**XAP5 CIRCADIAN TIMEKEEPER** Coordinates Light Signals for Proper Timing of Photomorphogenesis and the Circadian Clock in *Arabidopsis*

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Numerous, varied, and widespread taxa have an internal circadian clock that allows anticipation of rhythmic changes in the environment. We have identified **XAP5 CIRCADIAN TIMEKEEPER** (**XCT**), an *Arabidopsis thaliana* gene important for light regulation of the circadian clock and photomorphogenesis. **XCT** is essential for proper clock function: **xct** mutants display a shortened circadian period in all conditions tested. Interestingly, **XCT** plays opposite roles in plant responses to light depending both on trait and wavelength. The clock in **xct** plants is hypersensitive to red but shows normal responses to blue light. By contrast, inhibition of hypocotyl elongation in **xct** is hyposensitive to red light but hypersensitive to blue light. Finally, **XCT** is important for ribulose-1,5-bisphosphate carboxylase/oxygenase production and plant greening in response to light. This novel combination of phenotypes suggests **XCT** may play a global role in coordinating growth in response to the light environment. **XCT** contains a XAP5 domain and is well conserved across diverse taxa, suggesting it has a common function in higher eukaryotes. Downregulation of the **XCT** ortholog in *Caenorhabditis elegans* is lethal, suggesting that studies in *Arabidopsis* may be instrumental to understanding the biochemical activity of **XCT**.

**INTRODUCTION**

As a consequence of the rhythmic, predictable cycles in light and temperature conferred by the Earth’s rotation, organisms have evolved an internal mechanism to anticipate these changes. First reports of an endogenous oscillator in plants date back to 1729, when de Mairan observed leaf movement rhythms persisted in constant darkness (de Mairan, 1729). Since then, evidence for an internal circadian clock has been observed in nearly all eukaryotes and some prokaryotes. This suggests an evolutionary advantage in the capacity to predict environmental changes; indeed, a functional circadian clock has been shown to provide a physiological advantage when matched in periodicity to the external environment (Dodd et al., 2005; Johnson, 2005). However, individual components of the core oscillator are not related across higher taxa (Young and Kay, 2001).

In *Arabidopsis thaliana*, the core clock has been suggested to consist of a negative feedback loop involving the morning-phased genes **CIRCADIAN CLOCK-ASSOCIATED1** (**CCA1**) and **LATE ELONGATED HYCOTYL** (**LHY**) and the evening-phased gene **TIMING OF CAB EXPRESSION1/PSEUDO RESPONSE REGULATOR** 1 (**TOC1/PRR1**) (Alabadi et al., 2001). **CCA1** and **LHY** inhibit **TOC1** expression by binding to the evening element motif found in its promoter and are thought to regulate many other evening-phased genes through the same mechanism (Alabadi et al., 2001; Harmer and Kay, 2005). **TOC1** in turn has a positive effect on expression of **CCA1** and **LHY** through an unknown mechanism. However, this simple model fails to explain all published data (Salomé and McClung, 2004), and the plant clock likely consists of multiple, interlocking feedback loops, similar to other systems (Emery and Reppert, 2004). Recently, genes such as **GIGANTEA** (**GI**) (Locke et al., 2005; Mizoguchi et al., 2005; Gould et al., 2006; Martin-Tryon et al., 2007), **LUX ARRHYTHMO**/**PHYTOCLOCK1** (**LUX/PCL1**) (Haizen et al., 2005; Onai and Ishiura, 2005), and **EARLY FLOWERING4** (**ELF4**) (Kikis et al., 2005) have been suggested to form parallel evening loops with **TOC1**. Each of these components promotes expression of **CCA1** and **LHY**, perhaps by acting together as a protein complex. Additionally, morning-phased loops comprised of **PRR9**, **PRR7**, **CCA1**, and **LHY** probably further act to ensure correct clock period and resetting to light (Farré et al., 2005; Locke et al., 2006; Zellinger et al., 2006). Other components, such as **ELF3** (McWatters et al., 2000; Covington et al., 2001; Liu et al., 2001), **ZETIPLUE** (**ZTL**) (Mas et al., 2003b), and **LIGHT INSENSITIVE PERIOD1** (**LKP1**) (Kevei et al., 2007), appear to function in entrainment of the clock to light, while the site of action of genes such as **SENSITIVITY TO RED LIGHT REDUCED1** (**SRR1**) (Staiger et al., 2003) and **TIME FOR COFFEE** (**TIC**) (Hall et al., 2003; Ding et al., 2007), remains undefined. Inconsistencies between published data and current models suggest that additional components of the clock remain to be discovered.

Light input to the clock is mediated through multiple photoreceptors, including the F-box protein **ZTL**, phytochromes (**PHYs**) and cryochromes (**CRYs**) (Somers et al., 1998a; Devlin and Kay, 2000; Kim et al., 2007). Generally speaking, **PHYs** perceive and transmit red and far-red light signals, while **CRYs** and **ZTL** mediate blue light responses. **CRYs** are conserved in both...
structure and function in many taxa, serving an important role in clock entrainment in plants and insects and in addition acting within the core oscillator in some animals (Cashmore, 2003). PHYs are photoreceptors that mediate light regulation of many processes, including the shade avoidance response and seed germination, as well as entrainment of the plant circadian clock to light (Millar, 2004). Interactions between PHY and CRY signals play an important role in directing photomorphogenic responses, such as the inhibition of hypocotyl elongation, through regulation of both repressors and promoters of photomorphogenesis.

To uncover components of the circadian system, we mutagenized seeds with ethyl methanesulfonate (EMS) and identified plants with altered free-running rhythms (Martin-Tryon et al., 2007). One such short period mutant was characterized and its molecular defect localized to a gene encoding a protein of unknown function. This protein contains an X-CHROMOSOME ASSOCIATED PROTEINS5 (XAP5) domain, a region with uncertain biochemical function but that is highly conserved in many eukaryotes. Accordingly, we named this protein XAP5 CIRCADIAN TIMEKEEPER (XCT). We show that wild-type XCT inhibit red light input to the circadian clock and has additional functions in photomorphogenesis. Intriguingly, these functions are dependent upon wavelength, as XCT acts to inhibit growth in red light but promote growth in blue light. XCT therefore likely functions as a light quality integrator that coordinates the activities of blue and red light signaling pathways on plant growth.

**RESULTS**

**Multiple Circadian Outputs Are Disrupted in xct Mutants**

EMS-mutagenized *Arabidopsis* plants of the Columbia-0 (Col) ecotype transgenic for the COLD-CIRCADIAN RHYTHM–RNA BINDING2/GLYCINE-RICH RNA BINDING PROTEIN7 (CCR2/GRP7) promoter fused to the luciferase (LUC) reporter protein (CCR2_pro:LUC) (Strayer et al., 2000) were entrained in light/dark (LD) cycles and then screened in constant darkness for alterations in circadian regulation of LUC activity. One mutant, later named *xct-1*, retains robust circadian rhythms but with a period ~1.5 h shorter than the parental control when assayed in constant darkness (Figure 1A, Table 1). As some clock mutants display differential defects under specific conditions, we examined *xct-1* in a variety of light conditions. A similar short-period phenotype for CCR2_pro:LUC activity was also observed when plants were assayed in different colors of constant light (Figures 1B and 1C, Table 1). Furthermore, we examined the expression of 10 clock-associated genes using quantitative RT-PCR (qRT-PCR) and found all showed short-period rhythmic expression in *xct-1* (see Supplemental Figure 1 online). We next determined whether this mutation affected a whole-plant output by monitoring leaf movement rhythms in constant white light. Similar to the transcriptional outputs, leaf movement rhythms in *xct* mutants were shortened ~1.5 h relative to the wild type (Figure 1D, Table 1). Thus, multiple circadian outputs are altered in *xct-1* under a variety of light conditions, suggesting XCT functions either within the core oscillator or in a clock input pathway.

**XCT Is Well Conserved in Many Eukaryotes and Is Nuclear Localized**

We initially localized *xct-1* to the upper arm of chromosome 2 through bulked segregant analysis (Michelmore et al., 1991; Lukowitz et al., 2000) and then further mapped it to a 92-kb region containing 33 genes. Sequencing of candidate genes in this region revealed a G-to-A transition within At2g21150 (Figures 2A and 2B). This mutation occurred at the 5’ splice site of intron 7, changing the sequence from GC to AC, a nonconsensus splice site. Sequencing of *xct-1* cDNA products indicates that the mutated splice site is not recognized by RNA splicing machinery, and a GT nine nucleotides upstream of the normal splice junction is used instead (Figure 2B), generating mRNA encoding a protein with an internal deletion of three amino acids.

We also noted multiple XCT splice isoforms in *xct-1* and Col (Figure 2B; see Supplemental Figure 2 online). A minor splice variant is observed in Col; sequencing of this band revealed that intron 5 had not been removed, and translation of this message would result in a truncated protein. In *xct-1*, this alternate form is not observed, but two other variants are generated. Sequencing reveals retention of intron 7 in one and both introns 6 and 7 in the other. Both of these forms contain premature stop codons and if translated would generate truncated proteins. The *xct-1* period phenotype is recessive, suggesting that the alternatively spliced forms are nonfunctional. It is likely that the *xct-1* phenotype is caused by the in-frame deletion in the predominant message rather than generation or loss of the minor alternatively spliced forms.

To confirm that the *xct-1* phenotypes were due to the mutation in At2g21150, we obtained two lines from the Salk collection (Alonso et al., 2003), each with a T-DNA insertion within this gene, which we confirmed by sequencing. SALK_134513 (*xct-2*) contains an insertion in exon 4, and SALK_108639 (*xct-3*) contains an insertion in intron 4 (Figure 2A). No normal message is observed in *xct-2*, suggesting that it is a null allele. By contrast, *xct-3* expresses a small amount (<10% of the wild type) of correctly spliced message (see Supplemental Figure 2 online). *xct-3* exhibits a short period phenotype in constant light similar to that of *xct-1* (Figure 1, Table 1). However, in constant darkness, the short period phenotype of *xct-2* is more severe than *xct-1* (Figure 1A, Table 1), indicating that *xct-1* may be a partial loss-of-function allele. Although a change in amplitude of CCR2_pro:LUC activity is observed in *xct-3* (Figures 1B and 1C), levels of endogenous clock gene expression are not altered in *xct-3* in constant light (see Supplemental Figure 1 online), and *xct-3* shows no change in period for any output tested (Figure 1, Table 1; see Supplemental Figure 1 online). The reduction in luciferase expression in *xct-3* is likely due to silencing of the LUC transgene, as we have observed previously in other Salk insertion lines (Martin-Tryon et al., 2007), and is consistent with the loss of kanamycin resistance (presumably due to silencing of the knockout T-DNA) observed in this line.

To verify that the *xct-1* and *xct-2* phenotypes are caused by alterations in At2g21150, we crossed these recessive mutants to each other. The resulting F1 has a short period phenotype similar to both homozygous parents, demonstrating a failure of complementation (Figure 2C). Furthermore, the short period
phenotypes of both xct-1 and xct-2 can be rescued by transformation with a genomic copy of XCT (Table 1, Figure 2D). Notably, xct-2 mutants transformed with XCT driven by a strong viral promoter (xct-2 35Spro:XCT) also show a near wild-type period (P > 0.1, Student’s t test) (Figure 2D, Table 1). In combination with the wild-type period seen in xct-3 plants, this indicates that the plant clock is relatively insensitive to levels of XCT expression but that loss of XCT function causes a short-period phenotype.

XCT encodes a novel protein of 337 amino acids that is highly conserved with proteins found in the genomes of many eukaryotes, including rice (Oryza sativa), human, zebra fish, sea urchin, and fission yeast (Schizosaccharomyces pombe). Alignment of these protein sequences reveals conservation of amino acids across the entire protein but most notably in the C-terminal 225 amino acids, which comprises a XAP5 domain. The amino acids surrounding the xct-1 deletion lie within the XAP5 domain and are widely conserved (see Supplemental Figure 3 online). Comparison of amino acid sequences between the entire Arabidopsis protein and its orthologs reveals 34 to 84% amino acid identity (Figure 2E), a remarkable degree of conservation between these distantely related taxa (Figure 2F). Amino acid identity when just the XAP5 domains are considered is even more impressive: these regions are 94% identical between Arabidopsis and rice, 64% identical between Arabidopsis and human, 47% identical between Arabidopsis and Caenorhabditis elegans, and 39% identical between Arabidopsis and S. pombe. In Arabidopsis, similar to the genomes of rice and Medicago truncatula, XCT is the only XAP5 domain-containing protein. To reflect this conserved domain and the role of At2g21150 in the clock, we have named it XAP5 CIRCADIAN TIMEKEEPER (XCT).

The S. pombe XCT homolog was found to be nuclear localized in a genome-wide study (Matsuyama et al., 2006), and XCT

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**Figure 1.** xct Mutants Display Short Period Rhythms for Multiple Circadian Clock Outputs.

After entrainment to 12:12 LD cycles for 6 d, CCR2pro:LUC displays rhythmic short-period expression in xct mutants held in constant darkness (A), constant red light (B), and constant blue light (C). Similarly, xct mutants demonstrate short period leaf movement rhythms in constant white light (D). Each data point is the average of 8 to 36 seedlings for CCR2pro:LUC and 42 to 80 cotyledons for leaf movement analysis, and error bars represent SE. Error bars are presented only on every 12th data point in (A) for clarity. Shaded and closed or open and shaded bars on the x axis represent subjective day and subjective night, respectively.
contains a predicted nuclear localization sequence (KKRK) at amino acids 112 to 115 (Horton et al., 2007). To determine the intracellular localization of XCT, we generated plants expressing XCT fused to yellow fluorescent protein (YFP) and the hemagglutinin epitope tag (HA) under control of the native XCT promoter, which rescues the XCT phenotype (Figures 2D and 3E, Table 1). We found that XCT protein is restricted to and present in the nuclei of all cell types examined, including trichome, hypocotyl, and root cells of light-grown seedlings (Figures 3A to 3D). XCT-YFP-HA is also found in the nuclei of etiolated seedlings, juvenile leaf mesophyll, and adult leaves, stems, and flowers (see Supplemental Figure 4 online; data not shown), indicating that light is not required for XCT expression and that XCT protein is present in the nucleus throughout development. XCT translationally fused to YFP at the N terminus was also present in nuclei (see Supplemental Figure 4 online), indicating that this localization pattern is not an artifact of the fusion protein.

### Regulation of XCT Protein Levels Is Complex

Many, but not all, clock-associated genes show rhythmic regulation of mRNA levels. To examine whether XCT expression is under clock control, we entrained wild-type seedlings in LD cycles and then released them to constant light (LL) and collected time-course samples. XCT mRNA levels do not show 24-h rhythms either in LL or LD (data not shown). However, using an HA antibody to detect tagged XCT expressed under the control of its own promoter or the constitutively expressed 35S promoter, we found that XCT protein levels fluctuate in 6-d-old entrained seedlings. When plants are maintained in LD, XCT protein levels are low during the middle of the day and early evening (ZT6 to ZT12) and highest shortly after dawn (ZT3), regardless of whether expression is driven by the 35S or native promoter (Figure 4). Thus, a posttranscriptional mechanism regulates XCT abundance during the day.

To distinguish between effects caused by light versus the circadian clock, we examined XCT levels in plants maintained in LL or in LD conditions. LL samples 15 to 24 were harvested during the subjective night, corresponding to times when the plants were in the dark during entrainment but were exposed to light during the collection period. There is no obvious difference in XCT protein levels during the true and subjective nights (LD and LL samples, respectively) when XCT-YFP-HA is expressed under control of the 35S promoter (Figure 4A). By contrast, more XCT protein accumulates during the subjective night than during the true night when XCT-YFP-HA is expressed under the control of the native XCT promoter (Figure 4B). No consistent difference in XCT mRNA level is observed when entrained plants are held in constant light versus diurnal cycles (data not shown), suggesting that this light-induced increase in XCT protein at night might also be due to posttranscriptional regulation.

### XCT Inhibits Clock Gene Expression in Diurnal Cycles

The plant circadian clock is thought to consist of multiple interlocked transcription/translation feedback loops (Salomé and McClung, 2004). We therefore examined the effect of XCT mutations on the expression levels of many known clock-associated genes. As expected, rhythmic expression of all genes assayed in LL showed a short-period phenotype in xct-1 and xct-2 but a near wild-type period in xct-3 (see Supplemental Figure 1 online). Immediately after release to constant environmental conditions, TOC1, ELF4, PRR3, and PRR5 showed significantly higher peak expression levels in xct-1 and xct-2 compared with Col (see Supplemental Figures 1A to 1D online; P < 0.05 for Student’s t test comparison of peaks), with these differences generally decreasing by the second and third days in LL. Although there was no consistent significant difference in peak expression for PRR7, PRR9, LHY, CCA1, GI, or LUX (see Supplemental Figures 1E to 1J online), some of these genes appeared to also have elevated peak expression early in this time course.

The difference in expression levels primarily seen shortly after the transition to LL prompted us to examine expression levels of these genes in short-day (8:16) LD cycles. ELF4, PRR5, PRR7, and PRR9 showed an increase in peak expression levels in short-day conditions consistent across 2 d of collection (see Supplemental Figures 5A to 5D online; P < 0.05 for Student’s t test comparison of peaks). These data suggest that XCT does not strongly affect expression levels of known clock genes in

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Period Estimate (Variance Weighted Mean ± se [n]) in Hours</th>
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<tr>
<td></td>
<td>DD</td>
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<tr>
<td>Col</td>
<td>25.64 ± 0.36 (6)</td>
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<tr>
<td>xct-1</td>
<td>24.17 ± 0.24 (8)</td>
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<tr>
<td>xct-2</td>
<td>22.71 ± 0.23 (8)</td>
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<td>xct-3</td>
<td>25.28 ± 0.44 (7)</td>
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<td>xct-1 XCTpro:XCT</td>
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<td>xct-2 XCTpro:XCT</td>
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Intensities of constant light conditions are presented in µE (µmol m⁻² s⁻¹). CCR2pro:LUC activity was determined in constant darkness (DD), constant red light (cRL), constant blue light (cBL), or the combination of constant red and blue light (cR+B). Cotyledon movement rhythms (LMRA) were monitored in constant white light. xct mutants transformed with a genomic copy of XCT under the control of the native XCT promoter (XCTpro:XCT) or the globally expressed cauliflower mosaic virus 35S promoter (35Spro:XCT) were assayed in the T1 generation, with similar rescued periods observed in resulting T2 and T3 families. ND represents data not determined; se is the standard error for (n) individuals.
Figure 2. Identification of the XCT Locus.
constant conditions but can modulate the expression level of a subset of these genes under entrained conditions.

In the short-day LD samples, clear phase advances consistent with the short period phenotype of \textit{xct} can be seen for \textit{ELF4}, \textit{TOC1}, \textit{LUX}, and \textit{PRR3} but not for \textit{PRR5}, \textit{PRR7}, \textit{PRR9}, or \textit{GI} (see Supplemental Figure 5 online). \textit{PRR9} likely shows a normal dawn phase because it is directly light inducible (Tepperman et al., 2001), and increased expression and duration of \textit{PRR5} and \textit{PRR7} may mask a slightly earlier phase of expression of these genes. However, the lack of an early phase of \textit{GI} expression in \textit{xct-1} and \textit{xct-2} (see Supplemental Figure 5F online) motivated us to examine the photoperiodic pathway in these plants. Like \textit{GI}, we found no change in the phase of \textit{CONSTANS} expression in \textit{xct} plants grown in short days (see Supplemental Figure 6 online). Consistent with the normal phases of expression of these genes, \textit{xct} mutants grown in short days do not flower early, unlike other short-period mutants, such as \textit{gi-200}, \textit{toc1-2}, and \textit{lhy-100} (see Supplemental Figure 7 online). \textit{xct} mutants also flower with the same number of leaves as Col when grown in long days (see Supplemental Figure 7 online), indicating that \textit{XCT} does not play an important role in the control of flowering time.

**XCT Coordinates Plant Developmental Responses to Light**

Although \textit{xct-1} and \textit{xct-2} plants assayed in constant light have very similar period phenotypes (Figure 1, Table 1), \textit{xct-2} demonstrates a light-dependent phenotype not seen in \textit{xct-1}. When grown in any fluence or wavelength of light tested, \textit{xct-2} does not show a phase advance consistent with the \textit{xct} phenotype (Figure 1B, Table 1). Consistent with this observation, \textit{xct-2} mutants grown in any fluence or wavelength of light tested do not flower early, unlike other short-period mutants, such as \textit{gi-200}, \textit{toc1-2}, and \textit{lhy-100} (see Supplemental Figure 7 online). \textit{xct} mutants also flower with the same number of leaves as Col when grown in long days (see Supplemental Figure 7 online), indicating that \textit{XCT} does not play an important role in the control of flowering time.

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**Figure 2.** (continued).

(A) Gene structure of \textit{XCT}: white blocks indicate exons and black lines introns; hatched bars indicate the 5' and 3' UTRs. Locations of mutations are indicated: \textit{xct-1} G1712A, \textit{xct-2} (SALK_134513) insertion after 771 nucleotides, and \textit{xct-3} (SALK_108639) insertion after 1287 nucleotides.

(B) \textit{xct-1} contains a G → A transition 1712 nucleotides after the translational start, which alters a 5' intronic splice site and leads to missplicing of the \textit{XCT} message.

(C) \textit{xct-2} fails to complement \textit{xct-1}, with the F1 demonstrating a short period similar to both parents.

(D) \textit{xct-1} was rescued by transformation with \textit{XCT} under the control of its own promoter (\textit{xct-1 XCTpro:XCT}), and overexpression of \textit{XCT} by the 3SS promoter also produced a near normal free-running period in \textit{xct-2} (\textit{xct-2 3SSpro:XCT}, \(P > 0.1\)). For (C) and (D), plants were entrained and assayed as in Figure 1B, and error bars represent SE.

(E) Percentage of identical amino acids between species across the entire XAP5 protein is presented in a similarity matrix.

(F) Neighbor-joining phylogenetic tree showing the relationships between XAP5 proteins from various species. Bootstrap values (10,000 replicates) are presented near each branch, and branch length represents the number of amino acid changes per site in accordance with the scale bar. Species of XAP5 proteins in (E) and (F) are Arabidopsis thaliana, Oryza sativa, Mus musculus, Strongylocentrotus purpuratus, Homo sapiens, Xenopus laevis, Danio rerio, Drosophila melanogaster, Caenorhabditis elegans, and Schizosaccharomyces pombe.
cotyledons initially appear yellow and only turn green 5 to 6 d after germination (Figure 3E). A similar phenotype is apparent as postembryonic tissues emerge; the shoot apical meristems of xct-2 plants maintain a yellow appearance throughout development, and floral organs, such as sepals, also demonstrate delayed greening (data not shown). This suggests that chloroplast development is impaired in xct mutants, so we examined levels of the abundant chloroplast protein ribulose-1,5-bisphosphate carboxylase/oxygenase (Rubisco). Indeed, we found Rubisco levels are greatly decreased in light-grown xct-2 plants (Figure 4B) and that both the delayed greening and low Rubisco phenotypes are rescued by transformation with genomic XCT (Figures 3E and 4B). However, overexpression of XCT in the Col background does not lead to upregulation of Rubisco (Figure 4A) or enhanced greening of tissues (data not shown).

Many mutants with alterations in circadian function also display defects in photomorphogenesis (Nozue and Maloof, 2006). We therefore examined inhibition of hypocotyl elongation in xct plants in a variety of light conditions. Hypocotyl length of etiolated xct mutants was virtually identical to that of the wild type (see Supplemental Figure 8 online). Like many other clock mutants, xct plants are tall in constant red light (Figure 5A; P < 0.01 at all fluence rates). Unlike other clock mutants, however, xct mutants show the opposite phenotype of a shortened hypocotyl when grown in constant blue light (Figure 5B; P < 0.01 at all fluence rates), constant white light (Figure 5C; P < 0.01 at all fluence rates), or white LD cycles (data not shown). All of these phenotypes are rescued by transformation with a genomic copy of XCT expressed under control of the native promoter (Figure 5).

Thus, XCT promotes the inhibition of hypocotyl elongation in response to red light but negatively regulates this response in blue or white light (Figure 8).

**XCT Mediates Red Light Input to the Clock**

Since XCT plays a positive role in red light and a negative role in blue light regulation of photomorphogenesis, we next...
investigated its involvement in light input to the clock. Increased light intensity causes the internal circadian clocks of diurnal organisms, such as *Arabidopsis*, to run at a faster pace (Aschoff’s rule; Aschoff, 1979; Millar, 2004). We therefore examined the relationship between fluence rate and free-running period in xct plants maintained in either monochromatic red or blue light. xct-1 and xct-2 mutants are hypersensitive to red light, exhibiting a steeper slope of the period response to fluence rate compared with Col (Figure 6C; P < 0.01). In contrast, xct and Col plants show a very similar response to increasing fluence rates of constant blue light (Figure 6B, P > 0.1). Therefore XCT plays a role in red light, but not blue light, input to the circadian clock.

The short-period and tall hypocotyl in red light phenotypes of xct mutants are also seen in the recessive *toc1* allele toc1-2 (Más et al., 2003a). We therefore investigated whether toc1-2 plants are hypersensitive to red light input to the clock. Just as for xct-1 and xct-2, we found the clock to be hypersensitive to increasing fluence rates of constant red light in toc1-2 (Figure 6C; P < 0.01). By contrast, the short-period semidominant toc1-1 allele and Col showed similar responsiveness to increasing fluence rates, as previously reported (Somers et al., 1998b; Figure 6C). This indicates that red light input to the clock is altered in toc1-2 but not toc1-1, consistent with the toc1-1 allele retaining some function (Strayer et al., 2000; Alabadi et al., 2001).

A further means of examining light signal transduction to the clock is by determining the change in phase of a dark-adapted circadian rhythm in response to a pulse of light. The clock modulates the magnitude of response, such that depending on circadian time of the light pulse, the clock will advance or delay to varying degrees. Dark-adapted xct mutants were tested over two consecutive days for a change in phase of *CCR2pro-LUC* activity in response to a pulse of red light. xct-1 plants show nearly wild-type responses, whereas xct-2 shows stronger phase advances than the Col control, particularly during the subjective day (Figure 6D). This confirms that the clock in xct-2 plants is hypersensitive to red light and suggests that XCT may play an important role in inhibiting light input to the clock during the subjective day.

**XCT Acts as a Light Quality Sensor Directing Both Negative and Positive Transcriptional Regulation**

Since many light signaling and some clock genes are acutely induced by light (Tepperman et al., 2001), we examined the effect of light on XCT expression in etiolated plants. In Col, treatment of etiolated plants with white light causes a slow and modest increase in XCT levels, with peak expression ∼6 h after light onset immediately followed by a reduction; by contrast, red light has little effect on message levels (Figure 7A). White light treatment of xct-1 causes an increase in XCT message with similar kinetics to Col but greater fold induction; however, in xct-1, red light exposure leads to a rapid and pronounced increase in XCT expression (Figure 7A). XCT message levels remain elevated in xct-1 relative to Col many hours after transfer from darkness to either red or white light (Figure 7A). Thus, the xct-1 mutation causes enhanced induction of XCT mRNA in response to light, suggesting that XCT acts to inhibit its own expression (Figure 8).

Since the acute induction of XCT message in response to light is altered in xct-1, we next examined regulation of *LIGHT HARVESTING COMPLEX B5 (LHCBS)*, which is induced by both red and white light (Zimmermann et al., 2004). *LHCBS* induction is severely impaired in etiolated xct-2 mutants transferred to red light (Figure 7B), suggesting that XCT is necessary for induction of *LHCBS*. However, induction of *LHCBS* is very similar in xct-1 and Col in response to red light (Figure 7B), suggesting that the three–amino acid deletion present in xct-1 does not affect its function in this process. Upon transfer to white light, both xct-1 and xct-2 show similar upregulation of *LHCBS*, with more rapid kinetics than seen in Col (Figure 7C); however, *LHCBS* levels are lower in xct-2 than the wild type by the end of this time course. Therefore, XCT appears to play a positive role in the induction of *LHCBS* in response to red light, but in the acute response to white light, XCT acts to inhibit and delay its expression to the appropriate phase. Sustained upregulation of *LHCBS* in response to either red or white light requires XCT function that can be provided by the xct-1 but not the xct-2 allele.
Considered along with the variable phenotypes of xct mutants grown in red or blue light, these differential effects on gene expression in response to red or white light indicate that XCT plays different roles in different light qualities. XCT may therefore play an important role in coordinating plant responses to the light environment.

**DISCUSSION**

We have cloned and characterized *Arabidopsis* XCT, a nuclear protein containing a XAP5 domain that negatively regulates red light input to the clock. XCT functions beyond the circadian clock as well, coordinating growth and gene expression in response to light signals and playing a role in chloroplast development. As the XCT protein is highly conserved across varied taxa, it is likely that XAP5 proteins in diverse organisms have similar biochemical functions.

**XCT Is Posttranscriptionally Regulated**

We did not observe rhythmic expression of XCT mRNA either when plants were grown in LL or LD (data not shown). However, XCT protein levels show a consistent increase ~3 h after dawn followed by a decrease during the rest of the day, with a trough of expression at ZT6. Consistent with this being a posttranscriptional effect, a similar pattern was observed whether the XCT or...
35S promoter was used to drive XCT expression (Figure 4). One possible explanation for this pattern would be destabilization of XCT protein, either in response to light or by a clock-regulated protein with peak activity between CT4 and CT8. Regulation of protein degradation is known to be an important regulatory mechanism in both light and clock signaling (Lechner et al., 2006).

Interestingly, light exposure during the subjective night leads to an increase in XCT protein levels in plants expressing the XCTpro:XCT-YFP-HA construct (Figure 4B) but not the 35Spro:XCT-YFP-HA construct (Figure 4A). Despite the marked increase in XCT protein in LL, no similar change in XCT message was observed under these conditions (data not shown), again suggesting that a posttranscriptional mechanism might be at work. One important difference between these constructs is that the 35S-driven XCT contains the viral 5′ untranslated region (UTR), while the XCT-driven construct contains the native 5′ UTR. Some 5′ UTR sequences are known to control translation (Kawaguchi and Bailey-Serres, 2002). Of particular interest, translation of both LHY (Kim et al., 2003) and many genes implicated in photosynthesis (Berry et al., 1988, 1990; Hansen et al., 2001; Tang et al., 2003) is light regulated. Although we cannot unequivocally conclude that translation of XCT message and degradation of XCT protein are light and clock regulated, these are interesting possibilities that merit further study. Since a low level of XCT expression is sufficient to maintain wild-type period and gene expression profiles in xct-3 (Table 1, Figure 1; see Supplemental Figure 1 online) and overexpression of XCT does not lead to a lengthened period (Table 1), it seems likely that posttranscriptional regulation of XCT is more important than control of its transcript level.

**XCT Regulates Red Light Input to the Clock**

We found that xct mutants are hypersensitive to both continuous red light (Figure 6A) and pulses of red light (Figure 6D). However, the free-running period of xct mutants shows normal responsiveness to increasing fluence rates of blue light (Figure 6B), indicating that XCT specifically regulates red light input to the clock. Similarly, we found the clock in toc1-2 mutants to be hypersensitive to red light but show normal blue light responsiveness (Figure 6C; data not shown). xct and toc1-2 mutants share other phenotypes as well; they both have tall hypocotyls in red light and short free-running periods. It is therefore possible that XCT and TOC1 have related functions in red light signaling and clock pathways. The localization of XCT to the nucleus (Figures 3A to 3D) places it in the same compartment of the cell as TOC1 and other clock-associated proteins, such as ELF3, GI (Kim et al., 2007), LIP1 (Kevei et al., 2007), TIC (Ding et al., 2007), and SRR1 (Staiger et al., 2003).

However, unlike toc1-2 mutants, xct plants don’t show reduced expression of clock genes such as CCA1 and LHY (see

![Figure 8. XCT Has Variable Functions in Inhibition and Activation of Downstream Responses, such as Clock Pace, Hypocotyl Elongation, and Leaf Greening.](image-url)
Supplemental Figure 1 online; Alabadi et al., 2001); instead, some clock-associated genes show transiently enhanced expression soon after the transition from entrained to free-running conditions (see Supplemental Figure 1 online). This enhancement can be seen more strongly in plants harvested in LD cycles; we observed consistent upregulation of ELF4, PRR5, PRR7, and PRR9 near the expected peak of expression in diurnal cycles in xct plants (see Supplemental Figure 5 online). Therefore, a function of XCT is to inhibit expression of these genes, either directly or indirectly, in diurnal conditions. Enhanced expression of these genes is consistent with the increased sensitivity of xct plants to red light–induced clock resetting.

Interestingly, PRR5, PRR7, and ELF4 are phased with peak expression coinciding with the trough of XCT protein levels in diurnal cycles (Figure 4), suggesting that XCT could act directly to inhibit the expression of these genes. Alternatively, since many clock genes appear to be upregulated to a certain extent in xct mutants in diurnal cycles (see Supplemental Figure 1, times 0 to 12, and Supplemental Figure 4 online), this may be a general consequence of the clock being more sensitive to light input in the absence of XCT. A similar environment-dependent phenotype was recently reported for another clock input mutant; levels of TOC1 expression in lip1 plants are similar to the wild type in constant light but reduced in LD cycles (Kevei et al., 2007).

xct mutants display a shortened circadian period for multiple clock outputs in all light conditions tested, including constant darkness (Figure 1, Table 1; see Supplemental Figure 1 online). Other components involved in light entrainment of the circadian system also have phenotypes in both constant darkness and constant light. For example, ZTL regulates light input to the clock, but ztl mutants have long-period phenotypes in all light conditions tested, including constant darkness (Somers et al. 2004). ZTL interacts with TOC1 and targets it for degradation; this interaction is light independent, and ZTL destabilizes TOC1 even in the dark (Más et al., 2003b; Kim et al., 2007). Thus, ZTL has both light-dependent and light-independent functions within the circadian system. Similarly, TOC1 also plays separable roles in clock input and core clock function, since toc1-2, but not toc1-1, is hypersensitive to red light input to the clock (Figure 6C) despite the similar short-period phenotypes of these alleles. Thus, it is possible that XCT acts near or within the core oscillator in both light-dependent and light-independent ways.

### XCT Coordinates Environmental Signals to Direct Photomorphogenesis

The opposite hypocotyl phenotypes of xct mutants in red and blue light are very striking and suggest that XCT has different functions in PHY- and CRY-mediated regulation of photomorphogenesis (Figure 8). Plants with consistently opposite hypocotyl phenotypes across a broad range of red and blue light fluence rates have not been previously reported, either in circadian or classical photomorphogenic mutants. However, OB4 BINDING PROTEIN3 has been suggested to play a positive role in PHYB-mediated inhibition of hypocotyl elongation and a negative role in CRY1-mediated cotyledon expansion (Ward et al., 2005). A number of signaling components are thought to act similarly downstream of both PHY and CRY photoreceptors (Osterlund et al., 2000; Pepper et al., 2001; Kang et al., 2005). It is possible that in xct mutants such shared signaling components are skewed away from the PHY pathway and toward the CRY pathway, leading to reduced red light and enhanced blue light responses. It seems likely in natural, white light conditions, that XCT coordinates the activity of blue and red light signaling pathways to control hypocotyl elongation (Figure 8).

Throughout development, xct-2 but not xct-1 plants display delayed greening of new tissues (Figure 3E), suggesting that xct-1 represents a partial loss-of-function allele. This delay in greening is also observed when seedlings are grown in monochromatic red or blue light (data not shown). Thus, one function for XCT is to direct the process of chlorophyll development (Figure 3E) and Rubisco expression (Figure 4) after exposure to light, potentially through transcriptional activation of key components in the process (Figure 8). Notably, xct-1 and xct-2 display similar short period phenotypes in constant light of various wavelengths (Table 1), indicating that the role of XCT in the accumulation of photosynthetic machinery is biochemically separable from its function within the clock.

It is interesting that the role of XCT in greening is wavelength independent but allele dependent (this phenotype is observed in xct-2 but not xct-1). By contrast, the xct-1 and xct-2 hypocotyl phenotypes are wavelength dependent but similar to each other (Figure 5). Acute light-mediated induction of gene expression cannot be neatly summarized in this manner. A stronger effect on the acute induction of both XCT and LHCB expression is seen in etiolated xct plants treated with red rather than with white light (Figure 7), suggesting wavelength dependence on immediate responses. However, by 12 h after transfer to either red or white light, xct-2 but not xct-1 seedlings have lower LHCB levels than the wild type (Figures 7B and 7C), suggesting a wavelength-independent but allele-dependent effect on this gene. It is likely that such longer-term, allele-specific but wavelength-independent effects on gene expression underlie the delayed greening seen in xct-2. Furthermore, these data indicate that XCT can have both positive and negative effects on gene expression depending upon the allele, the light quality, and the duration of treatment.

### XCT May Act as a Link between the Clock and the Chloroplast

The circadian clock affects chloroplast development through coordination of pigment synthesis (Beator and Kloppstech, 1993), and chloroplasts may influence nuclear function through retrograde transcriptional signaling (Ruckle et al., 2007), suggesting that chloroplast status might influence the circadian clock. Anomalous greening in response to light occurs in some clock mutants; etiolated plants overexpressing TOC1 show delayed greening upon transfer to light, whereas plants overexpressing CCA1 green earlier than Col after transfer (Kato et al., 2007). However, no similar deficiency in greening has been reported in light-grown TOC1-overexpressing or CCA1-overexpressing plants, although overexpression of CCA1 does cause strong growth defects in very short days (Green et al., 2002). The loss of XCT more severely disrupts chloroplast development than overexpression of core clock components, suggesting that...
one function of XCT may be within a feedback loop between light signaling, the clock, and chloroplast pigment development.

XCT Regulates Light Input and the Clock

The strong similarity between XCT orthologs in divergent species raises the possibility that XCT represents a link between clocks of diverse taxa. Interestingly, RNA interference–mediated down-regulation of the XCT homolog in C. elegans causes embryonic lethality, suggesting an early and essential developmental requirement for this protein (Piano et al., 2002). Although the human XAP5 gene is ubiquitously expressed, levels are higher in fetal relative to adult tissues, suggesting that it may also play an important role in early mammalian development (Mazzarella et al., 1997). The human XAP5 gene is located in Xq28, a gene-dense region of the X chromosome. The presence of polymorphic numbers of trinucleotide repeats in the human 5′ UTR has been linked to mental retardation when altered (for review, see Chiurazzi et al., 2000). However, currently nothing is known about the molecular function of XAP5 domain-containing proteins in humans or other organisms. Since XCT function is required for viability in C. elegans (Piano et al., 2002) but not plants, Arabidopsis may be an excellent model system in which to investigate the biochemical activity of this intriguing protein.

METHODS

Plant Materials and Genotyping

Arabidopsis thaliana seeds of the Col ecotype were mutagenized as previously described (Martin-Tryon et al., 2007) and mutants mapped through bulked segregant analysis (Michelmore et al., 1991; Lukowitz et al., 2000) followed by fine scale mapping in a Landsberg erecta outcross population to isolate xct-1. The mutation was confirmed with a derived cleaved- amplified polymorphic sequence marker, F 5′-GTAAGAAGGTTATATTCG-3′ and R 5′-GAC- CTCTTCTCTTCTCGA-3′, and linkage analysis indicates that XCT is within the interval for many X-linked genes that cause mental retardation when altered (for review, see Chiurazzi et al., 2000). However, currently nothing is known about the molecular function of XAP5 domain-containing proteins in humans or other organisms. Since XCT function is required for viability in C. elegans (Piano et al., 2002) but not plants, Arabidopsis may be an excellent model system in which to investigate the biochemical activity of this intriguing protein.

Leaf Movement Rhythm Analysis

Plants were germinated on Murashige and Skoog (MS) medium containing 3% sucrose in plates held at a 45° angle in 12:12 LD cycles of 55 μmol m⁻² s⁻¹ for 2 d before being released to constant light conditions of 20 μmol m⁻² s⁻¹ provided by cool white fluorescent bulbs (Sylvania). Images were automatically acquired at 30-min intervals using LabView (National Instruments) and a Pixelink PL-A781 6.6 Mp camera equipped with a 16-mm Fujinon CF16HA-1 lens. The positions of cotyledon tips were analyzed using ImageJ (http://rsb.info.nih.gov/ij/) and normalized to the lowest position for each tip. Data represent the averages and se of 42 to 80 individual cotyledons and are indicative of two independent replicates.

qRT-PCR

Quantitative RNA profiles of 6-d-old seedlings were generated as previously described (Martin-Tryon et al., 2007) using two to three technical replicates for each sample normalized to PROTEIN PHOSPHATASE 2a subunit A3 (PP2a). Briefly, real-time qRT-PCR was performed using an iCycler (Bio-Rad) and SYBR Green I (Molecular Probes) on cDNA generated from each sample, a pool of 10 whole seedlings. Starting quantity was estimated from critical thresholds compared with the standard curve of amplification. All primer sets contain one primer that bridges an intron to reduce genomic amplification, melt curve analysis was performed following amplification to confirm specificity of products over primer dimers, and a no reverse transcriptase control was used to ensure products detected were from cDNA rather than genomic DNA. Data in Figure 7 are representative of two independent biological replicates, whereas data in Supplemental Figures 5 and 6 are internally replicated over the collection time course. Due to practical limitations, data presented in Supplemental Figure 1 online (LL) represent a single biological replicate (composed of a pool of 10 seedlings); however, similar findings are present for the two loss-of-function alleles xct-1 and xct-2, supporting the reproducibility of the expression profiles. XCT qRT-PCR primers are F 5′-TGAGAAGAGTTATATTCG-3′ and R 5′-GCA-ACTCTCCTCTCCTCGA-3′, LHCBS qRT-PCR primers are F 5′-CGG-TGAAGTGTGGAGATTATTG-3′ and R 5′-TGCTGATGATGATT-CAAA-3′, ELF4 qRT-PCR primers are F 5′-CAAGAGCGCTTCCTCGCA-3′ and R 5′-CGAATCATCACTCCAGG-3′, and LUX qRT-PCR primers are F 5′-CGGATCGGAAAGACAAAG-3′ and R 5′-TACTCTC- CATACGCGGTTGA-3′. Primers for LHY, CCA1, TOC1, GI, PRR3, PRR5, PRR7, PRR9, and CO are as described in Mockler et al. (2004). PP2a primers, F 5′-TAACGGGCAAATGATGC-3′ and R 5′-GCTCTCC- CACCCGAATGT-3′, were described by Czechowski et al. (2005). XCT splice variation and expression normalized to UBD-10 were monitored as previously described (Martin-Tryon et al., 2007) using XCT-specific primers flanking the mutation and insertion sites F 5′-TCGAAAGAGAAAGATCGG-3′ and R 5′-TGTCTCAGGCTTCTCGA-3′.

Alignment, Phylogenetic Analysis, and Similarity Matrix

Alignment of protein sequences was performed with AlignX (Vector NTI; Informax) and ClustalW in Mega4 (Tamura et al., 2007) before Mega4 was used for phylogenetic analysis. Evolutionary relationships were deduced using the neighbor-joining method (Saitou and Nei, 1987) with bootstrap values (10,000 replicates) (Felsenstein, 1985) with the Schizosaccharomyces pombe gene designated as the outgroup since it has the lowest degree of homology to all the other sequences. Evolutionary distances were computed with the JTT matrix-based method (Jones et al., 1992) and represent amino acid substitutions per site. Pairwise deletion was used to eliminate gaps in pairwise sequence comparisons. The similarity matrix was generated in Mega4 using pairwise sequence comparison of 10 sequences to determine the p-distance, the number of amino acid substitutions per site. Identity is shown as 1 – (p-distance)/100.
Rescue and Overexpression Constructs

Two types of genomic rescue constructs were generated under the control of the native promoter, −2 kb of the upstream region of XCT. Using the primers F 5′-AACCGGCGCGGCCGATGATTAATA-3′ and R 5′-ATACCCCATG-GACTGTGTGACCC-3′ and the 35S promoter pEG101 fragment was flanked by F 5′-CACCGGATCCAGATTAATAATTTA-3′ and R 5′-ATCCCCATG-GACTGTGTGACCC-3′. The native promoter XCTpro:XCT-YFP-HA pEG301/101 construct was generated by subcloning the XCT pro and 5′ region from the XCT pEG301 construct into the pEG101 backbone containing the remaining XCT sequence and tags. All clones were verified by sequence analysis.

YFP Imaging

xct-2 plants containing the XCTpro:XCT-YFP-HA pEG301/101 construct were imaged using an Eclipse 600 microscope (Nikon) and a Plan-Apo 60 objective with the YFP filter set (Chroma). Images were collected with MetaMorph software (Molecular Devices) and an Orca100 camera (Hamamatsu). Plants generated by five independent transformation events, all with rescued period, produced identical localization patterns.

Immunoblot

xct-2 or xct-2 plants containing XCTpro:XCT-YFP-HA pEG301/101 were germinated on filter paper (Whatman) on MS media containing 3% sucrose and stored at 80°C until collection. Samples were collected in liquid nitrogen, and RNA was prepared with TRIzol reagent (Invitrogen) for analysis by qRT-PCR. Data are representative of two independent replicates each with 18 individuals per genotype in short days and 9 to 25 individuals per genotype in long days.

Period and Hypocotyl Fluence Rate Response Curves

The response of circadian period and hypocotyl length after 6 d of growth to increased fluence rate was determined as previously described (Martin-Tryon et al., 2007). Difference in slope of period fluence rate response was determined by the interaction between genotype and fluence in ANOVA for general linear fixed-effects models. Response curves are representative of three independent replicates, with 5 to 20 individuals in each condition, in each replicate. Rescued hypocotyl phenotypes are representative of three rescued lines generated by independent transformation events.

Phase Response Curve

After germination on MS media containing 3% sucrose and entrainment in 12:12 LD cycles of 55 μmol m−2 s−1 for 6 d, plants containing the CCR2prom:LUC (Strayer et al., 2000) reporter were moved to constant darkness at subjective dawn (CT 0) for imaging. A subset of individuals (n = 16) received a single 3-h pulse of 40 μmol m−2 s−1 red light at various time points over the course of the next 48 h. After the pulse, plants were returned to constant darkness for imaging. Phase estimates were generated from the time of the first peak of LUC activity after the pulse, corrected to circadian time, and plotted against the circadian time of the light pulse for each plant as previously described (Covington et al., 2001) and are representative of two independent replicates each with 12 to 16 individuals.

Etiolated Pulse Response

Seeds were plated on MS media containing 3% sucrose and stratified for 3 d at 4°C before a 12-h white light pulse of 50 μmol m−2 s−1 to induce germination. Plates were then wrapped in foil and held at 22°C for 108 h before release at subjective dawn (CT 0) to constant red light of 40 μmol m−2 s−1 or constant white light of 50 μmol m−2 s−1, and controls were held in darkness at 22°C until collection. Samples were collected in liquid nitrogen, and RNA was prepared with TRizol reagent (Invitrogen) for analysis by qRT-PCR. Data are representative of two independent biological replicates and three technical replicates for each sample.

Flowering

Stratified seeds were germinated and grown individually on soil at 22°C in short-day cycles of 8 h light at 200 μmol m−2 s−1 and 16 h of darkness or long-day cycles of 16 h light at 100 μmol m−2 s−1 and 8 h of darkness; light was provided by cool white fluorescent bulbs (Sylvania and Philips). Rosette leaf number was counted when a 1-cm bolt was present. Data are representative of two independent replicates each with 18 individuals per genotype in short days and 9 to 25 individuals per genotype in long days.

Accession Numbers

Sequence data for XCT and other XAPS homologs can be found in the GenBank/EMBL data libraries under accession numbers At2g21150 (Arabidopsis XCT), Os09g0535300 (Oryza sativa), CAB46282 (Mus musculus XAPS), mCG48748 (M. musculus XAPS like), XP_001183761 (Strongyloteenotus purpuratus), NP_004690 (Homo sapiens XAPS), NP_036267 (H. sapiens XAPS like), NP_001080084 (Xenopus laevis), NP_001176336 (Danio rerio), NP_651595 (Drosophila melanogaster), NP_506625 (Cannorhabditis elegans), and NP_587947 (S. pombe). Sequence data for PP2a can be found under accession number At1g13320.

Supplemental Data

The following materials are available in the online version of this article.

Supplemental Figure 1. qRT-PCR Analysis of Expression Profiles of Clock Components.

Supplemental Figure 2. Analysis of XCT Expression in xct Mutants.
Supplemental Figure 3. Alignment of XAPS Proteins from Plants and Animals.

Supplemental Figure 4. N- and C-Terminal Fusions between XCT and YFP Are Found in the Nuclei of Juvenile and Adult Plants.

Supplemental Figure 5. Short-Day (8:16 LD) Expression Profiles of Clock Genes in xct Mutants.

Supplemental Figure 6. The Phase of CONSTANS Expression is Unaltered in xct Mutants.

Supplemental Figure 7. Leaf Number at Bolting for Various Clock Mutants Grown in Long or Short Days.

Supplemental Figure 8. Etiolated xct Seedlings Do Not Have a Hypocotyl Phenotype.

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