Title
CK1δ/ε protein kinase primes the PER2 circadian phosphoswitch.

Permalink
https://escholarship.org/uc/item/4kf5f80v

Journal
Proceedings of the National Academy of Sciences of the United States of America, 115(23)

ISSN
0027-8424

Authors
Narasimamurthy, Rajesh
Hunt, Sabrina R
Lu, Yining
et al.

Publication Date
2018-06-01

DOI
10.1073/pnas.1721076115

Peer reviewed
CK1δ/ε protein kinase primes the PER2 circadian phosphoswitch

Rajesh Narasimamurthy, Sabrina R. Hunt, Yining Lu, Jean-Michel Fustin, Hitoshi Okamura, Carrie L. Partch, Daniel B. Forger, Jae Young Kim, and David M. Virshup

*Programme in Cancer and Stem Cell Biology, Duke-NUS Medical School, 169857 Singapore; †Department of Chemistry and Biochemistry, University of California, Santa Cruz, CA 95064; ‡Department of Mathematics, University of Michigan, Ann Arbor, MI 48109; §Department of Computational Medicine and Bioinformatics, University of Michigan, Ann Arbor, MI 48109; ©Department of Systems Biology, Graduate School of Pharmaceutical Sciences, Kyoto University, Sakyoku, 606-8501 Kyoto, Japan; ‖Center for Circadian Biology, University of California, San Diego, La Jolla, CA 92033; ††The Michigan Institute for Data Science, University of Michigan, Ann Arbor, MI 48109; §§Department of Mathematical Sciences, Korea Advanced Institute of Science and Technology, 34141 Daejeon, Korea; and Department of Pediatrics, Duke University Medical Center, Durham, NC 27710

Edited by Joseph S. Takahashi, Howard Hughes Medical Institute and University of Texas Southwestern Medical Center, Dallas, TX, and approved April 27, 2018 (received for review December 4, 2017)

Multisite phosphorylation of the PERIOD 2 (PER2) protein is the key step that determines the period of the mammalian circadian clock. Previous studies concluded that an unidentified kinase is required to prime PER2 for subsequent phosphorylation by casein kinase 1 (CK1), an essential clock component that is conserved from algae to humans. These subsequent phosphorylations stabilize PER2, delay its degradation, and lengthen the period of the circadian clock. Here, we perform a comprehensive biochemical and biophysical analysis of mouse PER2 (mPER2) priming phosphorylation and demonstrate, surprisingly, that CK1δ/ε is indeed the priming kinase. We find that both CK1δ and a recently characterized CK1δ splice variant more efficiently prime mPER2 for downstream phosphorylation in cells than the well-studied splice variant CK1δ1. While CK1δ phosphorylation of PER2 was previously shown to be robust to changes in the cellular environment, our phosphoswitch mathematical model of circadian rhythms shows that the CK1 carboxyl-terminal tail can allow the period of the clock to be sensitive to cellular signaling. These studies implicate the extreme carboxyl terminus of CK1δ as a key regulator of circadian timing.

Characterization of circadian rhythm mutants has provided key insight into the role that phosphorylation plays in the clock mechanism. Mutations that alter phosphorylation of PER cause dramatic changes in the circadian period of Drosophila, mice, hamsters, and even humans (9–14). An inherited polymorphism of Ser-662 (S662G) in humans enhances PER2 degradation, shortens circadian period, and causes familial advanced sleep phase (FASP) syndrome (11). Despite the importance of the FASP site, it is still unclear how it gets phosphorylated. Two casein kinase 1 (CK1) genes, CSNK1D and CSNK1E, encode kinases (CK1δ and CK1ε, respectively) that phosphorylate PER2 at two key regions that control a “phosphoswitch” mechanism regulating PER2 stability (5, 15). While CK1δ is more abundant than CK1ε and may play a major role in regulating rhythms in most tissues (16–18), the fact that a single amino acid change in CK1ε (CK1εS662I, R178C) in hamsters and mice shortens period by 2 and 4 h in the heterozygote and homozygote, respectively, and loses temperature compensation indicates a major role for CK1δ in rhythms as well (12, 14, 19, 20).

Multiple studies and recent reviews have concluded that an additional but currently unidentified “priming” kinase is required to phosphorylate the FASP site before the downstream serines can be phosphorylated by CK1δ and/or CK1ε (4, 11, 13, 21). This is because members of the CK1 family preferentially phosphorylate primed sites—that is, sites where a phosphorylated residue drives recognition of a downstream serine in the +3 position (22). There are four serine residues with this spacing immediately downstream of S659 in mPER2 (S662 in humans) (Fig. 1 A). Based on in vitro assays using peptide substrates, it appears that the downstream serines are phosphorylated by CK1δ/ε only after S659 is primed. The importance of this S659 priming site is illustrated by mice with a phosphomimetic mutation (Ser to Asp)

The PERIOD (PER) proteins are the central regulators of the metazoan circadian (daily) clock. per was originally discovered in Drosophila as a gene whose mutation could lead to a short or long period, initiating the modern era of molecular circadian biology (1). In all metazoan clocks, PER expression oscillates at both the mRNA and protein levels, with posttranslational control of PER protein stability tightly regulated by phosphorylation (2, 3). PER phosphorylation also plays a critical role in a process known as temperature compensation, a defining feature of circadian rhythms that confers stable clock timing independent of ambient temperature (4–6). Due to its central role in controlling circadian period, pharmacological modification of PER2 phosphorylation is being pursued to alter circadian rhythms and ameliorate jet lag and seasonal affective disorder (7, 8). However, the complex process by which phosphorylation controls PER stability is still not well understood.

Characterization of circadian rhythm mutants has provided key insight into the role that phosphorylation plays in the clock mechanism. Mutations that alter phosphorylation of PER cause dramatic changes in the circadian period of Drosophila, mice, hamsters, and even humans (9–14). An inherited polymorphism of Ser-662 (S662G) in humans enhances PER2 degradation, shortens circadian period, and causes familial advanced sleep phase (FASP) syndrome (11). Despite the importance of the FASP site, it is still unclear how it gets phosphorylated. Two casein kinase 1 (CK1) genes, CSNK1D and CSNK1E, encode kinases (CK1δ and CK1ε, respectively) that phosphorylate PER2 at two key regions that control a “phosphoswitch” mechanism regulating PER2 stability (5, 15). While CK1δ is more abundant than CK1ε and may play a major role in regulating rhythms in most tissues (16–18), the fact that a single amino acid change in CK1ε (CK1εS662I, R178C) in hamsters and mice shortens period by 2 and 4 h in the heterozygote and homozygote, respectively, and loses temperature compensation indicates a major role for CK1δ in rhythms as well (12, 14, 19, 20).

Multiple studies and recent reviews have concluded that an additional but currently unidentified “priming” kinase is required to phosphorylate the FASP site before the downstream serines can be phosphorylated by CK1δ and/or CK1ε (4, 11, 13, 21). This is because members of the CK1 family preferentially phosphorylate primed sites—that is, sites where a phosphorylated residue drives recognition of a downstream serine in the +3 position (22). There are four serine residues with this spacing immediately downstream of S659 in mPER2 (S662 in humans) (Fig. 1 A). Based on in vitro assays using peptide substrates, it appears that the downstream serines are phosphorylated by CK1δ/ε only after S659 is primed. The importance of this S659 priming site is illustrated by mice with a phosphomimetic mutation (Ser to Asp)

Significance

Our innate circadian clocks control myriad aspects of behavior and physiology. Disruption of our clocks by shift work, jet lag, or inherited mutation leads to metabolic dysregulation and contributes to diseases, including diabetes and cancer. A central step in clock control is phosphorylation of the PERIOD 2 (PER2) protein. Here we conclusively identify the elusive PER2 priming kinase and find it to be the well-known circadian kinase, casein kinase 1 (CK1). Surprisingly, different forms of CK1 have differing abilities to phosphorylate the PER2 priming site, adding to the complexity of circadian regulation. These insights into the phosphoryregulation of PER2 will be of broad interest to circadian biologists, computational modelers, and those seeking to pharmacologically manipulate the circadian clock.


The authors declare no conflict of interest.

This article is a PNAS Direct Submission.

This open access article is distributed under Creative Commons Attribution-NonCommercial-NoDerivatives License 4.0 (CC BY-NC-ND).

Data deposition: The NMR chemical shift assignments for the mPER2 FASP peptide have been deposited in the Biological Magnetic Resonance Bank database (accession no. 27306).

To whom correspondence should be addressed. Email: david.virshup@duke-nus.edu.sg.

This article contains supporting information online at www.pnas.org/lookup/suppl/doi:10.1073/pnas.1721076115/-/DCSupplemental.

Published online May 21, 2018.

PNAS | June 5, 2018 | vol. 115 | no. 23 | 5986–5991

www.pnas.org/cgi/doi/10.1073/pnas.1721076115
Fig. 1. Phosphorylation of the mPER2 priming site by CK1δ is required for downstream phosphorylation of CK1 consensus sites. (A) Schematic diagram of the FASP serine cluster phosphorylation in a synthetic peptide. RKKK, polybasic motif for kinase assay. Dark gray shading indicates minimal FASP peptide used in this study, with phosphorylation sites shown in red; arrows demonstrate the potential for progressive phosphorylation of CK1 consensus sites. Additional downstream phosphorylation sites in PER2 (not included in the minimal FASP peptide) are shown in light gray shading with dashed arrows. (B and C) Time course of representative peptide phosphorylation assays with 20 nM (B) or 200 nM (C) CK1δ ΔC. Error bars represent SD for two biological replicates per assay. The experiment was repeated more than three times, with essentially identical results. (D) Zoom-in view of overlaid 18N/H heteronuclear single quantum correlation spectra of 200 μM 15N mPER2 FASP peptide alone (black) or 4 h after addition of 200 nM CK1δ ΔC (red) at 30 °C. NMR spectra were acquired after kinase reactions were quenched with 20 mM EDTA. (E) Quantification of peak volumes for indicated serines in the 15N FASP peptide from NMR time course (unphosphorylated shown in black; phosphorylated shown in red). Data points are fit to a one-phase exponential curve, except for S665 phosphorylation, which is fit to a linear regression. See SI Appendix, Table S1 for more details. (F and G) Quantification of peak volumes for indicated serine residues in 15N FASP S659A (F) and S662A (G) peptides, as in E. (H) Phosphorylation of S662 is dependent on the S659 site. Full-length wild-type and FASP mutant mPER2 were expressed with or without CK1δ1. Lysates were probed with indicated antibodies. The gel was spliced, as indicated, for clarity.

at the FASP site in a human PER2 transgene, which leads to a longer circadian period, contrasted with the shorter period observed with the Ser to Gly FASP polymorphism (13). The Nemo-like kinase was recently identified as a priming kinase for Drosophila PER, but the identity of the mammalian priming kinase responsible for phosphorylation of S659 in mPER2 remains a major open question in the field (23, 24).

This priming kinase theory is attractive from a systems biology perspective because its action could precisely control PER’s degradation rate, which is a key factor in regulating the timing of the mammalian circadian clock (25). Thus, it opens up the possibility of a signaling mechanism to regulate circadian period through posttranslational modifications of a single site. The delay in PER degradation caused by FASP priming and subsequent downstream site phosphorylation also was shown to be enhanced at higher temperatures, providing a mechanism for how the circadian clock can keep a 24-h period despite increasing reaction rates with increasing temperature (5). However, and despite much effort, the identity of the priming kinase has yet to be discovered.

Here, we show that CK1δ/ε itself is the priming kinase. Using an NMR-based assay that quantitatively probes phosphorylation with site-specific resolution, we demonstrate that phosphorylation of mPER2 S659 by CK1δ/ε is necessary and sufficient for the rapid phosphorylation of downstream consensus sites. In cells, CK1δ and a recently discovered splice variant of CK1δ (CK1δ2) that resembles CK1δ at the extreme carboxyl terminus are more-efficient priming kinases than CK1δ1. Interestingly, our previously proposed phosphoswitch model recapitulates salient features of the model, including the PER2 degradation pattern when CK1δ/ε is introduced as the priming kinase (5). Our modeling work suggests a robust yet fragile design to PER phosphorylation that allows the period of the circadian clock to be robust to environmental variations (e.g., changes in temperature) but also allows for regulatory changes in the CK1 carboxyl terminus to have a large effect on circadian period. This model makes the prediction that the CK1 tail preferentially controls phosphorylation on the FASP site, a prediction that is experimentally verified. Together, this presents a mechanism for regulation of circadian period that is surprisingly divergent from that used in Drosophila.

Results

Procesive Phosphorylation of the mPER2 FASP Region Is Dependent on S659 Phosphorylation. Phosphorylation of the FASP serine cluster of mPER2 by CK1δ/ε following a pSxxS consensus motif is thought to occur processively, but only after phosphorylation of an upstream priming site (S659 on mPER2) by an unidentified kinase, as illustrated in Fig. 1A. To identify the priming kinase and assess the activity of CK1δ/ε on primed peptides, we synthesized a peptide of the mPER2 FASP region containing three potential phosphorylation sites, complete with its native upstream sequence and an amino-terminal basic tag to facilitate peptide kinase assays (Fig. 1A and SI Appendix, Fig. S1A). As predicted, kinase reactions with limiting concentrations of CK1δ ΔC [a constitutively active form of recombinant CK1δ lacking its carboxyl-terminal autoregulatory domain (26)] led to efficient phosphorylation of a primed FASP peptide that was synthetically
phosphorylated on S659 (pS659). However, we noted that the unprimed wild-type peptide (FASP-WT) was also a potential substrate for CK1δ. Since CK1δ is found stably associated with PER1 and PER2 complexes in vivo (2, 27, 28), we reasoned that increasing the kinase concentration would better mimic the in vivo setting where kinase and substrate are found in a stoichiometric complex. Increasing the concentration of CK1δ by only 10-fold led to phosphorylation of the unprimed FASP-WT peptide, but not the S659A mutant (Fig. 1C), suggesting that CK1δ may be capable of acting as the priming kinase when its local concentration is increased relative to the mPER2 substrate. We observed that phosphorylation of the S662A mutant occurred at a rate similar to FASP-WT (Fig. 1C), suggesting that phosphorylation of the priming site at S659 by CK1δ is the rate-limiting step in regulation of the FASP region.

As an independent quantitative approach to study phosphorylation of the mPER2 FASP peptide by CK1δ, we developed an NMR-based kinase assay that utilizes uniformly ^15N-labeled FASP to monitor site-specific detection of phosphorylated residues. Addition of CK1δ to kinase-dependent perturbations of FASP peptide chemical shifts that only occurred in the presence of ATP, consistent with phosphorylation (Fig. 1D and SI Appendix, Fig. S1 B–E). By quantifying peak intensities over time after quenching the kinase assay with EDTA, we observed a progressive loss of intensity for unphosphorylated serines 659, 662, 665 and surrounding peaks, followed by a concomitant increase in intensity for new downfield peaks that correspond to phosphorylated serines (Fig. 1E), as seen in other NMR-based kinase assays (29, 30). CK1δ specifically targets S659 and downstream serines for phosphorylation, because a representative serine upstream of the priming site did not exhibit chemical shifts indicative of phosphorylation. We also observed similar results for kinase assays monitored in real time by NMR (SI Appendix, Fig. S1F). Peaks for phosphorylated S659 and S662 arise at essentially indistinguishable rates, consistent with earlier observations that phosphorylation of the priming site appears to be rate limiting, while phosphorylation of the consensus site downstream at S665 occurs nearly instantaneously after the priming site (SI Appendix, Table S1). Phosphorylation of S665 was noticeably slower, perhaps due to its location near the carboxyl terminus of our minimal FASP peptide (Fig. 1E and SI Appendix, Fig. S1F).

To test the role of priming phosphorylation on S659 for CK1δ activity on downstream sites, we examined activity of the kinase on the ^15N FASP S659A mutant. In the absence of the priming site, we found no detectable phosphorylation anywhere on the FASP peptide (Fig. 1F). This provides clear evidence that CK1δ requires S659 for priming phosphorylation of the mPER2 FASP region in vitro to elicit phosphorylation of downstream consensus sites at S662 and S665. We then used our NMR assay to examine the processivity of phosphorylation at these downstream consensus sites by CK1δ. If phosphorylation of the priming site at S659 establishes the pS659 CK1δ consensus motif, then loss of the second site with the S662A mutant should allow us to identify whether phosphorylation proceeds in a progressive manner down the FASP peptide. Although phosphorylation of the priming site in the S662A mutant occurred with a similar rate to FASP-WT, phosphorylation of the downstream site at S665 was abolished (Fig. 1G). These data demonstrate that the kinase phosphorylates S659 independently of S662 and uses a processive mechanism to phosphorylate target downstream serines in the mPER2 FASP region.

To test whether phosphorylation of S662 of mPER2 requires priming phosphorylation in full-length protein in cellular system, as an independent approach, we used a newly generated affinity-purified pS662-mPER2 antibody (Materials and Methods and SI Appendix, Fig. S2). As seen in Fig. 1H, mutation of the priming site, we found no detectable phosphorylation on S659 or S662, whereas phosphorylation on S665 occurred at a rate similar to FASP-WT. This provided clear evidence that phosphorylation is rate limiting in this context and that priming phosphorylation is required for phosphorylation of downstream sites at S662 and S665.
site (S659) abrogated phosphorylation of S662, confirming the processive nature of FASP phosphorylation in cells.

**CK1δ Protein Is Sufficient to Phosphorylate S659 of mPER2.** To facilitate identification of the mPER2 priming kinase, we generated affinity-purified phosphopeptide-specific antibodies recognizing pS659 of mPER2 (Materials and Methods). The pS659-PER2 antibody was highly specific for immobilized pS659-FASP peptide, recognizing the peptide even at a dilution of 1:32,000 (Fig. 2A). The pS659-PER2 antibody also recognized pS659, but not S659A, in full-length and truncated mPER2 in immunoblots (Fig. 2B). Confirming the phosphorylation dependency of the antibody, treatment of lysates with alkaline phosphatase specifically decreased binding of the pS659-PER2 antibody (SI Appendix, Fig. S3).

As noted by Fustin et al. (31), CK1δ has two splice variants, CK1δ1 and CK1δ2. Using the in vitro peptide kinase ELISA, we confirmed that CK1δ1 can phosphorylate the FASP-WT peptide at S659 in a concentration-dependent manner (Fig. 2C). Next, we tested whether CK1δ1 could phosphorylate the FASP priming site of mPER2 in full-length protein (Fig. 2D and E). Myc-tagged mPER2 expressed in HEK293 cells was immunoprecipitated and then incubated with recombinant full-length CK1δ1 protein. Priming-site phosphorylation was assessed by SDS/ PAGE and immunoblotting. As noted in Fig. 2D, mPER2 in cells is phosphorylated on S659 to some extent by endogenous kinases. However, addition of increasing amounts of recombinant CK1δ1 protein was sufficient to increase the phosphorylation of S659 in full-length mPER2.

**CK1δ is the Priming Kinase in Cells.** Having established that CK1δ1 could phosphorylate the priming site in the peptide and in the immunopurified protein, we asked whether CK1δ1 could phosphorylate the mPER2 priming site in intact cells (Fig. 2E). mPER2 was expressed alone or with increasing amounts of ectopic CK1δ1. In the absence of added CK1δ1, mPER2 was phosphorylated on S659, and the amount of phosphorylation increased markedly with coexpression of CK1δ1. Conversely, mPER2 with a S659A mutation (Fig. 2E, last lane) was not recognized by the pS659 antibody and displayed a mobility shift in the presence of ectopic CK1δ1, consistent with phosphorylation at the β-TrCP phosphodegron and other sites (15).

The preceding assays demonstrate that CK1δ1 is sufficient to phosphorylate the mPER2 priming site on peptides in vitro and in cells in the context of the full-length protein. To test whether CK1δ and/or CK1δ1 kinase is necessary for priming phosphorylation in cells, we performed knockdown and inhibitor assays. Knockdown of total CK1δ1 only partially inhibited the priming-site phosphorylation (Fig. 3A). Knockdown of CK1δ1, a kinase generally present in much lower abundance than CK1δ isoforms, also gave rise to a marked decrease in priming-site phosphorylation, and knockdown of both CK1δ and CK1δ1 together eliminated priming phosphorylation. Confirming that CK1δ1 can phosphorylate the priming site, purified CK1δ1 protein could phosphorylate the FASP peptide in vitro (Fig. 3B), and overexpression of CK1δ1 drove phosphorylation of the S659 site in cells (Fig. 3C). Lastly, as an independent test, we found that the dual CK1δ1 inhibitor PF670462 (7) and, to a lesser extent, the pan-CK1 inhibitor D4476 also markedly reduced mPER2 priming phosphorylation (Fig. 3D). We conclude that CK1δ and CK1δ1 are both necessary and sufficient to phosphorylate the mPER2 FASP priming and downstream sites in vitro and in cells.

**The Role of the CK1δ/δ1 Carboxyl Terminus in Priming-Site Phosphorylation.** Fustin et al. (31) suggested that CK1δ1 and CK1δ2 have differing activities in phosphorylation of the priming site. CK1δ2 differs from CK1δ1 only in the last 16 amino acids due to inclusion of a penultimate exon in CK1δ2 that alters the reading frame (Fig. 4A). In fact, CK1δ2 more closely resembles CK1δ at the extreme carboxyl terminus. We assessed the relative priming activity of the three kinases in cells. CK1δ2 and CK1δ1 are more active than CK1δ in phosphorylating the priming site, as illustrated in the immunoblot in Fig. 4B and as presented quantitatively in Fig. 4C. Consistent with this, Fustin et al. (31) found that overexpression of CK1δ2, more active on the FASP site, lengthens the circadian period in cells, whereas specific knockdown of CK1δ1 shortens period. This suggests a previously unappreciated role for the extreme carboxyl terminus of CK1δ in influencing the activity of the kinase. Confirming this, truncation of CK1δ1 at amino acid 400, removing the last 16 residues, increased the activity of the kinase on the priming site to that of CK1δ2 and CK1δ1 (Fig. 4B and C). Thus, the activity of CK1δ/δ1 as a priming kinase is tightly regulated by the extreme carboxyl terminus of the protein.

**Revising the Phosphoswitch Mathematical Model.** We previously proposed a phosphoswitch model in which the PER2 protein switches between two fates (5). When the β-TrCP site is phosphorylated by CK1δ/δ1, PER2 is rapidly degraded. Based on previous experimental data (32), we also proposed a priming kinase that phosphorylates the FASP site, stabilizes PER2, and allows for sequential phosphorylation of PER2 downstream from the FASP site by CK1. With the identification of CK1δ as the priming kinase, we asked whether the phosphoswitch model was still predictive and accurate. We modified our previous phosphoswitch model by incorporating the finding that CK1δ/δ1/δ2 functions as the priming kinase (see SI Appendix, Materials and Methods for details). This revised model continues to accurately simulate the unusual kinetics of PER2 degradation where, during phases when PER2 accumulates in the cell, its degradation curve contains a plateau (Fig. 4D). Furthermore, the model successfully reproduces the negligible period change of CK1δ/δ1 mutant mice (33), the longer period of CK1δ/δ1 mutant mice (18, 33), and the shorter period of FASP humans and mice (11, 13) (Fig. 4E). CK1 phosphorylation of PER2 is temperature compensated in vitro by balancing the higher dissociation.
constant and higher phosphorylation rate at higher temperatures, which is proposed as a temperature compensation mechanism of circadian period (4, 6). Consistent with this finding, when the dissociation constant of CK1 and phosphorylation rates for both the priming site and the β-TrCP site of PER2 increase together, the period is nearly constant in the model (SI Appendix, Fig. S4).

Discussion

Regulation of PER2 abundance controls circadian timing, yet understanding the phosphorylation of the key control point has been elusive. Here, we show by multiple approaches that CK1δ/ε can function as the PER2 priming kinase, resolving a longstanding question in circadian biology. Additionally, we find that CK1δ1 and CK1ε differ markedly in their ability to phosphorylate the priming site. CK1δ2, which has residues at the extreme carboxyl terminus that more closely resemble CK1ε, displays increased priming kinase activity like CK1ε, suggesting that control of splicing can also regulate priming and, hence, clock timing (31). These studies highlight the role of the CK1δ/ε carboxyl terminus (Fig. 4G). Prior studies demonstrated that while CK1ε does not require its carboxyl terminus to bind to PER proteins, inclusion of the tail can significantly enhance the interaction (34, 35). Because CK1δ/ε is also regulated by phosphorylation and dephosphorylation of the carboxyl terminus, this also suggests a mechanism for cellular signaling pathways to regulate PER2 priming rates (26, 36–40). For example, changes in phosphorylation of the CK1δ/ε carboxyl terminus by cell cycle-dependent kinases has recently been shown to alter CK1δ activity on PER2 (41). Other signaling pathways that impinge on CK1δ/ε carboxyl-terminal phosphorylation, such as metabotropic glutamate and Wnt signaling, could further influence priming and, hence, alter the clock period (42, 43).

CK1δ/ε has the additional feature of being temperature compensated—that is, the activity of the kinase on selected substrates is relatively constant as temperature increases (4). A molecular mechanism for this has recently been proposed, involving key residues adjacent to the substrate recognition motif (6). Since CK1 phosphorylation of PER2 is temperature compensated in vitro and CK1 is involved in both priming and degradation, how does the time required for PER2 degradation lengthen at higher temperatures, a property we showed is essential for the temperature compensation of circadian period (5)? The answer may lie in a better understanding of how the carboxyl terminus of the CK1δ/ε family members regulates temperature compensation on different substrates. The regulation of a fraction of the CK1δ/ε/δ1/δ2 kinase pool (in which each member has a different tail sequence and, thus, priming phosphorylation rate), may provide a mechanism for temperature-compensated regulation of circadian period. Additionally, CK1 may have different Q10 on the priming and β-TrCP sites in PER2 so that temperature compensation of the circadian clock utilizes the differential phosphorylation of the priming and β-TrCP sites to regulate the phosphoswitch controlling mPER2 stability (5). This is consistent with the data from Ueda and coworkers (4), who reported different Q10 for different forms of recombinant CK1. However, it is unfortunately challenging to study temperature compensation in vitro because of the rapid inactivating autophosphorylation of full-length CK1δ/ε in the presence of ATP. In contrast,
in vivo, the net phosphorylation of the carboxyl terminus of CK1δ/ε is highly dynamic, balancing active autophosphorylation and phosphorylation by other kinases with active dephosphorylation by multiple phosphatases (36, 37, 42). In the phosphoswitch model, when the phosphorylation rate for the priming site is increased, which we now show strongly depends on the CK1 carboxyl terminus (Fig. 4 B and C), the period changes dramatically (Fig. 4 F). On the other hand, when the phosphorylation rates for both the priming site and the β-TCP site increase equally, the period is nearly constant (Fig. 4 F). This shows that the CK1 phosphorylation of PER2 follows a “robust yet fragile” paradigm that is emerging in systems biology, where cellular systems are robustly resistant to environmental changes yet can still react to specific signaling pathways.

The differential activity of CK1δ and CK1ε on priming phosphorylation must also be viewed in the context of their relative protein abundance. Knockout studies have demonstrated that CK1δ plays a major role in regulation of the circadian clock in vivo (17, 33). Quantitative mass spectrometry studies have recently found that CK1δ protein was over 20-fold more abundant than CK1ε in liver and that CK1δ is more readily detectable in PER-containing macromolecular circadian complexes (16, 27, 28). However, we found that CK1δ is significantly more active than CK1ε as a priming kinase, which may explain why the tau mutation of CK1δ has a semidominant phenotype (19). Together, the data here and from Fustin et al. (31) indicate that dynamic post-transcriptional splicing and posttranslational phosphorylation of CK1δ and CK1ε can regulate priming and, hence, PER2 activity, providing important flexibility to regulate clock speed.

Materials and Methods

A detailed description of reagents, methods, and mathematical models, including the various parameters analyzed, equations applied, and the Mathematica code, can be found in SI Appendix, Materials and Methods. The rabbit polyclonal antibodies against pS659 and pS662 of mouse PER2 were developed at AbFrontier (Young In Frontier Co.) using the phosphopeptides GAEPeSVSLS-Tys and KAeSVpSLSQ-Sys, respectively.

ACKNOWLEDGMENTS. We thank Dai Wook Kim for assistance with the mathematical models. This work was funded by the National Medical Research Council of Singapore Grant NMRC/CIG/1465/2017 (to D.M.V.), the National Research Foundation of Korea grant and the POSCO TJ Park Foundation Science Fellowship (to J.K.K.), the National Institutes of Health Grants R01 GM107069 and R01 GM121507, as well as funds from the NIH Office of the Director under Award S10OD018455 (to C.L.P.), and the National Science Foundation Grant DMS-1714094 (to D.B.F.).