.

To study the integration and transduction of circadian and environmental signals under naturally fluctuating conditions, we selected a well-characterized environmental signalling pathway as an experimental model. This comprises the regulation by the circadian clock of SIGMA FACTOR 5 (SIG5), which in turn regulates the transcription of *psbD* (Fig. 1A). *CCA1* and *SIG5* are nuclear encoded, and *psbD* is chloroplast encoded. We chose this pathway because it is relatively straightforward, consisting of three major components, each of which provides distinct regulatory points of signal transduction. Therefore, the pathway provides a relatively low level of complexity to evaluate circadian and environmental signal integration and transduction under realistic field conditions. CCA1 is a key component of the Arabidopsis circadian oscillator, and *CCA1* transcript abundance can be used as a proxy for the status of the circadian oscillator (Fig. 1A). SIG5 is a nuclear-encoded regulator of chloroplast transcription, which is regulated closely by the circadian oscillator under constant conditions [20]. Based on its responses under controlled conditions [19-30], we hypothesized that under natural conditions SIG5 might integrate information concerning circadian regulation, light quantity, light quality, temperature, and abiotic stress. Therefore, *SIG5* transcript abundance presents a read-out several environmental signal integration processes (Fig. 1A). It is thought that SIG5 is imported into chloroplasts, and communicates the integrated environmental information to chloroplast gene expression by regulating transcription from the blue light responsive promoter of *psbD* (*psbD* BLRP) [22] that encodes the D2 protein of Photosystem II (Fig. 1A). This chloroplast transcript provides an experimental read-out of a later step in this signalling pathway (Fig. 1A) [19, 20, 22].

We investigated the temporal dynamics of this signalling pathway in a natural habitat of the perennial *Arabidopsis* species, *Arabidopsis halleri* subsp. *gemmifera* (referred to here as *A. halleri*) [55]. The close-relatedness of *A. halleri* and *A. thaliana* makes it possible to identify pairs of homologous genes based on the sequence similarity (indicated by *Ahg* or *At* prefixes

to gene names) [56]. The circadian clock-SIG5-*psbD* BLRP pathway is present in *A. thaliana* and *A. halleri*, and well-conserved across the vascular plants [31, 32]. We obtained a number of time series, during two seasons of the year, that monitored pathway function under representative light and temperature conditions. We interpreted these data using dynamic linear models, which are a type of state space model derived from control theory. In these models, the state of the system can be predicted from the prior state of the system, onto which can be superimposed external effects. This allows the estimation of the dynamics of the system that arise from its internal dynamics and external factors (such as environmental cues). Using this approach, we identified key roles for temperature and the circadian clock in the regulation of this pathway under natural conditions, and obtained evidence for temporal gating of responses of the pathway to environmental cues. Our approaches could be applicable to the study of many circadian-regulated processes under naturally fluctuating conditions.

Results

Biological data underlying models of signal transduction

Under controlled conditions of constant light, *AtCCA1* and *AtSIG5* transcript abundance are very well correlated (Fig. S1A-D; data from [20]). This correlation between *AtCCA1* and *AtSIG5* transcript abundance is absent under light/dark cycles (Fig. S1E, F), suggesting that the integration of light and dark cues alters the diel regulation of *AtSIG5* transcript accumulation [19, 20]. We acquired time-series of transcript abundance during spring (March) and autumn/fall (September), close to the spring or autumn equinox (Fig. 1B-K; Fig. S2). Although both the spring and autumn equinoxes share 12-h photoperiods, they provide contrasting temperature regimes (cool and warm, respectively) (Fig. 1B, C; Fig. S2A, B), with irradiance levels determined by weather conditions (Fig. 1D, E; Fig. S2C, D). This allowed us to investigate temperature, light and seasonal influences upon SIG5-mediated signalling to chloroplasts, because the pathway is known to be affected by light and temperature in *A.*

thaliana [19, 21, 22, 26, 31]. We obtained data from areas with open sky and with vegetational shade, to include within our models the transcriptional responses to a wider range of irradiance levels (Fig. 1D, E; Fig. S3). The “sun” and “shade” sampling sites were chosen by measurement of the ratio of red to far-red light (R:FR) (Fig. S3C, D) and availability of plant patches, because *A. halleri* does not grow in deep shade at this location. The total light intensity at the sun sampling site was 5 to 10-fold greater during March 2015 than during September 2015, depending on the time of day, due to weather differences (Fig. 1D, E). During March 2015, the study site temperature at both sun and shade sites ranged from 0 °C to 17 °C (Fig. 1B, C). The temperature was often above 20 °C during September 2015, with greater diel fluctuations at the sun site (Fig. 1B, C).

We compared the pathway dynamics between the spring and autumn sampling periods by using a smooth trend model, and identified differences in pathway regulation (Fig. 1F-K and Fig. S2E-J). We estimated the parameters of a smooth trend model by Bayesian inference to visualize the differences in transcript abundance between the spring and autumn sampling. The morning peak accumulation of transcripts encoding the circadian clock component *AhgCCA1* was significantly greater during the autumn sampling compared with the spring, under both light conditions tested (Fig. 1F, G). During both sampling seasons, *AhgSIG5* transcripts reached peak abundance between the middle and end of the photoperiod (Fig. 1H, I). This differs from the phase of *AtSIG5* transcript accumulation under square-wave light/dark cycles under controlled conditions, where *AtSIG5* transcript abundance peaks around dawn [20]. The peak of the diel fluctuation of *AhgSIG5* was significantly greater during the March sampling period than during the September sampling period (Fig. 1H, I). Furthermore, the pre-dawn accumulation of *AhgSIG5* transcripts occurred at an earlier time during the dark period during September than during March (Fig. 1H, I). This delay in pre-dawn transcript accumulation might be due to weaker circadian control during the spring sampling period, as suggested by the significantly decreased peak height of *AhgCCA1* transcript oscillations during March compared with September (Fig. 1F, G). Transcripts

encoding the SIG5 regulatory target *AhgpsbD* BLRP (Fig. 1A) had a significantly greater peak of accumulation during the September sampling season compared with the March season, but only under the shade light conditions (Fig. 1J, K).

AhgCCA1 transcript abundance was significantly greater under shade conditions during the photoperiod, during both sampling seasons (Fig. S2E, F). This is reminiscent of the greater *AtCCA1* promoter activity that occurs directly after dawn under controlled conditions of far red light compared with red light [33]. We did not identify the diminished *AtCCA1* oscillation that occurs under constant light with a very low R:FR [34] or on the shaded western side of crop fields around dawn [16]. As with *AhgCCA1*, *AhgSIG5* transcript abundance was significantly greater under shade than sun conditions, with this difference restricted to the end of the photoperiod (Fig. S2G, H). *AhgpsbD* BLRP transcript levels were unaltered by the two light environments (Fig. S2I, J).

Time delays between signalling pathway components

We assumed that SIG5-mediated signalling to chloroplasts involves a hierarchically-organized pathway, whereby *AhgCCA1* is positioned upstream from the regulation of *AhgSIG5* transcript accumulation, and *AhgpsbD* BLRP is positioned downstream of AhgSIG5 activity (Fig. 1A). We also assumed that environmental signals might influence *AhgCCA1*, *AhgSIG5* and *AhgpsbD* BLRP transcript accumulation independently (Fig. 1A) [35]. To understand the dynamics of this process, we first considered the temporal relationship between *AhgCCA1*, *AhgSIG5* and *AhgpsbD* BLRP transcript accumulation under natural conditions (*t*1, *t*2; Fig. 1A). The abundance of each of these related transcripts was monitored at each timepoint, but their responses to each other might not be instantaneous. For example, in *A. thaliana* under controlled square-wave light/dark cycle conditions, *AtCCA1* transcript abundance peaks at dawn, *AtSIG5* approximately 3 h after dawn, and *AtpsbD* BLRP approximately 6 hours after dawn [20]. Comparable dynamics are present in our field data, whereby *AhgCCA1* peaks at or after solar dawn (Fig. 1F, G),

AhgSIG5 mid-photoperiod (Fig. 1H, I), and *AhgpsbD* BLRP towards the end of the photoperiod under those conditions where it is rhythmic (Fig. 1J, K). Therefore, we reasoned that there would be a time lag in the regulation of *AhgSIG5* by *AhgCCA1* (*t1* in Fig. 1A), and in the regulation of *AhgpsbD* BLRP by *AhgSIG5* (*t2* in Fig. 1A).

We were interested to quantify these time lags, and use the information arising to construct models that assess the regulation of the pathway by specific environmental variables. We developed dynamic linear models that predict the abundance of *AhgSIG5* from *AhgCCA1* transcript abundance, and predict *AhgpsbD* BLRP from *AhgSIG5* transcript abundance, together with temperature and irradiance as explanatory variables. In these models, we used the transcript abundance of the upstream component as an explanatory variable, and the transcript abundance of the target component as a response variable within this analysis. Therefore, *AhgSIG5* is the response variable in the first model with *AhgCCA1* as the explanatory variable, whilst in the second model, *AhgSIG5* is used as the explanatory variable for *AhgpsbD.* We tested the quality of model fit for a range of time delays (lags) between the genes in the pathway (Fig. 1A). For this, we compared three model selection parameters to estimate the time delay that provides the best estimation of the downstream transcript (response variable). For a prediction of *AhgSIG5* from *AhgCCA1*, a model containing a 6 h time lag produced the best model fit, according to three model selection parameters (Fig. 2A, B, C). For a prediction of *AhgpsbD* BLRP from *AhgSIG5*, a model containing a 4 h time lag produced the best model fit for two out of three model selection parameters (Fig. 2D, E, F).

We detected differences between the two sampling seasons in the time lags that produced the best model selection parameters (Fig. S4). During the March sampling season, the best prediction of either *AhgSIG5* or *AhgpsbD* BLRP arose when time lags of 6-8 h (*AhgSIG5* prediction from *AhgCCA1*) and 4-8 h (*AhgpsbD* BLRP prediction from *AhgSIG5*) were tested (Fig. S4A-F). This was relatively longer than during the September sampling season, when time lags of 0 or 4 h (*AhgSIG5* prediction from *AhgCCA1*) and 4 h (*AhgpsbD* BLRP

prediction from *AhgSIG5*) produced the best model fit estimates (Fig. S4G-L). This suggests that the low temperature in March delays the speed of signal transduction. Taken together, these analyses suggest that time delays in signalling pathways are detectable under field conditions, and that environmental conditions (seasonal differences in temperature, or seasonal regulation) might affect the speed of signal transduction.

Dynamics of environmental regulation of signalling pathway

Environmental fluctuations are complex, noisy, and occur in simultaneous combinations. This presents a challenge for interpreting time-series transcript data from the field within the context of environmental signalling. We elaborated upon our modelling approach to investigate the relationship between key environmental variables and SIG5-mediated signalling to chloroplasts under field conditions. We used statistical models, rather than models of biochemical kinetics [36], because this provides an effective tool for interpreting diel and seasonal transcriptome dynamics [9, 12, 37, 38]. Comparable approaches have allowed the investigation of diel and seasonal changes of transcriptome dynamics in *A. halleri* [12, 37, 38] and rice [9].

We represented the behaviour of the pathway components using dynamic linear models, into which the time delays that produced the best model fit were incorporated (Fig. 2). The output of the Bayesian estimation reproduced well the essential dynamics of the observed *AhgCCA1* transcript level (Fig. 3A, B). The model estimated a significant positive relationship between ambient temperature and *AhgCCA1* transcript abundance between midnight and midday, with no effect of temperature at other times (Fig. 3C). There was no significant effect of irradiance upon the estimation of *AhgCCA1* transcript abundance (Fig. 3D).

Diel fluctuations of *AhgSIG5* transcript abundance were reproduced well by the model (Fig. 3E, F). We identified a significant negative correlation between ambient temperature and *AhgSIG5* transcript level towards the end of the light period (Fig. 3G), whereas there was no

significant effect of irradiance upon the prediction of *AhgSIG5* transcript abundance (Fig. 3H). *AhgSIG5* is regulated by the circadian clock, and we included within the model *AhgCCA1* transcript abundance as a proxy for circadian clock dynamics. There was a significant positive coefficient of regression between *AhgCCA1* and *AhgSIG5* during the dark period, and around the middle of the photoperiod (Fig. 3I).

Diel fluctuations of chloroplast *psbD* BLRP transcript abundance were also predicted well (Fig. 3J, K). In this case, there was a significant positive coefficient of regression between ambient temperature and *psbD* BLRP transcript abundance, which was restricted to the light period (Fig. 3L). There was no significant coefficient of regression between irradiance and *psbD* BLRP transcript abundance (Fig. 3M). *psbD* BLRP transcript accumulation is regulated in *A. thaliana* by SIG5 [22], and within our model, there was a significant positive coefficient of regression between *AhgSIG5* and *AhgpsbD* BLRP transcript levels during part of the light period (Fig. 3N).

Together, this analysis identifies that the ambient temperature, rather than the irradiance, was important for predicting the dynamics of all pathway components under naturally fluctuating conditions. In addition, the effect of the circadian clock (*AhgCCA1*) contributed to the prediction of *AhgSIG5* transcript abundance (Fig. 3I), and the effect of SIG5 contributed to the prediction of *AhgpsbD* BLRP transcript abundance (Fig. 3N). A feature within these predictions was the restriction to specific times of day of significant coefficients of regression between transcripts abundance and certain variables (such as for temperature in the prediction of *AhgCCA1* (Fig. 3C) and *AhgSIG5* (Fig. 3G)). These 24-h fluctuations in the coefficient of regression are suggestive of the concept of circadian gating, which is the process whereby the circadian clock constrains certain biological processes to specific times in the 24 h cycle [39]. In plants, this often takes the form of a circadian rhythm in the magnitude of the response to identical environmental stimuli given at different times of day [8].

Temporal gating of temperature regulation of SIG5-mediated signalling to chloroplasts under natural conditions

Our dynamic linear modelling analysis suggested that under natural conditions, greater ambient temperatures upregulate *AhgCCA1* and *AhgpsbD* BLRP transcript levels, whereas lower ambient temperatures upregulate *AhgSIG5* transcript levels (Fig. 3C, G, L). We tested this hypothesis by applying moderate temperature manipulations to adjacent patches of *A. halleri* plants, in the field, using custom-designed equipment (Fig. 4A; Fig. S5). We collected 24-h time-series of RNA samples from these plant patches, and interpreted the data with smooth trend models. The moderate temperature increase caused a small significant upregulation of *AhgCCA1* transcript abundance after dawn relative to the control, whereas the temperature reduction treatment was without effect (Fig. 4B). The moderate temperature increase was without effect upon *AhgSIG5* transcript abundance, whereas the temperature reduction treatment upregulated *AhgSIG5* transcripts significantly immediately after dawn, relative to the control, and caused a significant reduction in transcript abundance during the afternoon (Fig. 4C). This is consistent with the negative coefficient of regression between *AhgSIG5* and temperature under naturally fluctuating conditions (Fig. 3G), and with the upregulation of *A. thaliana SIG5* by a short cold treatment under laboratory conditions [22]. The restriction of the response of *AhgSIG5* transcripts to the moderate temperature reduction (Fig. 4C) is consistent with the 24-h cycle of the magnitude of the coefficient of regression of temperature for *AhgSIG5* transcript abundance (Fig. 3G). This further supports the notion of temporal gating of the influence of temperature upon this pathway under naturally fluctuating conditions.

Transcripts for the chloroplast target of SIG5, *AhgpsbD* BLRP, were also altered by temperature manipulation. The moderate temperature elevation significantly increased *AhgpsbD* BLRP transcript levels relative to the control, whereas the moderate temperature reduction significantly reduced *AhgpsbD* BLRP transcripts relative to the control. These significant alterations were restricted to the photoperiod, which might be because chloroplast

DNA binding and transcription by PEP generally requires light [40-44]. Furthermore, the positive regulation of *AhgpsbD* BLRP transcript abundance by the temperature manipulations (Fig. 4D) is consistent with the coefficient of regression between *AhgpsbD* BLRP transcript abundance and temperature under naturally fluctuating conditions (Fig. 3L).

Discussion

We established that circadian regulation and ambient temperature are potential regulators of *AhgSIG5*-mediated signalling to chloroplasts, in a natural population of *A. halleri*. Our analysis identified a significant regulation of *AhgSIG5* by *AhgCCA1* from midnight to morning (Fig. 3I), and significant regulation of *AhgpsbD* BLRP by *AhgSIG5* towards the end of the photoperiod (Fig. 3N). These significant relationships suggest that under natural conditions, a signal is communicated from the circadian oscillator (using *AhgCCA1* as a proxy) to the signalling pathway output of *AhgpsbD* BLRP. One interpretation is that the pathway couples the circadian oscillator and temperature response processes to chloroplast gene transcription under naturally fluctuating conditions.

We identified seasonal differences in the maximum accumulation of *AhgCCA1*, *AhgSIG5* and *AhgpsbD* BLRP. *AhgCCA1* and *AhgpsbD* BLRP had significantly lower peak accumulation during the spring sampling period compared with the autumn sampling season. In comparison, *AhgSIG5* had significantly greater peak accumulation during the spring compared with the autumn sampling season. The difference in *AhgCCA1* dynamics between these sampling seasons likely reflects the decreased amplitude of the circadian oscillator that occurs under lower temperature conditions, in both controlled environments and the field [12, 45-47]. The difference in dynamics of *AhgSIG5* compared with *AhgCCA1* suggests that an additional temperature input into this pathway occurs between the circadian oscillator and *AhgSIG5*. In *A. thaliana*, *SIG5* transcripts are upregulated by short cold temperature treatments [22] and in our field experiment, *AhgSIG5* transcript accumulation had a negative coefficient of regression with the temperature (Fig. 3G, Fig. 4C). This

negative coefficient of regression predicts that under lower temperature conditions, *AhgSIG5* transcript abundance will increase. Therefore, the lower temperatures of the spring sampling season compared with the autumn sampling season (Fig. 1A, B) might explain the greater levels of *AhgSIG5* transcript accumulation during the spring.

Because we considered *AhgpsbD* BLRP to represent the ultimate output from the signalling pathway (Fig. 1A), our analysis suggests that environmental inputs occurred within at least three positions in the pathway; first, in the regulation of *AhgCCA1* transcript accumulation by the season or temperature, second, in the regulation of *AhgSIG5* transcript accumulation by temperature, and, a third environmental input occurring downstream of *AhgSIG5* transcript accumulation for the regulation of *AhgpsbD* BLRP. This is evidenced by the differences in temperature responses of *AhgCCA1* (positive relationship), *AhgSIG5* (negative relationship), and *AhgpsbD* BLRP (positive relationship) (Fig. 3C, G, L). These environmental inputs might occur through biologically independent processes, such as temperature inputs to the circadian clock mediated by temperature-responsive components such as the evening complex [48, 49]. One of these mechanisms could be the regulation of *AhgSIG5* by HY5, which is a known regulator of SIG5 that participates in low-temperature gene regulation [22, 25, 50] and binds the SIG5 promoter in *A. thaliana* [51]. Furthermore, there might be direct effects of light upon sigma factor activity in chloroplasts through, for example, redox regulation [52] or light- and temperature-regulation of chloroplast protein import. We did not consider here the long history of light or temperature conditions upon leaves prior to experimentation [53], or other biotic or abiotic factors such as water availability, relative humidity, and atmospheric CO_2 concentration.

Statistical modelling of the transcriptome of field-grown *Oryza sativa* (rice) concluded that the main environmental driver of *OsSIG5* (*Os05g0586600*) transcript accumulation is temperature [9]. In this case, the temperature had a negative regression coefficient with *OsSIG5* [9]. This is consistent with our finding of a negative coefficient of regression between temperature and *AhgSIG5*. The study of the rice transcriptome in the field [9] did

not monitor chloroplast-encoded transcripts, so a direct comparison between *AhgpsbD* BLRP and our data is not possible.

A key finding from our work is the detection of a 24 h fluctuation in the coefficient of regression between the three genes and temperature (Fig. 3C, G, L). One interpretation of this is that there is a diel cycle of sensitivity of these pathway components to temperature cues, with their response to temperature restricted to certain times of day. This is reminiscent of circadian gating, which is the phenomenon whereby the circadian oscillator restricts the response to a stimulus to certain times of day [39]. These findings are corroborated by laboratory experiments, which demonstrate that the circadian oscillator gates its own response to temperature [54], and the response of *AhgSIG5* to blue light is gated by the circadian oscillator [20]. This is important, because it suggests that processes of circadian gating might operate under naturally fluctuating conditions to modulate the environmental responses of plants.

Our investigation provides insights into molecular aspects of signal transduction in plants under field conditions. This represents a relatively under-studied topic, and we developed new quantitative approaches to interpret transcript data collected under complex fluctuating environments, to investigate a specific pathway. This allowed us to identify potential time-delay steps within a signalling mechanism, multiple positions of environmental inputs, and temporal gating of a response to temperature. The approaches used provide a framework to study environmental signal integration in plants and other organisms under field conditions, which might be valuable to understanding rhythmic biological responses within an increasingly unpredictable climate.

Materials and Methods

Field site and plant material

Our experiments used a naturally-occurring population of *Arabidopsis halleri* subsp. *gemmifera* (Matsum.) growing beside a forested stream in Hyogo Prefecture, Japan (Omoide-gawa site; 35°06' N, 134°55' E, elevation 190–230 m) [12, 37, 55] (Fig. 1B, C). We selected *A. halleri* as an experimental model for several reasons [56]. First, it has a high nucleotide sequence identity and good synteny with *A. thaliana* [57]. Second, unlike *A. thaliana*, the perennial life history of *A. halleri* allows investigation of transcriptional responses across the seasons [2, 55]. Many individuals are clones because the species propagates by producing clonal rosettes as well as by seeds, which allows repeated sampling from single genotypes. Furthermore, *A. halleri* is metal tolerant and occurs in natural habitats that are relatively free from other vegetation due to contamination by heavy metals, which provides experimentally-convenient sites enriched with many *A. halleri* plants [58]. *Arabidopsis halleri* subsp. *gemmifera* at this site was previously identified by examination of museum and herbarium specimens, and a nearby population provided material for sequencing the *A. halleri* genome [55, 57]. Sampling occurred during 24 – 26 March 2015, 15 – 17 September 2015, and 13 - 14 September 2016, where March and September correspond to spring and autumn (fall) at the field site, respectively.

The *A. halleri* homologs of the *A. thaliana* genes *CCA1* and *SIG5* are loci *g25274* (*AhgSIG5*) and *g097040* (*AhgCCA1*), respectively. These were identified from *A. halleri* genome Version Ahal2.2 [57]. *AhgSIG5* has 94.9% coding sequence identity and 95.0% protein sequence identity with the *A. thaliana* homolog. *AhgCCA1* has 94.8% coding sequence identity and 93.3% protein sequence identity with the *A. thaliana* homolog. Chloroplast-encoded *psbDC* is not annotated within Version Ahal2.2 of the *A. halleri* genome, and we identified this instead within scaffold 2 of an *A. halleri* reference transcriptome [59]. The

AhgpsbD BLRP promoter region, which was our focus, has a 100% sequence identity with *psbD* BLRP of *A. thaliana* [41].

Sampling under natural and manipulated conditions

The first sets of samples were obtained under natural conditions without environmental manipulation. For this, we sampled during two different seasons, March 2015 and September 2015, on dates that were close to the spring and autumn equinox. We exploited variations in environmental conditions across the field site, and sampled leaves from the locations nominated as “sun” and “shade” sites. At “sun” locations, plants received direct sunlight during the day, and at “shade” locations plants received sunlight filtered by surrounding vegetation for most of the day with the sites identified by measurement of the ratio of red to far red light (Fig. S3; R:FR calculated as the photon irradiance from 660 to 670nm divided by the photon irradiance from 725 to 735nm [60]). In each case, sampling occurred for at least 24 h. During March 2015, plants received more direct sunlight, whereas during September 2015 the light was scattered through sky overcast with clouds.

We expanded the range of environmental conditions by manipulating the temperature conditions around patches of plants (September 2016). In addition to control plants that were not manipulated (Fig. S5A), we applied two temperature treatments. These were (1) a continuous temperature increase (Fig. S5B), whereby plants were covered with clear plastic horticultural domes to block air currents and trap warm air; (2) a continuous temperature reduction, using a custom device that passed air through a duct within a heat-exchanging ice-filled polystyrene box and expelled the chilled air into a clear horticultural dome covering the plants, with chilling augmented by small ice packs within the dome (Fig. S5C).

Field sampling for transcript analysis

Across all experimental conditions, the same sampling and RNA isolation procedures were used. At 2 h intervals, a fully expanded rosette leaf was excised with dissecting scissors

from 6 replicate plants for each condition. The time-courses using naturally occurring sun and shade conditions each comprised 13 sampling timepoints over a total of 26 hours, and the time-courses involving artificial temperature manipulations comprised 15 sampling timepoints over a total of 30 hours. Sampled leaves were placed immediately into individual microtubes containing at least 400 µL RNALater (Invitrogen). Scissors and forceps were cleaned with 70% (w/v) ethanol between samples. After sampling, tubes were placed temporarily on dry ice for up to 2 hours, at -40 °C for 3 days in a portable freezer during transfer to the laboratory, and then at -80 °C until RNA isolation. During hours of darkness, sampling occurred using green-filtered head torches. Each sampling timepoint was from the same set of replicate plants. We obtained a separate reference standard for all RT-qPCR experiments in the study, by pooling RNA from 10 leaves sampled at midday during March 2015 from healthy plants located randomly across the study site. This provided a reference cDNA sample against which all RT-qPCR analyses from all sampling seasons were normalized, to allow comparability between all datasets. This reference RNA sample was collected during March 2015. In all experiments, dawn and dusk were defined as the astronomical (solar) time of sunrise and sunset.

RNA isolation and RT-qPCR

Frozen samples containing RNALater were defrosted in a cold room for 4 hours, the RNALater was removed, and leaf tissue was transferred to new dry tubes and frozen in liquid nitrogen. Frozen tissue was ground with a TissueLyzer and total RNA was isolated from the powdered plant material using Macherey-Nagel Nucleospin II RNA extraction kits (Thermo-Fisher). cDNA was synthesized using a High Capacity cDNA Reverse Transcription Kit (Applied Biosystems) supplemented with RNAase inhibitor, as described previously [19, 20]. RNA concentrations were determined using a Nanodrop spectrophotometer (Thermo Scientific). cDNA was synthesized using an ABI High Capacity cDNA Reverse Transcription Kit (Applied Biosystems) according to the manufacturer's instructions, using random primers for the cDNA synthesis reaction. 1:500 cDNA dilutions were analysed using Brilliant III Ultra-

Fast SYBR Green QPCR master mix (Agilent Technologies) and required primer pairs (Table S2). Primers were designed using the PrimerQuest™ Tool from Integrated DNA Technologies. Results were normalized using the ΔΔCt method to *AhgACTIN2* [19, 20]. *AhgACTIN2* is encoded in *A. halleri* by locus *g21632* [57] and has 97.8% coding sequence identity with *A. thaliana ACTIN2* (*At3g18780*). Statistical comparisons within transcript abundance data were conducted using the SPSS software package.

Environmental monitoring

The temperature and irradiance were measured beside the plants during sampling. The temperature at each location, for each environmental manipulation, was monitored with EL-USB-2 data loggers (Lascar Electronics) at 5-minute intervals. Temperature loggers were wrapped in aluminium foil to prevent surface heating by solar radiation. Irradiance was measured using a CC-3-UV-S cosine corrector connected to a USB2000+ spectrometer with a QP400-2-UV-VIS fibre optic cable (Ocean Optics). Ambient light spectra (200 nm to 900 nm) were collected every 5 minutes over the 14 hours of light during each day of sampling using OceanView software (Ocean Optics) on a laptop PC, controlled by a custom script. The spectrometer and computer were powered using portable lithium battery packs (Powertraveller, Hampshire, UK).

Smooth trend model analysis

The smooth trend model (STM) to analyze the difference in transcript abundance between March and September under sun and shade conditions (Fig. 1) was defined by the equations:

$$\mu_{1,t} \sim Normal(2\mu_{1,t-1} - \mu_{1,t-2},\ \sigma_{\mu 1}^2), \quad (1)$$

$$\delta_t \sim Cauchy(\delta_{t-1},\ \sigma_{\delta}^2), \quad (2)$$

$$\mu_{2,t} = \mu_{1,t} + \delta_t, \quad (3)$$

$$y_{1,t} \sim Normal(\mu_{1,t},\ \sigma_y^2), \quad (4)$$

$$y_{2,t} \sim Normal(\mu_{2,t},\ \sigma_y^2), \quad (5)$$

where μ_1 and μ_2 are the smooth trend components in March and September in 2015, respectively, δ_t is the time-varying difference between the two seasons, and y_1 and y_2 are the observed transcript abundance in the two seasons. $t = (1, 2, \cdots, 13)$ is the time point at two-hour intervals. The same STM was used to analyze the difference in transcript abundance between sun and shade conditions in March and September (Fig. S1).

The parameters of the models were estimated by Bayesian inference. The statistical models were written in the Stan language and the programs were called by the rstan package (using version 2.21.0 of R). After 2,000 warm-up steps, 1,000 Markov Chain Monte Carlo (MCMC) samples were obtained by thinning out 6,000 MCMC samples for each of four parallel chains. Thus, 4,000 MCMC samples were obtained in total.

For the models of the three (ambient, warm and chill) conditions in the local environment manipulation experiment, additional δ, μ and y were considered:

$$\delta_{2,t} \sim Cauchy(\delta_{2,t-1},\ \sigma_{\delta 2}^2), \quad (6)$$

$$\mu_{3,t} = \mu_{1,t} + \delta_{2,t}, \quad (7)$$

$$y_{3,t} \sim Normal\left(\mu_{3,t},\ \sigma_y^2\right). \quad (8)$$

Dynamic linear model

The dynamic linear model (DLM) to analyze the time-varying effect of environmental variables on transcript abundance (Fig. 2) was defined by the equations:

$$\mu_t \sim Normal(\mu_{t-1},\ \sigma_\mu^2), \tag{9}$$

$$\beta_{temp,t} \sim Normal(\beta_{temp,t-1},\ \sigma_{\beta temp}^2), \tag{10}$$

$$\beta_{light,t} \sim Normal(\beta_{light,t-1},\ \sigma_{\beta light}^2), \tag{11}$$

$$\alpha_{MarSun,t} = \mu_t + \beta_{temp,t} \cdot temp_{MarSun,t} + \beta_{light,t} \cdot light_{MarSun,t}, \tag{12}$$

$$\alpha_{MarShade,t} = \mu_t + \beta_{temp,t} \cdot temp_{MarShade,t} + \beta_{light,t} \cdot light_{MarShade,t}, \tag{13}$$

$$\alpha_{SepSun,t} = \mu_t + \beta_{temp,t} \cdot temp_{SepSun,t} + \beta_{light,t} \cdot light_{SepSun,t}, \tag{14}$$

$$\alpha_{SepShade,t} = \mu_t + \beta_{temp,t} \cdot temp_{SepShade,t} + \beta_{light,t} \cdot light_{SepShade,t}, \tag{15}$$

$$y_{MarSun,t} \sim Normal(\alpha_{MarSun,t},\ \sigma_y^2), \tag{16}$$

$$y_{MarShade,t} \sim Normal(\alpha_{MarShade,t},\ \sigma_y^2), \tag{17}$$

$$y_{SepSun,t} \sim Normal(\alpha_{SepSun,t},\ \sigma_y^2), \tag{18}$$

$$y_{SepShade,t} \sim Normal(\alpha_{SepShade,t},\ \sigma_y^2), \tag{19}$$

where μ is the trend component, β is the time-varying regression coefficient, α is the true state of transcript abundance, y is the observed transcript abundance, and σ^2 is the variance. The subscripts, $temp$, $light$, Mar, Sep, Sun and $Shade$ represent temperature, irradiance, March, September, sun condition and shade condition, respectively. $t = (1, 2, \cdots, 13)$ is the time point at two-hour intervals.

In the *AhgSIG5* and *AhgpsbD* BLRP models, the effects of the upstream genes (i.e., *AhgCCA1* in the *AhgSIG5* model and *AhgSIG5* in the *AhgpsbD* BLRP model) were additionally considered. Thus, the equations of α are modified as follows:

$$\alpha_{MarSun,t} = \mu_t + \beta_{temp,t} \cdot temp_{MarSun,t} + \beta_{light,t} \cdot light_{MarSun,t} + \beta_{gene,t} \cdot gene_{MarSun,t}, \quad (20)$$

$$\alpha_{MarShade,t} = \mu_t + \beta_{temp,t} \cdot temp_{MarShade,t} + \beta_{light,t} \cdot light_{MarShade,t} + \beta_{gene,t} \cdot gene_{MarShade,t}, \quad (21)$$

$$\alpha_{SepSun,t} = \mu_t + \beta_{temp,t} \cdot temp_{SepSun,t} + \beta_{light,t} \cdot light_{SepSun,t} + \beta_{gene,t} \cdot gene_{SepSun,t}, \quad (22)$$

$$\alpha_{SepShade,t} = \mu_t + \beta_{temp,t} \cdot temp_{SepShade,t} + \beta_{light,t} \cdot light_{SepShade,t} + \beta_{gene,t} \cdot gene_{SepShade,t}, \quad (23)$$

where $gene$ is the mean transcript abundance of the upstream genes, and the other symbols are the same as above. The lagged effects of the upstream genes were tested by using values at previous time points (e.g., using $gene_{MarSun,t-1}$, $gene_{MarSun,t-2}$, $gene_{MarSun,t-3}$ or $gene_{MarSun,t-4}$ for $\alpha_{MarSun,t}$). The same DLM was used in Fig. 2 and S4.

The parameters of the models were estimated by Bayesian inference. The statistical models were written in the Stan language and the programs were compiled using CmdStan (version 2.24). To operate CmdStan, the cmdstanr package (version 0.4.0) of R was used. After 3,000 warm-up steps, 1,000 MCMC samples were obtained for each of the four parallel chains, and thus 4,000 MCMC samples were obtained in total.

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Author contributions

DLCR, HN, JS, MNH, HK and AND designed and performed experimentation; HN, DLCR, TM, LLBD, HK and AND analysed and interpreted data, and DLCR, HN, LLBD, HK and AND wrote the paper.

Competing interests

The authors declare no competing interests

Figure legends

Fig. 1. Components of a circadian signalling pathway have diel fluctuations in a natural plant population. (A) Potential architecture of a signal transduction pathway underlying SIG5-mediated signalling to chloroplasts, with environmental inputs occurring at several positions. *t1* and *t2* represent the time taken for signal transduction between each pathway component. (B-E) Diel fluctuations in (B, C) ambient temperature and (D, E) total irradiance detected (200-900 nm), measured at 5-minute intervals. (F-K) Bayesian estimation of smooth trend model (STM) for March and September 2015. The output of STM for (F, G) *AhgCCA1*, (H, I) *AhgSIG5* and (J, K) *AhgpsbD BLRP*. In F-K, the upper graphs show the predicted relative transcript abundance for March (pink) and September (brown) with the mean of observed values (dots), and the lower graphs represent the differences in transcript abundance between March and September. The solid line and the shaded region are the median and

the 95% credible interval of the posterior distribution. When the 95% credible interval of the difference between March and September does not contain zero, the difference is considered significant.

Fig. 2. Time-delay steps are predicted within this signalling pathway under naturally-fluctuating conditions. Lagged effects of variables in Bayesian estimation of dynamic linear models (DLM) for transcript levels during March and September 2015. (A, B, C) RMSE, log-likelihood and correlation of the models to predict *AhgSIG5* against the observed values, incorporating time lags of the upstream *AhgCCA1*. (D, E, F) RMSE, log-likelihood and correlation of the models to predict *AhgpsbD BLRP* against the observed values, incorporating time lags of the upstream *AhgSIG5*. The time lags of temperature and irradiance are set to 0. Asterisks represent (A, D) the lowest RMSE, (B, E) the highest log-likelihood and (C, F) the highest correlation. Error bars represent the 95% Bayesian credible intervals.

Fig. 3. The circadian clock and ambient temperature are key regulators of SIG5-mediated signalling to chloroplasts under naturally-fluctuating conditions. Bayesian estimation of the dynamic linear model (DLM) for March and September 2015. (A-D) The output of DLM for *AhgCCA1* where relative transcript abundance for (A) sun condition and (B) shade condition, with the coefficient of regression for (C) temperature and (D) irradiance. (E-I) The output of DLM for *AhgSIG5*, where (I) the coefficient of regression for *AhgCCA1* is shown, with other plots the same as (A-D). (J-N) The output of DLM for *AhgpsbD BLRP*, where (N) is the coefficient of regression for *AhgSIG5* is shown, with other plots the same as (A-D). The predicted relative transcript abundance for March (orange) and September (blue) are shown with the mean of observed values (dots). In each graph, the solid line and the shaded region are the median and the 95% credible interval of the posterior distribution.

Fig. 4. Prediction of diel rhythms of gating of temperature response in a natural plant population. Bayesian estimation of smooth trend model (STM) for temperature manipulation

experiments in September 2016. (A) Temperature changes during the study period in each condition. (B-D) The output of STM for (B) *AhgCCA1*, (C) *AhgSIG5* and (D) *AhgpsbD BLRP*. In each panel, the upper graphs show the predicted relative transcript abundance for ambient (black), warm (red) and cool (light blue) conditions with the mean of observed values (dots), and the lower graphs represent the differences in transcript abundance against the ambient condition. In each graph, the solid line and the shaded region are the median and the 95% credible interval of the posterior distribution. When the 95% credible interval of the difference between conditions does not contain zero, the difference is considered significant.

Fig. S1. Close relationship between *AtCCA1* and *AtSIG5* transcript abundance under free-running conditions in *A. thaliana* under controlled conditions. (A-D) Relationship between *AtCCA1* and *AtSIG5* transcript abundance under conditions of constant light, from the transcriptome studies of (A) [3] (B) [53], (C) [4], (D) [6]. (E, F) Relationship between *AtCCA1* and *AtSIG5* transcript abundance under light/dark cycles with (E) long and (F) short photoperiods, from the transcriptome study of [54]. Blue lines indicate a regression line. Pearson's correlation coefficient (R) with p-values testing for the likelihood of a chance correlation are shown for each plot.

Fig. S2. Components of a circadian signalling pathway have diel fluctuations in a natural plant population. Bayesian estimation of smooth trend model (STM) comparing sun and shade conditions, sampled during 2015. (A-D) Diel fluctuations in total irradiance detected (A, B; 200-900 nm) and (C, D) ambient temperature, measured at 5-minute intervals. (E-J) The output of STM for (E, F) *AhgCCA1*, (G, H) *AhgSIG5* and (I, J) *AhgpsbD* BLRP. In E-J, the upper graphs show the predicted relative transcript abundance for sun (orange) and shade (light grey) conditions, with the mean of observed values (dots). The lower graphs represent the differences in transcript abundance between sun and shade conditions. The solid line and the shaded region are the median and the 95% credible interval of the

posterior distribution. When the 95% credible interval of the difference between sun and shade conditions does not contain zero, the difference is considered significant.

Fig. S3. Effects of the ratio of red to far-red light upon *A. halleri* plants in the field, during March and September sampling seasons. (A, B) Examples of rosette-stage plants growing under (A) sun and (B) shade conditions during the September sampling season. (C, D) Comparison of the ratio of red to far-red light received by plants under the sun- and shade conditions during (C) March 2015 and (D) September 2015 sampling seasons. The R:FR varied during the photoperiod during both sampling seasons, and the effect of shade on R:FR was ameliorated by heavy cloud cover.

Fig. S4. The nature of the time-delay steps within this signalling pathway depends on the sampling season. Lagged effects of variables in Bayesian estimation of the dynamic linear model (DLM) for March and September separately in 2015. (A, D, G, J) RMSE, (B, E, H, K) log-likelihood and (C, F, I, L) correlation of the models to predict *AhgSIG5* in March against the observed values, incorporating time lags of *AhgCCA1*. (D-F) RMSE, log-likelihood and correlation of the models to predict *AhgpsbD* BLRP in March against the observed values, incorporating time lags of *AhgSIG5*. (G-I) RMSE, log-likelihood and correlation of the models to predict *AhgSIG5* in September against the observed values, incorporating time lags of *AhgCCA1*. (J-L) RMSE, log-likelihood and correlation of the models to predict *AhgpsbD* BLRP in September against the observed values, incorporating time lags of *AhgSIG5*. Time lags of temperature and irradiance are set to 0. Asterisks represent the lowest RMSE (A, D, G, J), the highest log-likelihood (B, E, H, K) and the highest correlation (C, F, I, L). Error bars represent the 95% Bayesian credible intervals.

Fig. S5. Moderate temperature manipulations to adjacent patches of *A. halleri* plants, in the field, using custom-designed equipment. (A) The representative appearance of plant patches under naturally fluctuating conditions. (B) Plants covered with a plastic dome to raise temperature. (C) Plants covered with plastic dome undergoing temperature reduction with a

custom chilling device. In this device, cool air is introduced to enclosed plant patches after being driven slowly through a heat exchanger, positioned within an expanded polystyrene box filled with ice.

Fig. S6. Location of field sampling. Photographs of (A) upstream and (B) downstream views of Omoide river site, which has naturally occurring populations of *A. halleri*. The majority of plants at ground level on the stony river banks are *A. halleri*.

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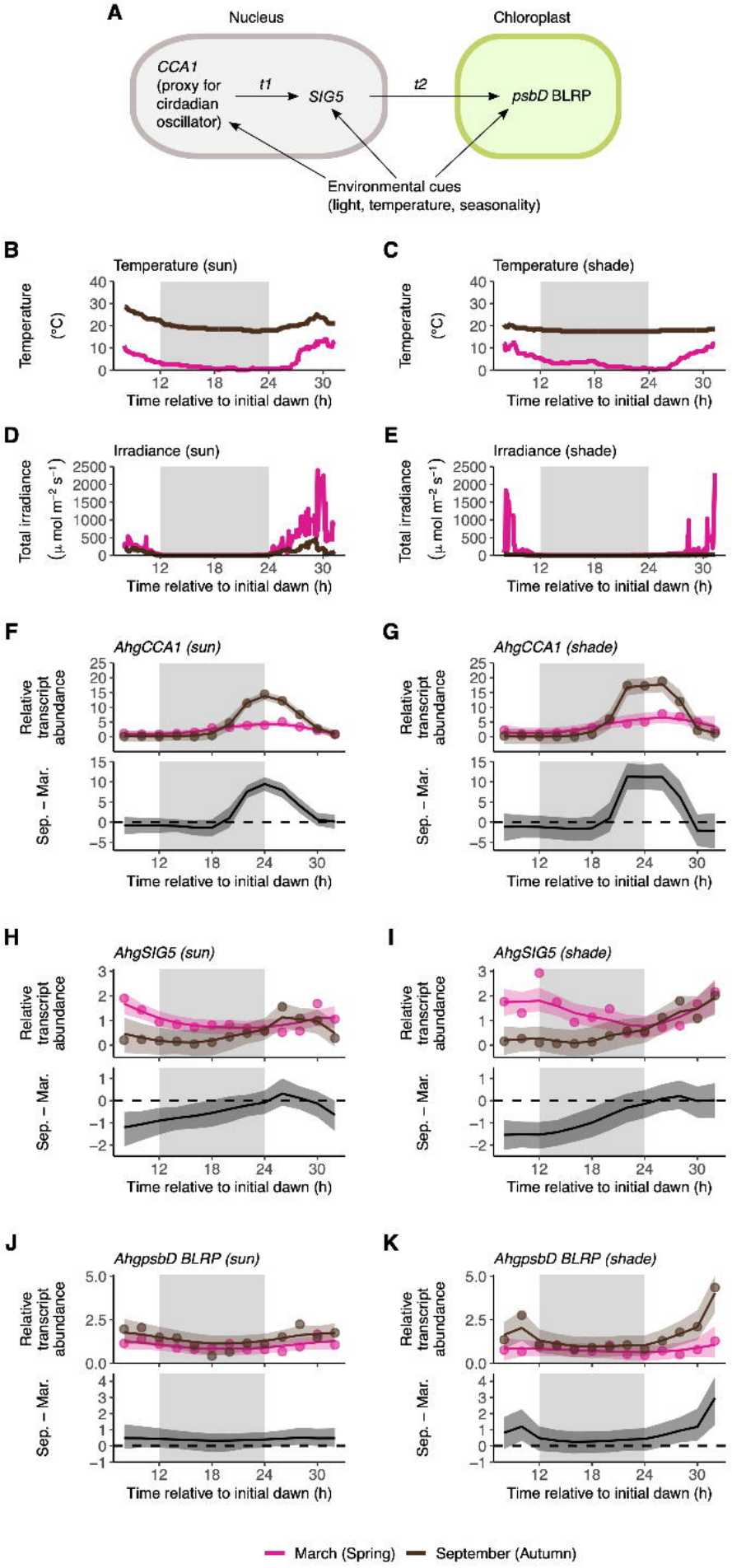
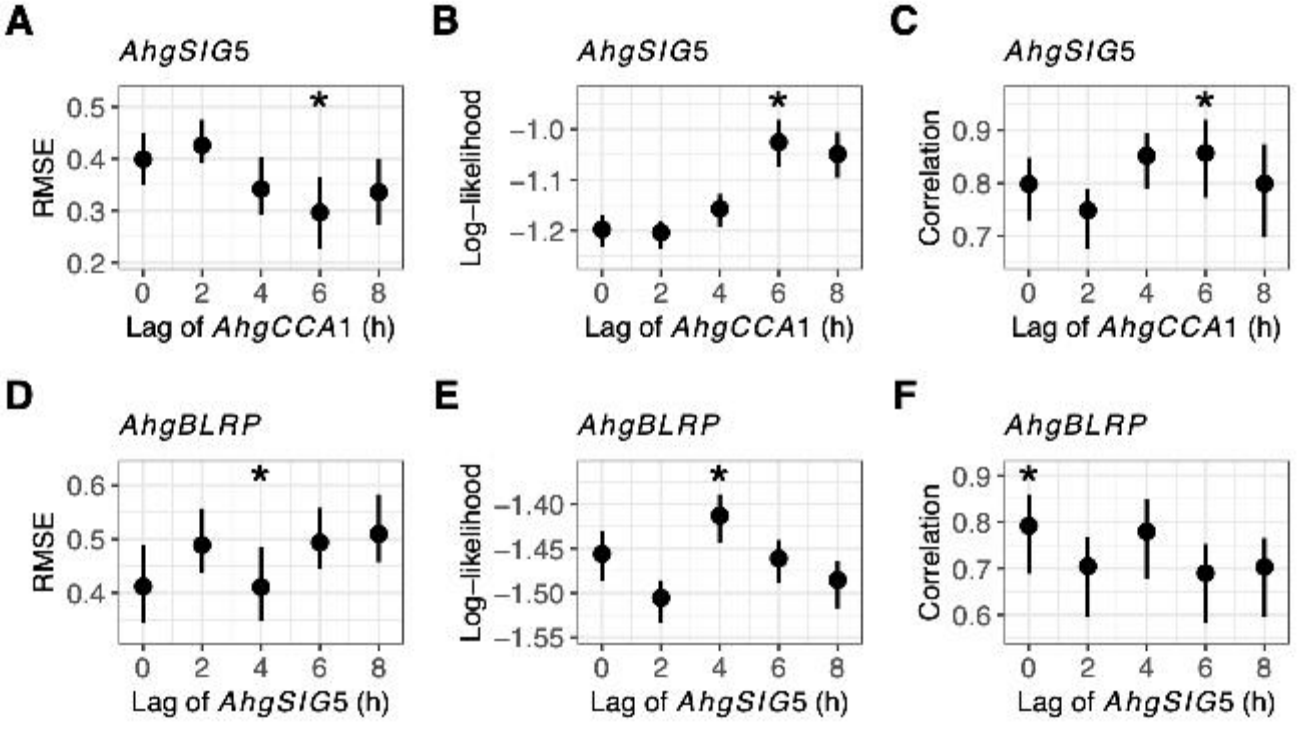
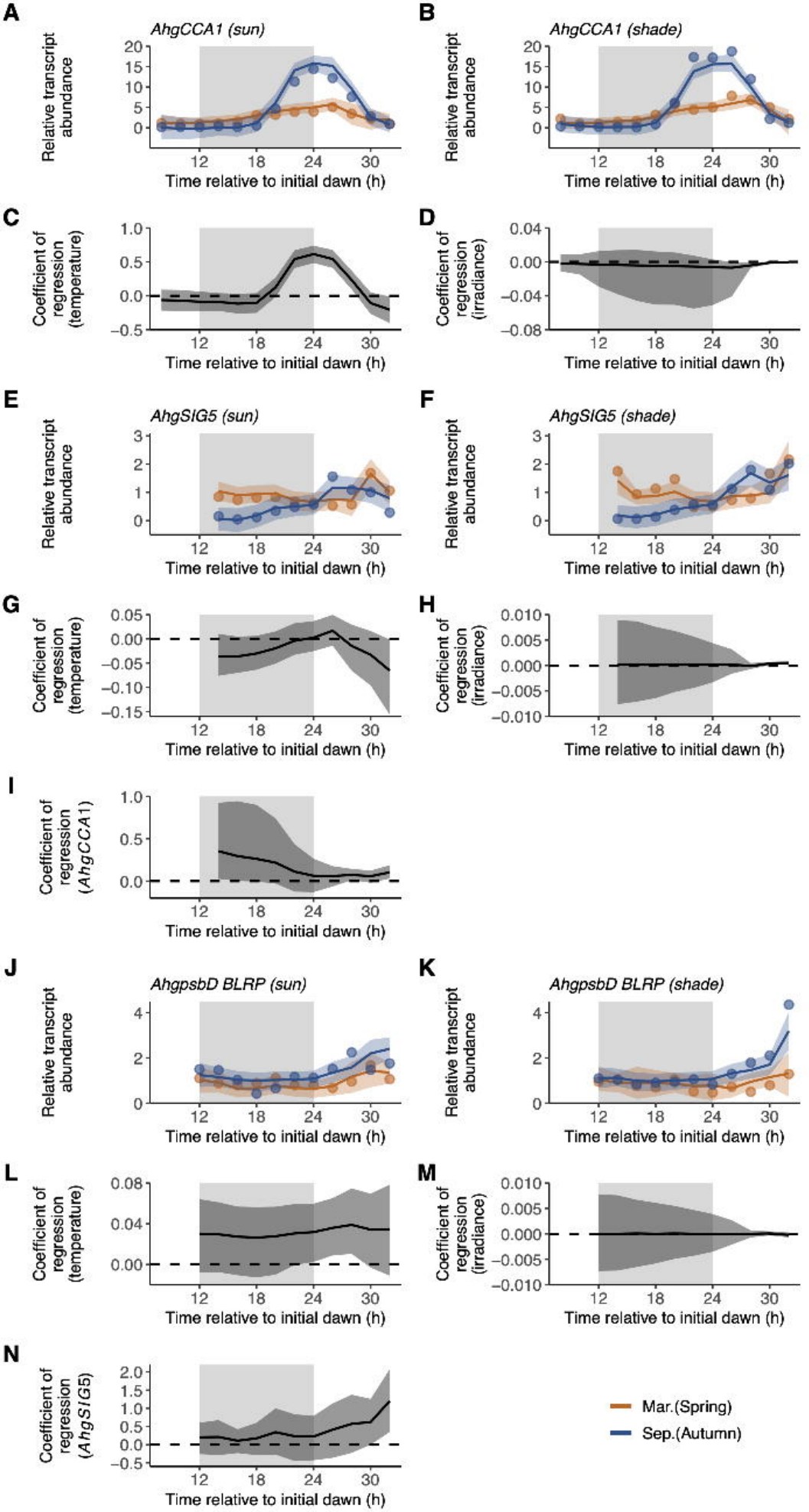
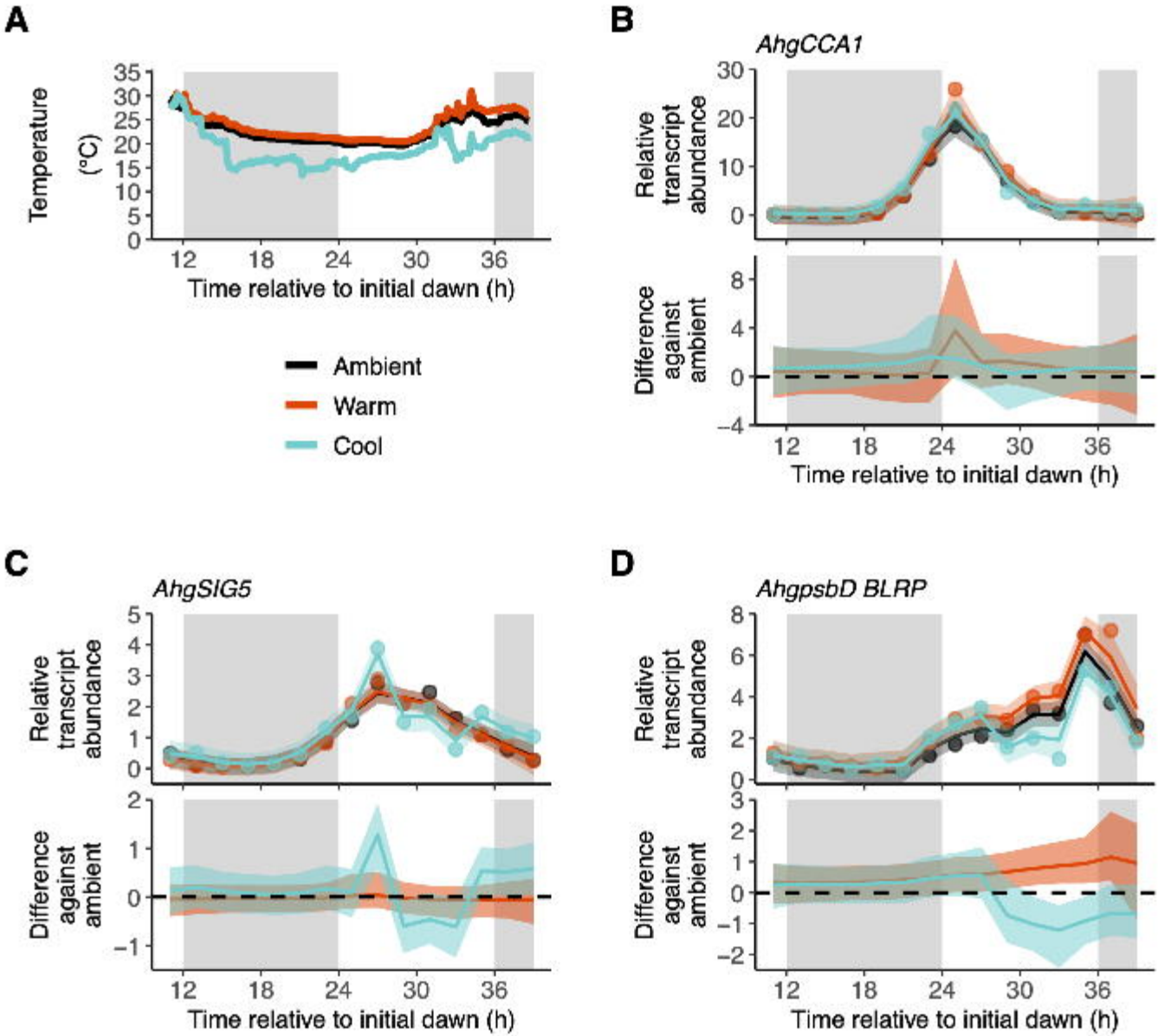

A
Nucleus
Chloroplast
CCA1 (proxy for cirdadian oscillator)
t1
SIG5
t2
psbD BLRP
Environmental cues (light, temperature, seasonality)
B
Temperature (sun)
Temperature (°C)
Time relative to initial dawn (h)
C
Temperature (shade)
D
Irradiance (sun)
Total irradiance (μ mol m⁻² s⁻¹)
E
Irradiance (shade)
F
AhgCCA1 (sun)
Relative transcript abundance
Sep. – Mar.
G
AhgCCA1 (shade)
H
AhgSIG5 (sun)
I
AhgSIG5 (shade)
J
AhgpsbD BLRP (sun)
K
AhgpsbD BLRP (shade)
March (Spring)
September (Autumn)


A
AhgSIG5
RMSE
0.5
0.4
0.3
0.2
*
0 2 4 6 8
Lag of AhgCCA1 (h)
B
AhgSIG5
Log−likelihood
−1.0
−1.1
−1.2
*
0 2 4 6 8
Lag of AhgCCA1 (h)
C
AhgSIG5
Correlation
0.9
0.8
0.7
*
0 2 4 6 8
Lag of AhgCCA1 (h)
D
AhgBLRP
RMSE
0.6
0.5
0.4
*
0 2 4 6 8
Lag of AhgSIG5 (h)
E
AhgBLRP
Log−likelihood
−1.40
−1.45
−1.50
−1.55
*
0 2 4 6 8
Lag of AhgSIG5 (h)
F
AhgBLRP
Correlation
0.9
0.8
0.7
0.6
*
0 2 4 6 8
Lag of AhgSIG5 (h)


A
AhgCCA1 (sun)
Relative transcript abundance
Time relative to initial dawn (h)
B
AhgCCA1 (shade)
Relative transcript abundance
Time relative to initial dawn (h)
C
Coefficient of regression (temperature)
Time relative to initial dawn (h)
D
Coefficient of regression (irradiance)
Time relative to initial dawn (h)
E
AhgSIG5 (sun)
Relative transcript abundance
Time relative to initial dawn (h)
F
AhgSIG5 (shade)
Relative transcript abundance
Time relative to initial dawn (h)
G
Coefficient of regression (temperature)
Time relative to initial dawn (h)
H
Coefficient of regression (irradiance)
Time relative to initial dawn (h)
I
Coefficient of regression (AhgCCA1)
Time relative to initial dawn (h)
J
AhgpsbD BLRP (sun)
Relative transcript abundance
Time relative to initial dawn (h)
K
AhgpsbD BLRP (shade)
Relative transcript abundance
Time relative to initial dawn (h)
L
Coefficient of regression (temperature)
Time relative to initial dawn (h)
M
Coefficient of regression (irradiance)
Time relative to initial dawn (h)
N
Coefficient of regression (AhgSIG5)
Time relative to initial dawn (h)
Mar.(Spring)
Sep.(Autumn)


A
Temperature (°C)
35
30
25
20
15
10
5
0
12
18
24
30
36
Time relative to initial dawn (h)
Ambient
Warm
Cool
B
AhgCCA1
Relative transcript abundance
30
20
10
0
Difference against ambient
8
4
0
−4
12
18
24
30
36
Time relative to initial dawn (h)
C
AhgSIG5
Relative transcript abundance
5
4
3
2
1
0
Difference against ambient
2
1
0
−1
12
18
24
30
36
Time relative to initial dawn (h)
D
AhgpsbD BLRP
Relative transcript abundance
8
6
4
2
0
Difference against ambient
3
2
1
0
−1
−2
12
18
24
30
36
Time relative to initial dawn (h)