Transcriptional Feedback Loop Regulation, Function, and Ontogeny in Drosophila

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The Drosophila circadian oscillator is composed of interlocked period/timeless (per/tim) and Clock (Clk) transcriptional feedback loops. These feedback loops drive rhythmic transcription having peaks at dawn and dusk during the daily cycle and function in the brain and a variety of peripheral tissues. To understand how the circadian oscillator keeps time and controls metabolic, physiological, and behavioral rhythms, we must determine how these feedback loops regulate rhythmic transcription, determine the relative importance of the per/tim and Clk feedback loops with regard to circadian oscillator function, and determine how these feedback loops come to be expressed in only certain tissues. Substantial insight into each of these issues has been gained from experiments performed in our lab and others and is summarized here.

INTRODUCTION

As in other organisms, the circadian clock in Drosophila controls daily rhythms in physiology, metabolism, and behavior through a self-sustaining oscillator that is synchronized to environmental cycles in light and temperature but keeps time even in the absence of environmental cues. The Drosophila circadian oscillator is composed of interlocked period/timeless (per/tim) and Clock (Clk) feedback loops that regulate rhythmic transcription in different phases of the circadian cycle (for review, see Hardin 2006; Yu and Hardin 2006). The transcriptional rhythms imparted by these feedback loops not only maintain circadian oscillator function, but also activate clock “output genes” that control physiological, metabolic, and behavioral processes in various tissues (Claridge-Chang et al. 2001; McDonald and Roshbash 2001; Ceriani et al. 2002; Y. Lin et al. 2002; Ueda et al. 2002; Wijnen et al. 2006). Because transcriptional regulation is critically important for circadian clock function in all organisms (Young and Kay 2001; Bell-Pedersen et al. 2005), a major focus within the circadian rhythms field has been to define the mechanisms through which transcriptional feedback loops mediate rhythmic transcription.

One of the best-characterized transcriptional feedback loops is the per/tim feedback loop in Drosophila (Fig. 1). This feedback loop is initiated when CYCLE (CYC) forms a heterodimer with CLK and binds E-box regulatory sequences to activate per and tim transcription around midday or zeitgeber time 6 (ZT6) (note: Zeitgeber time refers to time during a light-dark cycle where ZT0 is lights-on and ZT12 is lights-off [Darlington et al. 1998]). Although per and tim mRNAs accumulate to high levels around dusk (ZT12) (Hardin et al. 1990; Sehgal et al. 1995), PER and TIM proteins do not feed back to inhibit CLK-CYC transcription until midnight (ZT18) because of a phosphorylation-dependent delay in their accumulation and nuclear localization (Kloss et al. 1998, 2001; Price et al. 1998; Martinek et al. 2001; J.M. Lin et al. 2002; Akten et al. 2003). Degradation of PER and TIM in the early morning (ZT4) releases transcriptional inhibition to enable the next round of CLK-CYC transcriptional activation (Hunter-Ensor et al. 1996; Myers et al. 1996; Zeng et al. 1996; Naidoo et al. 1999; Grima et al. 2002; Ko et al. 2002). The per/tim feedback loop is necessary for, and intrinsically linked to, the Clk feedback loop, which drives rhythms in Clk mRNA expression that peak around dawn (ZT0) (Glossop et al. 1999). The Clk feedback loop is initiated when CLK-CYC binds E boxes to activate vrille (vri) and PAR domain protein 1ε (Pdp1ε) transcription (Cyran et al. 2003; Glossop et al. 2003). VRI protein accumulates to high levels in concert with vri mRNA during the early night (ZT15) and binds V/P boxes to inhibit Clk transcription (Cyran et al. 2003; Glossop et al. 2003). PDP1ε protein does not accumulate to high levels until late evening (ZT21), when it is thought to compete with decreasing levels of VRI for V/P-box binding to activate Clk transcription (Cyran et al. 2003). Although the per/tim and Clk feedback loops control rhythmic transcription within (and downstream from) the circadian oscillator, their relative contributions to oscillator function and overt rhythmicity are less well understood. Accumulating data from our lab and others suggest that the Clk feedback loop is not necessary for circadian oscillator function. Moreover, recent data from our lab argue that PDP1ε is a critical output factor, rather than a major Clk transcriptional activator, and that key factors controlling rhythmic transcription within the Clk loop are yet to be identified.

Circadian feedback loop oscillators function in several clusters of brain neurons and numerous peripheral tissues in Drosophila (Hall 2003; Helfrich-Forster 2005). Because CLK-CYC heterodimers initiate both per/tim and Clk feedback loop function, factors that activate Clk and cyc would then be primary determinants of oscillator cell fate. However, the situation is more complicated because CLK is also expressed in cells that do not harbor circadian oscillators (i.e., nonoscillator cells) (Houl et al. 2003).
2006); thus, not all Clk activators initiate oscillator function. The spatial expression of CYC has not yet been determined, but it may also be expressed in nonoscillator cells. Circadian oscillators in various cells and tissues begin to function at different times during development. Oscillators in three clusters of brain neurons begin to function during the first larval instar (Sehgal et al. 1992), whereas oscillators in other groups of brain neurons and in peripheral tissues do not start to function until the late pupal/early adult stage (Liu et al. 1988; Kaneko et al. 1997). How these various cells and tissues are fated to contain circadian oscillators is not known, but determining when CLK and CYC expression is initiated during development will provide insight into when these cell-fate decisions are taking place. Moreover, such analysis may suggest candidate Clk activators that not only establish oscillator cell fate, but maintain Clk transcriptional activation, and thus per/tim and Clk feedback loop function, in adults.

THE SIGNIFICANCE OF RHYTHMIC TRANSCRIPTION AND PER/TIM AND CLK FEEDBACK LOOP FUNCTION

Since the initial discovery that molecular feedback loops control rhythmic transcription of core circadian clock components in Drosophila (Hardin et al. 1990, 1992), considerable effort has been directed toward defining the mechanisms that regulate rhythmic transcription. Consequently, we have a detailed, although not comprehensive, understanding of the factors and interactions that control rhythmic transcription. In contrast, relatively little attention has been paid to determining whether rhythmic transcription is necessary to maintain feedback loop function. Although some studies argue that rhythmic transcription is not necessary for circadian oscillator function, there is a growing consensus that rhythmic transcription is indeed required.

The key regulatory events governing circadian transcription within the per/tim loop are transcriptional activation by CLK-CYC heterodimers and transcriptional repression by PER-containing complexes (Fig. 1). Transcriptional activation and repression are temporally separated: Activation occurs from midday (ZT6) through mid-evening (ZT18) and repression begins around mid-evening and is relieved around midday (for review, see Yu and Hardin 2006). This separation of transcriptional activation and repression is primarily regulated by phosphorylation of CLK, PER, and TIM. CLK is rhythmically phosphorylated in phase with CLK-CYC transcriptional activity: Hypophosphorylated CLK predominates when CLK-CYC target genes are activated and hyperphosphorylated CLK predominates when CLK-CYC target genes are repressed (Kim and Edery 2006; Yu et al. 2006). CLK hyperphosphorylation is PER-dependent and occurs in
CIRCADIAN GENE EXPRESSION

confront with the accumulation of phosphorylated PER in CLK-CYC complexes in the nucleus (Lee et al. 1998; Kim and Edery 2006; Yu et al. 2006). DOUBLE-TIME (DBT) kinase-dependent phosphorylation promotes PER degradation (Price et al. 1998), whereas TIM stabilizes PER by blocking DBT phosphorylation (Price et al. 1995; Ko et al. 2002). Phosphorylation of PER by casein kinase 2 (CK2) and TIM by SHAGGY (SGG) kinase promotes PER and TIM nuclear localization, respectively (Martinek et al. 2001; J.M. Lin et al. 2002; Akten et al. 2003; Nawathean and Rosbash 2004). TIM is degraded around dawn, which facilitates DBT-dependent degradation of hyperphosphorylated PER and CLK and transcriptional activation by accumulating levels of hypophosphorylated CLK (Hunter-Ensor et al. 1996; Myers et al. 1996; Zeng et al. 1996; Ko et al. 2002; Kim and Edery 2006; Yu et al. 2006).

Because posttranslational regulation of PER and TIM mediates CLK phosphorylation and transcriptional activity, is rhythmic transcription of per and tim (and by extension per and tim mRNA cycling) necessary for circadian oscillator function? Transgenic flies expressing constitutive levels of either per or tim mRNAs had little effect on molecular and behavioral rhythms (Cheng and Hardin 1998; Yang and Sehgal 2001). Likewise, about half of the transgenic fly lines that express constant levels of both per and tim mRNAs retained molecular and behavioral rhythmicity, suggesting that mRNA rhythms are not necessary for circadian oscillator function (Yang and Sehgal 2001). However, the lack of rhythmicity in half the transgenic lines and severe decrements in molecular and behavioral rhythmicity in the others suggest that mRNA cycling is important, if not essential, for circadian oscillator function. The transgenic lines used to constitutively express per and tim mRNAs (Yang and Sehgal 2001) were recently retested and found to display less than 20% rhythmicity that was generally weak and in a broad range of circadian periodicities, indicating that per and tim mRNA rhythms are indeed required for circadian oscillator function in Drosophila (Hall et al., this volume).

In the Clk feedback loop, rhythms in the VRI/PDP1 ε null mutant flies (Cyran et al. 2003). Activation of Clk by PDP1ε was unexpected because Clk mRNA levels are high in Clkε and cyc01 flies even there is little or no PDP1ε. Although it is possible that small amounts of PDP1ε could predominate over low levels of VRI to activate Clk in Clkε and cyc01 mutants, this would contrast with the relationship between these proteins in per01 and tim01 flies, where high levels of VRI predominate over consolidation of locomotor activity rhythms (Sato et al. 2004). Another potential function for the Clk loop is to drive outputs that require transcriptional activation around dawn. Although no output genes have been identified that are directly under Clk feedback loop control (i.e., activated by PDP1ε and/or repressed by VRI), microarray screens have identified a large number of potential Clk feedback loop target genes whose mRNAs peak at dawn (Claridge-Chang et al. 2001; McDonald and Rosbash 2001; Ceriani et al. 2002; Y. Lin et al. 2002; Ueda et al. 2002; Wijnen et al. 2006).

REGULATION OF RHYTHMIC TRANSCRIPTION WITHIN THE Clk FEEDBACK LOOP

The Clk feedback loop was first proposed to explain the opposite phase cycling of Clk mRNA with respect to per and tim mRNAs (Glossop et al. 1999). Clk transcription is repressed when Clk-CYC activity is high from midnight to midnight in wild-type flies and in per01 or tim01 mutants, whereas Clk transcription is activated when Clk-CYC activity is low from midnight to midday in wild-type flies and in Clkε or cyc01 mutants. The high levels of Clk mRNA in Clkε and cyc01 flies predict that Clk is activated by a factor that is not dependent on circadian oscillator function. In contrast, the low levels of Clk mRNA in per01 and tim01 mutants suggest that Clk-CYC activates a repressor.

One CLK-CYC-activated transcript identified in a screen for rhythmically expressed mRNAs encodes the bZIP (basic leucine zipper) repressor VRI (Blau and Young 1999). Although circadian phenotypes cannot be measured in vri null mutants due to developmental lethality (George and Terracol 1997), VRI overexpression represses Clk and CLK-CYC-dependent transcripts such as per and tim (Blau and Young 1999; Cyran et al. 2003; Glossop et al. 2003). VRI accumulates in phase with its mRNA from midday to early evening (Cyran et al. 2003; Glossop et al. 2003), consistent with the timing of Clk repression and the dependence of Clk repression on CLK-CYC activity (Fig. 1). Another rhythmically expressed transcript that is dependent on CLK-CYC, Pdp1ε, encodes a bZIP activator with high similarity to VRI (Claridge-Chang et al. 2001; McDonald and Rosbash 2001; Ceriani et al. 2002; Y. Lin et al. 2002; Ueda et al. 2002; Cyran et al. 2003; Wijnen et al. 2006). Pdp1ε mRNA and protein accumulate to high levels several hours later than vri mRNA and protein, suggesting that accumulating Pdp1ε could activate Clk transcription late at night as VRI levels fall (Fig. 1). Consistent with this possibility, PDP1ε binds V/P-box elements in vitro, PDP1ε competes with VRI to activate Clk transcription in cell culture, and little or no Clk mRNA is detected in Pdp1ε null mutant flies (Cyran et al. 2003). Activation of Clk by PDP1ε was unexpected because Clk mRNA levels are high in Clkε and cyc01 flies even there is little or no PDP1ε. Although it is possible that small amounts of PDP1ε could predominate over low levels of VRI to activate Clk in Clkε and cyc01 mutants, this would contrast with the relationship between these proteins in per01 and tim01 flies, where high levels of VRI predominate over
high levels of PDP1ε to repress Clk (Cyran et al. 2003). Pdp1ε produces multiple RNA and protein isoforms that are expressed in a variety of tissues including the central nervous system (CNS) (Reddy et al. 2000). Deletion of Pdp1 leads to severe defects in growth, mitosis, and endocytosis that cause lethality during larval stages (Reddy et al. 2006). It is possible that loss of all PDP1 isoforms in the Pdp1 deletion mutant alters clock neuron identity or development in larvae, and thus indirectly reduces Clk mRNA levels.

If Clk mRNA cycling is driven by competition between PDP1ε and VRI for V/P-box binding, then altering the PDP1ε/VRI ratio by reducing or increasing PDP1ε expression specifically in circadian clock cells should disrupt Clk mRNA cycling by producing a constant trough or peak levels of Clk mRNA, respectively. When PDP1ε was reduced to its normal trough level or below via RNA interference (RNAi), Clk mRNA continued to cycle similarly to the wild-type controls with the exception of a lower Clk mRNA level at ZT1 (Fig. 2). VRI levels continued to cycle in flies expressing low levels of PDP1ε, consistent with its role as a Clk repressor (Fig. 2). Similar results were seen when PDP1ε levels were increased to ≥5-fold above its normal peak: Clk mRNA and VRI protein levels continued to cycle with amplitudes comparable to wild-type controls (Fig. 3). These results demonstrate that PDP1ε levels, and thus the PDP1ε/VRI ratio, are not critical for Clk mRNA cycling or circadian oscillator function (Benito et al. 2007). Moreover, the wild-type levels of Clk mRNA in Pdp1 RNAi and Pdp1ε overexpression strains suggest that PDP1ε is not the major Clk activator, although a minor role in Clk activation cannot be discounted (Benito et al. 2007).

FUNCTION OF PDP1ε WITHIN THE CIRCADIAN CLOCK

Because circadian oscillator function is not disrupted in flies with constant low or high levels of PDP1ε, perhaps PDP1ε functions to control clock output. To test this possibility, locomotor activity rhythms were measured in Pdp1 RNAi, Pdp1ε overexpression, and control strains (Benito et al. 2007). Flies expressing low or high levels of PDP1ε show drastic reductions in behavioral rhythm compared to control strains (Table 1). Despite this loss in behavioral rhythm, oscillator function persists in locomotor activity pacemaker cells or lateral neurons (LNs), which indicates that PDP1ε controls clock output (Benito et al. 2007). Because PDP1ε is a rhythmically expressed bZIP transcriptional factor, it is likely to mediate behavioral rhythms by rhythmically activating effector genes. These PDP1ε-dependent rhythmic transcripts may represent some of those identified in previous microarray studies that peak in abundance around dawn (Claridge-Chang et al. 2001; McDonald and Rosbash 2001; Ceriani et al. 2002; Y. Lin et al. 2002; Ueda et al. 2002; Wijnen et al. 2006). These data suggest a revised model for clock function in Drosophila in which a constitutive activator and VRI mediate Clk mRNA cycling within the Clk feedback loop (Fig. 1). PDP1ε may have a minor role in regulating Clk transcription, but it is proposed to be a major regulator of output transcription required for (at least) behavioral rhythm (Benito et al. 2007). VRI may also function to control output transcription along with PDP1ε, but it is worth noting that VRI’s role within the clock is based on gain-of-function experiments. Eliminating VRI function within oscillator cells
will more definitively pinpoint VRI’s role within the clock.

The mammalian homologs of PDP1ε and VRI likely have an analogous role in regulating clock output. PDP1ε is related to three rhythmically expressed PAR domain-containing bZIP transcriptional activators in mammals: albumin gene site D-binding protein (DBP), thyroid embryonic factor (TEF), and hepatocyte leukemia factor (HLF) (Wuarin and Schibler 1990; Falvey et al. 1995; Fonjallaz et al. 1996). DBP knockout mice show lower locomotor activity levels and a shorter circadian period than wild-type animals, yet robust circadian oscillator function persists (Lopez-Molina et al. 1997). These results imply that DBP functions primarily to control clock output, consistent with PDP1ε function in flies.

DBP binds to the same regulatory element as adenovirus E4 promoter ATF site-binding protein (E4BP4), a rhythmically expressed bZIP repressor related to VRI (Mitsui et al. 2001). Because E4BP4 is expressed in the opposite phase than DBP (Mitsui et al. 2001), sequential binding of E4BP4 and DBP could control rhythmic target gene transcription.

### Table 1. Reducing and Increasing PDP1ε Levels Disrupts Locomotor Activity Rhythms

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Percent rhythmic (N)</th>
<th>Period (h) ± S.E.M.</th>
<th>Power ± S.E.M.</th>
<th>Activity ± S.E.M.</th>
</tr>
</thead>
<tbody>
<tr>
<td>w/+;+/+</td>
<td>75.0 (172)</td>
<td>23.8 ± 0.03</td>
<td>78.9 ± 3.7</td>
<td>17.8 ± 0.6</td>
</tr>
<tr>
<td>w;+/+;tim-Gal4/+</td>
<td>80.5 (41)</td>
<td>24.6 ± 0.07</td>
<td>76.7 ± 5.4</td>
<td>16.7 ± 0.9</td>
</tr>
<tr>
<td>w;+/+;pdf-Gal4/+</td>
<td>57.0 (35)</td>
<td>24.2 ± 0.13</td>
<td>68.7 ± 7.7</td>
<td>14.0 ± 0.8</td>
</tr>
<tr>
<td>w;PDP1a/+;PDP1b/+</td>
<td>77.8 (38)</td>
<td>23.4 ± 0.08</td>
<td>72.8 ± 5.3</td>
<td>28.3 ± 2.1</td>
</tr>
<tr>
<td>w;PDP1a/+;PDP1b;tim-Gal4</td>
<td>17.2 (29)</td>
<td>25.3 ± 0.23</td>
<td>35.3 ± 1.7</td>
<td>13.5 ± 1.0</td>
</tr>
<tr>
<td>w;PDP1a/+;PDP1b;pdf-Gal4</td>
<td>0 (27)</td>
<td>n.a.</td>
<td>n.a.</td>
<td>12.1 ± 0.7</td>
</tr>
<tr>
<td>w;+/+;+/+</td>
<td>96.0 (25)</td>
<td>23.5 ± 0.15</td>
<td>96.1 ± 6.4</td>
<td>19.9 ± 2.3</td>
</tr>
<tr>
<td>w;+/+;tim-Gal4/+</td>
<td>100 (31)</td>
<td>24.4 ± 0.21</td>
<td>78.4 ± 5.2</td>
<td>21.6 ± 2.0</td>
</tr>
<tr>
<td>w;+/+;pdf-Gal4/+</td>
<td>95.5 (22)</td>
<td>24.3 ± 0.09</td>
<td>76.4 ± 9.5</td>
<td>13.5 ± 2.3</td>
</tr>
<tr>
<td>w;PDP1a/PDP1b;+/+</td>
<td>73.9 (29)</td>
<td>24.5 ± 0.16</td>
<td>78.1 ± 11.7</td>
<td>27.1 ± 3.9</td>
</tr>
<tr>
<td>w;PDP1a/+;PDP1b;tim-Gal4</td>
<td>12.5 (31)</td>
<td>25.2 ± 0.12</td>
<td>24.5 ± 5.9</td>
<td>15.4 ± 1.8</td>
</tr>
<tr>
<td>w;PDP1a/+;PDP1b;pdf-Gal4</td>
<td>10.3 (29)</td>
<td>24.1 ± 0.02</td>
<td>27.2 ± 2.3</td>
<td>19.1 ± 1.5</td>
</tr>
</tbody>
</table>

Period and power were calculated for all rhythmic animals as described in Benito et al. (2007). Activity was calculated for all flies that survived to the end of the experiment, as described in Benito et al. (2007). n.a. indicates not applicable. (Reprinted, with permission, from Benito et al. 2007 ©The Society for Neuroscience.)
REGULATION OF CLK SPATIAL EXPRESSION

Circadian oscillator cells from *Drosophila* can be identified by the rhythmic expression of *per* and *tim* mRNA and protein (Hardin 1994; Plautz et al. 1997). In adults, oscillator cells have been identified in the brain, i.e., four clusters of lateral neurons (dorsal lateral neurons [LN]$_{0,5}$; small ventral lateral neurons [sLN]$_{0,5}$; large ventral lateral neurons [LNL]$_{0,5}$; and a lateral posterior neuron [LPN]) and three clusters of dorsal neurons (dorsal neuron 1 [DN1]; dorsal neuron 2 [DN2]; and dorsal neuron 3 [DN3]), and in peripheral tissues (e.g., the gut, fat body, Malpighian tubules, the antenna, compound eye, proboscis, wing, and leg) (Hall 2003; Helfrich-Forster 2005; Shafer et al. 2006). Although a subset of oscillator neurons in the brain control morning and evening activity and oscillator neurons in the antenna control olfactory responses (Krishnan et al. 1999; Grima et al. 2004; Stoleru et al. 2004), outputs from other adult brain and peripheral oscillator cells have not been characterized. Circadian control of tissue-specific processes in *Drosophila* and other animals is thought to enable coordinate temporal control of behavior, physiology, and metabolism. Despite the importance of oscillator function in different tissues, relatively little is known about how this tissue-specific pattern of oscillator expression is specified.

Because CLK-CYC initiates circadian oscillator function by activating *per*, *tim*, *vri*, and *Pdp1e* expression (Fig. 1), coexpression of CLK and CYC necessarily determines which tissues contain circadian oscillators. Such coexpression could arise by (1) expression of both CLK and CYC specifically in oscillator cells, (2) broad expression of CLK and oscillator-specific expression of CYC, (3) broad expression of CYC and oscillator-cell-specific expression of CLK, or (4) broad expression of CLK and CYC that overlaps specifically in oscillator cells. Localization of CLK has provided insight into which of these scenarios for CLK and CYC coexpression is correct.

In adults, CLK is expressed in all oscillator cells as expected, but it is also expressed in nonoscillator cells (Houl et al. 2006). This result was somewhat surprising because previous work had shown that ectopic expression of CLK in certain brain neurons could generate circadian oscillators (Zhao et al. 2003). Perhaps CLK is able to induce oscillator function only in cells that already express CYC and the kinases and phosphatases that mediate feedback repression by PER and TIM. CRY expression in ectopic oscillator cells, and thus the ability of these oscillators to entrain to light, may come from CLK-CYC-dependent induction of the candidate cryn activator PDP1e (Cyran et al. 2003). In any case, expression of CLK in nonoscillator cells indicates that oscillator cells are determined by either oscillator-cell-specific expression of CYC or the overlapping expression of CLK and CYC specifically in oscillator cells. These possibilities can be distinguished when reagents necessary to localize CYC are available.

Circadian oscillators in the brain start to be expressed at earlier times during development than those in peripheral tissues. Brain oscillator cells can be detected as early as the first larval instar and include precursors to the LNVs, DN2s, and a subset of DN1s (Sehgal et al. 1992; Kaneko et al. 1997; Helfrich-Forster 2005). PER expression in photoreceptors and the antenna is not detected until late during pupal development, indicating that functional oscillators are not expressed in these peripheral tissues until just before flies eclose (Liu et al. 1988). CLK expression precedes oscillator function in the larval brain and can be seen as early as embryonic stage 11, which indicates that brain oscillators are determined during mid embryogenesis (F.S. Ng et al., unpubl.).

Factors that activate CLK and/or CYC in oscillator cells have not yet been identified. Given the diverse array of brain cells and peripheral tissues that contain circadian oscillators, it is likely that multiple tissue-specific factors activate CLK and CYC in oscillator cells. CLK is activated in locomotor activity pacemaker neurons during embryogenesis, well before oscillator function is initiated in L1 larvae, and more than 1 week before these neurons control locomotor activity rhythms. Pacemaker neurons are unique in that they appear to be dedicated to controlling activity rhythms, yet are not required for locomotor activity per se. In contrast, peripheral oscillators are thought to control outputs inherent to a given tissue, where the tissue is necessary for the process being modulated. For instance, *Drosophila* olfactory sensory neurons (OSNs) control rhythms in electrophysiological responses to odors and are necessary for odor-dependent electrophysiological responses per se (Tanoue et al. 2004; Vosshall and Stocker 2007). CLK is presumably activated just before *per* and *tim* when OSNs and other clock-containing peripheral tissues are differentiating in late pupae (Liu et al. 1988). The activation of CLK during peripheral tissue differentiation implies that oscillator function is a core property of these tissues. When these activators are identified, it will be important to determine whether they also activate CYC and whether they maintain CLK activation in adults. Because circadian oscillators in the hypothalamic suprachiasmatic nucleus and peripheral tissues of mammals are analogous to the locomotor activity pacemaker neurons and peripheral oscillator tissues in flies, respectively, similar mechanisms may be responsible for specifying clock cell identity in mammals.

CONCLUSIONS

The core circadian timekeeping mechanism operates through interlocked *per/tim* and CLK feedback loops that regulate rhythmic transcription peaking around dusk and dawn, respectively. Although it is well established that phosphorylation-dependent rhythms in PER and TIM abundance are necessary for circadian oscillator function, mounting evidence indicates that rhythms in *per* and *tim* transcription are also required for circadian oscillator function. Presumably high levels of *per* and *tim* mRNAs at inappropriate times alters the overall levels, cycling phase, or activity of PER and TIM, thereby disrupting oscillator function. In contrast, reversing rhythms in CLK mRNA abundance disrupts neither circadian oscillator function nor CLK phosphorylation rhythms, indicating that CLK mRNA rhythms are dispensable. Taken together...
with the PER dependence of rhythms in CLK phosphorylation, these results argue that the per/tim feedback loop has a dominant role in maintaining circadian oscillator function. Despite its subservient role within the Drosophila circadian oscillator, the Clk feedback loop regulates rhythmic transcription in a phase opposite to that of the per/tim feedback loop. Clk feedback-loop-dependent transcription of genes such as Clk was initially thought to be mediated by competition between VRI and PDP1ε transcription at dusk because the VRI/PDP1ε ratio is high, and PDP1ε binds V/P boxes to activate Clk transcription at dawn because the VRI/PDP1ε ratio is low. However, we recently found that altering the VRI/PDP1ε ratio by reducing or increasing PDP1ε levels had little effect on Clk transcription or VRI cycling. Taken together with the constant high levels of Clk mRNA in mutants that express little if any VRI or PDP1ε (i.e., ClkεDK and cyeα), this result suggests a model in which VRI periodically represses the constant activation of Clk transcription. Although PDP1ε does not greatly affect Clk transcription, PDP1ε is required for rhythms in locomotor activity. We hypothesize that PDP1ε has a major role in activating genes that control rhythmic outputs, perhaps in conjunction with VRI. Such a role is consistent with that proposed for DBP and E4BP4, the mammalian homologs of PDP1ε and VRI, respectively.

Circadian oscillators are expressed in several clusters of brain neurons and a variety of peripheral tissues. This spatial distribution is controlled by factors that activate Clk and cye because CLK-CYC initiates circadian oscillator function. However, Clk expression is not restricted to oscillator cells, which suggests that CYC is either specifically expressed only in oscillator cells or that CYC is broadly expressed and specifically overlaps Clk expression in oscillator cells. Moreover, expression of Clk in nonoscillator cells indicates that Clk contributes to processes other than circadian oscillator function. Nevertheless, ectopic expression of Clk in certain brain cells can generate circadian oscillator function, presumably because these cells already express CYC and kinases/phosphatases normally found in oscillator cells. The developmental expression of Clk suggests that locomotor activity pacemaker cells are determined during mid embryogenesis. Clk appears to be activated in peripheral oscillator tissues around the time they differentiate in late pupae. Insight into oscillator cell determination and maintenance will come with the identification and characterization of Clk and cye activators.

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