

Chicktacking Pineal Clock

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Many tissues in non-mammalian vertebrates contain both photoreceptors and circadian clock systems. Among these photosensitive clock structures, the chick pineal gland has been characterized in detail from cellular and molecular aspects of the clock oscillation and entrainment. Analyses of the pineal photic-input pathway revealed a phase-shifting mechanism mediated by activation of G11, one of the Gq-type G-proteins. A major photoreceptive molecule, pinopsin, likely triggers this pathway by transmitting the light signal to the circadian oscillator. In the chick pineal oscillator, the transcription/translation-based autoregulatory feedback loop is composed of positive and negative elements (clock gene products) that are homologous to those identified in mammals. In the molecular cycling, a CACGTG E-box located in the promoter region of the negative element genes plays a central role in the transcriptional regulation. The phase of the molecular cycling is modulated by many regulatory components, among which E4BP4 and extracellular signal-regulated kinase (ERK) are closely associated with the photic entrainment. A light-responsive element was found in the promoter region of the *Pinopsin* gene, and the element included a CACGTG E-box, suggesting a novel role of the E-box as a point of convergence of light and circadian signals. These observations together point to general and unique features of the chick pineal circadian system among animal clocks.

Key words: circadian clock, E4BP4, mitogen-activated protein kinase, pineal gland, pinopsin.

The circadian clock regulates a variety of activities in animal physiology and behavior, such as the sleep-wake cycle, body temperature, production of hormones, and locomotor activities. Circadian clock systems generally contain three components: (i) input pathway(s) for resetting the oscillator, (ii) a self-sustained oscillator, and (iii) output pathway(s) for transmission of time signals to downstream effectors (reviewed in Ref. 1). Light plays a major role as a time cue that synchronizes the oscillator with the ambient 24-h light/dark cycle, and therefore the light-input pathway to the oscillator has been studied to understand the mechanism of the circadian-clock resetting.

In mammals, the “central oscillator” regulating the locomotor activity resides in the suprachiasmatic nucleus (SCN) in the hypothalamus (2; reviewed in Ref. 3). The phase of the central oscillator is reset by the light signal transmitted from the retina through the retinohypothalamic tract, as the SCN is not itself photosensitive. A photoreceptive molecule responsible for the resetting is called a “circadian photoreceptor,” and the retinal opsins including rhodopsin, cone opsins and melanopsin appear to operate together as the circadian photoreceptors activating the resetting pathway in a redundant manner (4, 5). In addition to the SCN, a variety of peripheral tissues contain the circadian oscillator (6). When isolated, mam-

malian peripheral tissues display self-sustained oscillation of *Per1* expression (7), but these oscillators, termed “peripheral clocks,” are not reset by light due to the light-insensitive nature of these tissues. Instead, they are reset by humoral factors such as glucocorticoid (8), retinoid (9), and glucose (10) that are probably regulated by the central clock in the SCN or by feeding-associated events (11–13).

In non-mammalian vertebrates, the distinction between the “central clock” and the “peripheral clock” is less clear than in mammals, in which most tissues are blind. In the zebrafish, peripheral tissues such as heart and kidney retain circadian clocks that are light-entrainable in isolated culture, indicating the presence of an intrinsic light-input pathway to the oscillator (14). A typical photosensitive clock structure present outside the hypothalamus is the pineal gland (15–19), which plays a major role in the circadian production of melatonin, a well-known mediator of the circadian physiology in animals. This review summarizes recent studies on this small photosensitive clock structure in the chick. The finding of the chick pineal photosensitivity by Deguchi (17, 19) was a landmark in this research field.

Pinopsin as a circadian photoreceptor in chick pineal gland

The pineal gland of non-mammalian vertebrates is tightly linked with a light-input pathway(s) inherent in the gland (reviewed in Refs. 20–22). This forms a clear contrast to the mammalian pineal gland, which is a light-

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insensitive neuroendocrinal organ synthesizing melatonin in a circadian rhythmic manner under the control of the SCN. More than 20 years ago, Deguchi demonstrated that the chick pineal gland is light-sensitive and has the ability to produce melatonin in a circadian rhythmic and light-dependent manner in culture (16, 17, 19). Since then, the chick pineal gland has been widely used as one of the best experimental models for the study of the animal circadian clock (20–22). The photosensitivity and the clock function of chick pineal cells are well-maintained in dissociated cell culture, and this great advantage allows several experiments to be performed that are difficult in other systems.

Light has two distinct effects on the chick pineal melatonin rhythm. One is an acute inhibitory effect on melatonin synthesis (acute effect), and the other is a phase-shifting effect on the circadian oscillator. In 1981, Deguchi reported an action spectrum for the acute effect of light and suggested the involvement of a rhodopsin-like molecule (19). Consistent with this prediction, an opsin-like molecule was identified in the chick pineal gland in 1994 and named pinopsin (23). Pinopsin showed nearly equal similarities in amino acid sequence to chicken retinal rod and cone visual pigments (24, 25), indicating that the *pinopsin* gene is a distant relative of the retinal opsin genes. Based on knowledge of the retinal phototransduction mechanism, pinopsin was considered to couple with a heterotrimeric G-protein to trigger the downstream biochemical cascade (21–23).

Immunocytochemical analysis of chick pineal sections and molecular screening of a pineal cDNA library revealed the expression of several kinds of heterotrimeric G-protein α -subunits, among which $G_{t1}\alpha$ (rod transducin α -subunit) and $G_{11}\alpha$ (α -subunit of G_q -subtype G-protein) were colocalized with pinopsin in the outer segment-like membrane structures of the chick pinealocytes (26–30). To determine whether these G-proteins are involved in the photic-input pathway, m1 or m2 subtype of muscarinic acetylcholine receptor (mAChR) was transiently expressed in cultured pineal cells, to which the AChR agonist carbachol was administered to activate endogenous G_{11} (via m1 receptor stimulation) or G_{t1} (via m2 receptor stimulation). The carbachol treatment of m1 receptor-expressing cells induced a phase-dependent phase-shift of the melatonin rhythm, and the effect was indistinguishable from the effect of light (30). On the other hand, the carbachol treatment of m2 receptor-expressing cells had no effect on the rhythm. This study was unique in that the phase-shifting light-signaling pathway was explored in the dark by administering “non-photic” pharmacological stimuli to the clock cells expressing a foreign receptor mimicking the endogenous photoreceptor(s). This strategy allows the G_{11} cascade to be triggered without activating other possible photic-input pathways that might operate in a redundant manner, and the results demonstrate the contribution of G_{11} -mediated signaling pathway to the photic-input mechanism. This is consistent with the pioneering study showing that pertussis toxin blocks the acute effect of light but not the phase-shifting effect (31).

It is likely that pinopsin couples with two G-proteins, G_{11} and G_{t1} , in the gland, and that the pinopsin- G_{11} cascade inputs to the oscillator. Besides pinopsin, the

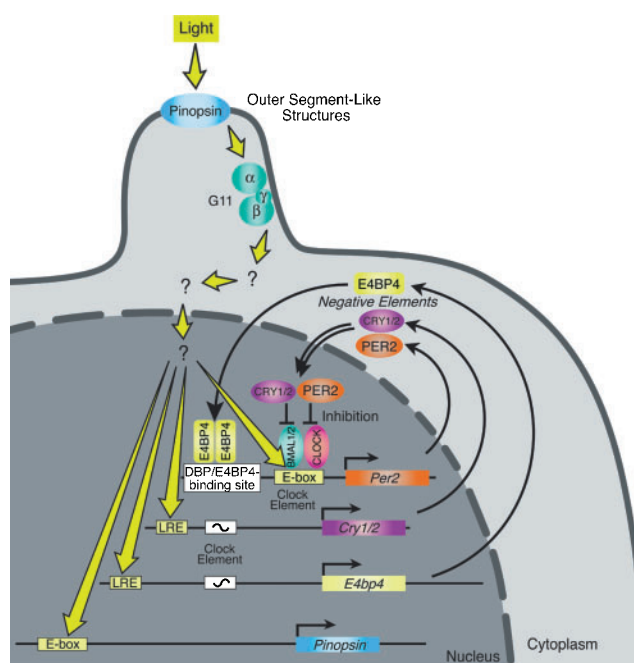


Fig. 1. A model for the role of clock-related molecules in circadian oscillation and light entrainment of the chick pineal clock. LRE, a putative light-responsive element. This model was drawn with reference to mammalian models for the transcription/translation-based autoregulatory negative feedback loop (70).

putative photoreceptive molecule melanopsin in the chick pineal gland (Provencio *et al.*, Genbank accession no. AY036061) may couple with G_{11} to activate the photic-input pathway, although further biochemical and immunohistochemical characterization is necessary in order to define the contribution of this less-characterized opsin and its signaling pathway to the photic-entrainment.

Core clock elements in the chick pineal clock

The clock gene period was first identified in *Drosophila*, and later in mouse (*mPer1-3*). Since the identification of *mPers* during 1997–1998, extensive studies have identified CLOCK, BMAL1, and CRY1/2 in several vertebrate species, and these proteins have been shown to constitute the core feedback loop of the circadian oscillator (reviewed in Refs. 22 and 32). Recently BMAL2 (MOP9 or CLIF) was identified in human and in some other vertebrates (33–37), but it is not yet known whether the *Bmal2* gene is essential for the clock oscillation. In chicken, a series of orthologues of the mammalian clock genes, chicken *Per2* (*cPer2*) (37), *cPer3* (38), *cBmal1* (37, 39), *cBmal2* (37), *cCry1* (38), *cCry2* (38), and *cClock* (40), have been identified to date (Fig. 1). Birds appear to lack a *Per1* gene.

Recent dramatic advances in the field of the circadian biology have facilitated the construction of a model for the molecular oscillation based on the transcription/translation-based autoregulatory negative feedback loop (Fig. 1). In the chick pineal clock system, a CACGTG E-box element exists in the *cPer2* promoter region, and cCLOCK-cBMAL1/2 multimer shows significant transactivation ability through this element. Interestingly, cBMAL2 shows an inhibitory effect depending on its

dose, implying its unique modulatory role in the E-box-mediated transactivation (37). In the chick pineal gland, the mRNA level of each clock gene oscillates in a circadian manner with a peak at its unique phase (37), and the transcript levels of *cPer2*, *cCry1*, and *cCry2* are up-regulated by light captured by the endogenous photoreceptor in the pineal cells (Fig. 1) (38). The molecular oscillatory mechanism of the chick pineal clock seems very similar to that of the mammalian clock in the SCN (Figs. 1 and 2), but the chick pineal clock may be more susceptible to light than the mammalian SCN clock in terms of light-responsiveness of the clock (related) genes.

E4BP4 as a key molecule for phase-delaying process

Light-responsiveness of the clock (related) genes is important in regulating the phase of the molecular clock (1, 3, 22). To identify genes whose expression is regulated by light in a phase-dependent manner, more than 5,000 transcripts expressed in the chick pineal gland were screened by differential display analysis (41). This screening revealed only a few transcripts that are subject to regulation by both the circadian clock and light, implying the physiological importance of the transcripts. One of these transcripts encoded cE4BP4, a member of PAR family transcription factors, having a basic leucine zipper motif for its DNA-binding (41). Interestingly, a cE4BP4-binding site was found in *cPer2* promoter (Figs. 1 and 2), and cE4BP4 repressed the transcription of a reporter gene from *cPer2* promoter through the binding site (41). The temporal expression pattern of *cE4bp4* had its peak at ZT10 (ZT, Zeitgeber time) and CT12 (CT, circadian time) under LD cycles and DD condition, respectively, and this is almost antiphasic to that of *cPer2* peaking at ZT2 and CT4 (41). Because the change in E4BP4 protein level rapidly follows that in mRNA level (42), it is possible that cE4BP4 may be involved in the down-regulation of *cPer2* mRNA level occurring from midday to evening in the chick pineal gland (Fig. 2).

More importantly, the light-dependent up-regulation of *cE4bp4* mRNA level suggests that cE4BP4 plays a critical role in the phase-shifting mechanism of the pineal clock. The prolongation of the light period to the early night shifts backward the clock phase by delaying the rising phase of *cPer2* in the next morning, and this phase-shift is not accompanied by light-dependent up-regulation of *cPer2* expression (41). Such behavior of *cPer2* expression is well explained by the light-dependent induction of cE4BP4, which would suppress the *cPer2* expression from evening to midnight (Fig. 2). It is most probable that cE4BP4 is a key mediator of the evening light signal that causes the phase-delay (Fig. 1) (41).

The binding site of E4BP4 is shared with another member of the PAR family, albumin D-site binding protein (DBP) (43, 44). DBP and E4BP4 act as a positive and a negative regulator, respectively, both acting on the same DNA-binding site (44). mDBP (*mDbp*) shows robust circadian oscillation in the mRNA and protein levels in the mouse SCN (45, 46), and activates transcription of *mPer1* gene through a DBP/E4BP4-binding site in *mPer1* promoter (46). In addition, the temporal expression pattern of *mDbp* in the SCN is a few hours earlier than that

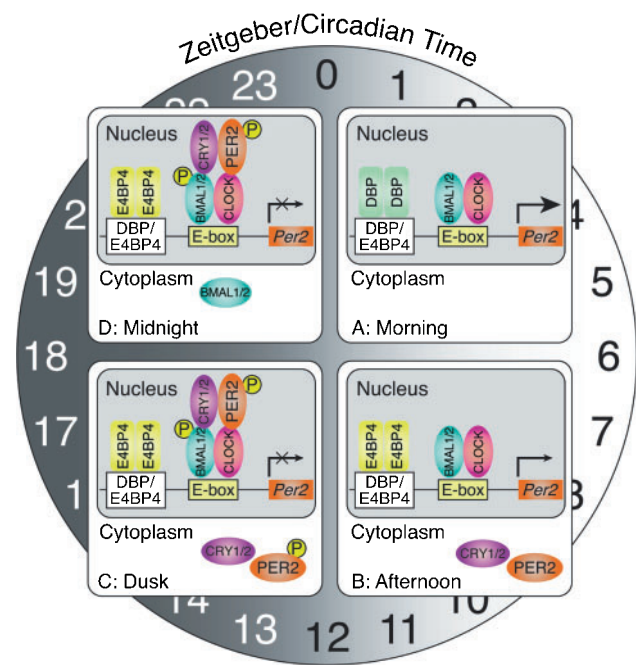


Fig. 2. Ticktacking of the circadian oscillator in the chick pineal gland. (A) Early morning to midday: Transcription of *cPer2* genes is activated through the CACGTG E-box element by an activator complex composed of cCLOCK and cBMAL1/2. cDBP has not been identified in the chicken, yet it may bind DBP/E4BP4-binding site to enhance the *cPer2* transcription. (B) Midday to evening (Afternoon): Stimulation of *cPer2* transcription leads to cytosolic accumulation of cPER2 protein, which then associates with cCRY1/2 (chicken Cryptochrome 1/2). Transcription of *cE4bp4* leads to accumulation of cE4BP4, which then inhibits the *cPer2* transcription by binding to DBP/E4BP4-binding site. (C) Evening to midnight (Dusk): The cPER2-cCRY1/2 complex enters the nucleus to inhibit the cCLOCK-cBMAL1/2 complex, resulting in suppression of *cPer2* transcription. (D) Midnight: The cPER2-cCRY1/2 inhibitor complex is gradually down-regulated through post-translational steps such as phosphorylation and destruction, with cytoplasmic cPER and cCRY1/2 exhausted. BMAL1/2 proteins accumulate before restarting the *cPer2* transcription (A). PER and BMAL1 may be phosphorylated by casein kinases (CKI ϵ and CKI δ) and MAPK, respectively (50–53, 62).

of *mPer1* and is nearly antiphasic to that of *mE4bp4*, suggesting agonistic and antagonistic roles of *mDbp* and *mE4bp4* in the transcriptional regulation of *mPer1* (44). Therefore, the circadian oscillation of the balance between DBP and E4BP4 activities may contribute to the stabilization of the core negative feedback loop. It would be interesting to investigate a similar role of *cDbp* in the chick pineal clockwork and to ask whether a light-signal might also affect *cDbp* expression.

Role of protein kinases in the pineal clock

Not only the transcriptional control but also posttranslational regulations such as protein phosphorylation, nuclear entry and degradation contribute to maintenance of stable 24-h oscillation by driving or delaying the molecular cycling. Recent studies on the animal clock systems have demonstrated that casein kinase I (CKI ϵ /CKI δ), *Shaggy* kinase (GSK3 β) and two members of the mitogen-activated protein (MAP) kinase family (ERK and p38) are involved in the circadian clockwork. The

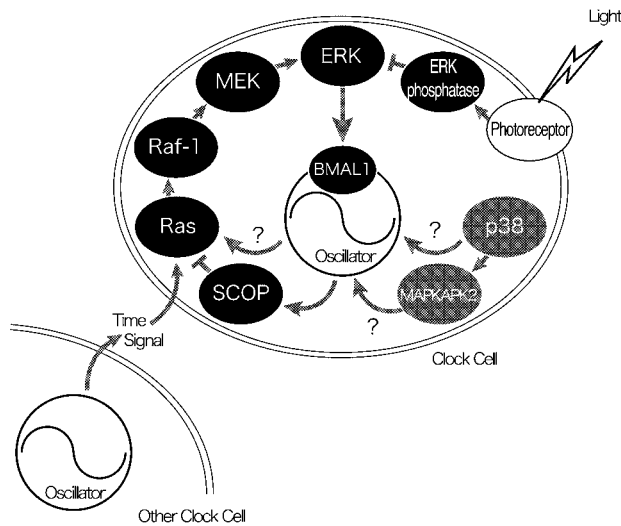


Fig. 3. A model for the roles of MAP kinases, ERK and p38, in circadian oscillation and light entrainment of the chick pineal clock system. SCN circadian oscillatory protein (SCOP) found in the rat SCN is a negative regulator of K-Ras (61) and tentatively included in this model, although its expression has not been examined in the chick pineal cells.

clock-associated function of CKI ϵ was first identified in *Drosophila doubletime* (*dbt*) mutants having mutations in the *dbt* gene, which encodes a protein kinase highly related to mammalian CKI ϵ (47, 48). The period length of the circadian rhythmicity of these mutants is lengthened (in *dbt^L* mutant) or shortened (in *dbt^S* mutant) (47, 48), and later *Ckl ϵ* was shown to be responsible for *tau* mutant phenotype in hamster (49). CKI ϵ (or DBT) and CKI δ directly phosphorylate PERs and consequently alter the stability or subcellular localization of PER proteins (50–52). Although the functions of CKI ϵ and CKI δ have not been examined in non-mammalian clock structures, potential sites for CKI ϵ phosphorylation (Ser residues in Ser-X-X-Ser-X-X-Ser-X-X-Ser-X-X-Ser) identified in hPER2 (53) are conserved in the corresponding region of cPER2.

The protein level of CKI ϵ is constant over the day in the mouse liver (54), whereas the regulation of CKI activity is not fully understood in clock structures. On the other hand, it was clearly shown that phosphorylation and activity of ERK is circadian-regulated in a number of clock structures such as the mouse SCN (55, 56), chick pineal gland (57), bullfrog retina (58), and chick retina (59). In the bullfrog retina and chick pineal gland, ERK activity is low during the (subjective) day and peaks at midnight. ERK oscillation is likely regulated *via* a classical Ras and ERK cascade (60), and a novel K-Ras modulator SCOP (SCN circadian oscillatory protein) might be one of the upstream regulators of circadian activation of Ras (61; Fig. 3). It should be noted that the phase of the pineal clock is affected by inhibiting MEK (ERK kinase) activity during the subjective night, indicating that the ERK activation signal inputs to the oscillator. Therefore, the ERK cascade is likely to form a secondary loop that may contribute to stabilization of the core feedback loop (57). Just like ERK in the mammalian SCN, the chick pineal ERK activity is regulated not only by the circadian

clock but also by light. A light stimulus given during the subjective night leads to rapid dephosphorylation (and inactivation) of ERK in the pineal gland without affecting the activity of upstream MEK (57, 60). This indicates that the pineal phototransduction pathway activates a phosphatase that dephosphorylates ERK. Thus, in the chick pineal clock, ERK seems to represent a converging point of two signals, time and light (Fig. 3).

Identification of *in vivo* substrates of ERK is an important outstanding issue for understanding the physiological role of the circadian-regulated ERK. Among the chicken clock-related gene products, BMAL1 directly associated with ERK, and was efficiently phosphorylated by activated ERK *in vitro* (62). In the transcriptional assay in 293EBNA cells, activation of ERK by expression of constitutive active MEK resulted in partial suppression of the transactivation from the CACGTG E-box element by CLOCK and BMAL1 (62). This suppressive effect was abrogated when one of the ERK phosphorylation sites Thr 534 in BMAL1 was mutated to alanine (62). ERK has the ability to negatively regulate the transactivation from the E-box element through the phosphorylation of BMAL1 at Thr 534.

Considering the physiological role of the ERK cascade in the clockwork, an interesting question is whether the circadian regulation is an intracellular event or involves intercellular signal transmission. In the former case, ERK may contribute to a circadian time-keeping mechanism by generating an appropriate time delay in the E-box-dependent transcriptional activation. In the latter case, the ERK cascade would be activated by a signal generated by neighboring pineal clock cells, and hence it may act as a synchronizer among the individual clock cells (Fig. 3).

p38, another member of the MAP kinase family, is also present in the chick pineal gland (63). Both the p38 protein level and its phosphorylation (activation) were almost constant over the day in the chick pineal gland, but interestingly, chronic application of p38 inhibitor delayed the phase of the pineal melatonin rhythm in a time-of-day specific manner (63). These observations suggest that p38 plays a time-of-day-specific role in the pineal clock oscillation. Although the downstream cascade of p38 in the pineal gland is not clear, MAP kinase-activated protein kinase 2 (MAPKAPK2) has been suggested as a downstream target of p38 (63; Fig. 3).

Light-responsive element indispensable for the light-dependent gene expression

Transcription of *mPer1* is induced by light in the mouse SCN *in vivo*, and this seems to be associated with the light-dependent phase-shift of the locomotor activity rhythm (64). As described, transcripts of *cPer2*, *cCry1/2*, and *cE4bp4* are up-regulated by light in the chick pineal gland in culture (38, 41). These observations suggest an idea that the light-dependent transcription of the clock (related) gene(s) is essential for the phase-shift. The light-dependent gene expression regulated by light-responsive elements (LREs) has been extensively studied in plants (reviewed in Ref. 65). In contrast, LREs and LRE-containing promoters have been less well characterized in animal cells (66), probably due to the lack of an appropriate assay system to evaluate enhancer activi-

ties under the light and dark conditions. The transcriptional analysis established in the primary culture of the chick pineal cells has made it possible to measure the light-dependent enhancer activity. This was employed to search the promoter region of the *pinopsin* gene for an LRE, because the mRNA level of *pinopsin* is positively regulated by light in the chick pineal gland *in vivo* and in tissue culture (67, 68). Pinopsin LRE was found in an 18-bp region (TGGCACGTGGGGTTCCCTC) that included a CACGTG E-box element (68). Mutation of the E-box sequence abolished the light-responsiveness, indicating the functional importance of the E-box sequence (68). Interestingly, the CACGTGG sequence, termed the G-box, is known to operate as an LRE in plants (69), and this implies a light-dependent mechanism common to animals and plants. A putative LRE-binding factor was detected in the chick pineal nuclear extract by electrophoretic mobility shift assay (EMSA). EMSA using double-stranded oligonucleotide competitors for *cPer2* or *arginine vasopressin* E-box sequence indicated that the pinopsin LRE-binding factor has an affinity to these E-box sequences as well (69). Therefore, not only the circadian time signal but also the light signal may input to the CACGTG E-box element found in the promoter region of several clock (related) genes (Fig. 2).

Final Comments

The chick pineal gland and the pineal cells in culture are good models for the study of the animal circadian clock and its photic-input pathway. Characterization of the light-dependent regulatory mechanism of gene expression is feasible only in the light-sensitive clock cells, which would help to clarify in detail the phase-resetting mechanism of the clock. Comparative studies on the clock system of mammalian SCN and avian pineal gland are of great importance in addressing how the clock system has developed. Elucidation of a core mechanism conserved among a wide variety of living organisms should lead to understanding of the origin of the circadian clock.

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