Circadian Rhythm and cDNA Cloning of the Clock Gene period in the Honeybee Apis cerana japonica

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ABSTRACT—Isolated individual foragers of Apis cerana japonica could be entrained under a light-dark cycle, and the predominant activity was concentrated to the later part of the photophase. Foragers showed circadian rhythm under conditions of constant light and constant dark with free-running periods of more and less than 24 hr, respectively. These observations indicated that A. cerana possesses a circadian clock controlling locomotor activity. To investigate the molecular mechanism underlying the circadian system we cloned cDNA for a homolog of the clock gene period (per) from the honeybee by a PCR-strategy. The cloned per-cDNAs consisted of two types, α and β, encoding a putative protein of 1124 amino acids and 1116 amino acids, respectively. The sequences of types α and β were identical except that the former possessed an additional 24 bp stretch corresponding to 8 amino acids in the conserved C2 block. These two types were assumed to be differentially spliced variants and found also in per-cDNA of A. mellifera. In support of this idea, Southern blotting experiments showed that per of A. cerana is a single copy gene. RT-PCR analysis and subcloning of the products revealed that the both types α and β are expressed in the brain of the forager. A quantitative RT-PCR assay by which the level of per mRNA in one single brain can be detected was established. Per mRNA level showed daily oscillation under a light-dark cycle with a change of the ratio of type α to β.

INTRODUCTION

Many organisms including unicellular organisms have been shown to possess endogenous circadian clocks that provide temporal synchronization of life processes and adaptation of organisms to environmental cycles (Aschoff, 1960; Decoursey, 1983). Circadian rhythms driven by these clocks oscillate with a free-running period of about 24 hr under constant environmental condition (Pittendrigh, 1981; Saunders, 1982). The molecular mechanisms responsible for these circadian clocks are under extensive investigation using many organisms including insects (Giebultowicz, 1999) and several genes of the components constructing the clocks have been identified (Dunlap, 1999). Our knowledge about the mechanisms comes largely from genetic and biochemical studies in the fruitfly Drosophila melanogaster. The first clock gene, period (per), an essential component of the circadian clock machinery, was originally cloned in Drosophila (Zehring et al., 1984; Bargiello et al., 1984). The period gene was extensively characterized, and the molecular mechanism of the Drosophila clock is generally thought to be based on negative feedback in which transcription of the per gene is regulated by its protein product PER (Dunlap, 1999). Rhythmic expression of the per gene caused by this feedback regulation has been proposed to be the main mechanism generating daily rhythmicity in Drosophila. In another insect, the moth Antheraea pernyi, per was also cloned and its function was analyzed (Reppert et al., 1994; Levine et al., 1995; Sauman et al., 1996a, 1996b). The silkmoth per gene is also a necessary element of the circadian system (Sauman et al., 1996b), although the molecular details of per expression and regulation are different between the silkmoth and fruitfly (Sauman et al., 1996a). Recently, per genes were cloned and investigated in Musca domestica and Lucilia cuprina, dipteran species other than Drosophila (Piccin et al., 2000; Warman et al., 2000). Mammalian per genes have been cloned (Dunlap, 1999), and the gene products were shown to constitute a molecular circuit with other clock components such as Timeless, Clock and BMAL1, which are also common among fruitflies and mammals (Dunlap, 1999). Thus, isolation and analysis of the per gene has been critical to understanding the molecular mechanisms of circadian systems of insects and mammals.
It was reported that honeybees (*Apis mellifera*) showed distinct free-running rhythms in activity at the level of individual and also at the colony level. The circadian activity rhythm of individual forager honeybees has been well investigated and the free-running period of less than 24 hr under constant darkness (DD) and greater than that under constant light (LL) have been observed (Spangler, 1973; Moore and Rankin, 1985). The circadian rhythm can be entrained to light-dark and temperature cycles (Moore and Rankin, 1985; 1993). In addition to these physical conditions, feeding cycles and social interaction also influence the circadian rhythms represented by colonies (Frisch and Aschoff, 1967; Moritz and Kryger, 1994; Moritz and Sakowski, 1991; Frisch and Koeniger, 1994). For example, introduction of a queen into a worker group that was entrained to a phase-shifted light/dark cycle caused a shift of the free-running phase under DD conditions (Moritz and Sakowski, 1991). The ontogenetic development of circadian activity was reported in honeybee workers: the newly emerged bees had no circadian rhythm but the aged foragers showed a clear rhythm (Moore et al., 1998; Sasaki, 1992). Further the endogenous circadian system of *Apis* is involved in sun compass and “time memory” which enables bees to remember the time of the day at which nectar sources are available (Saunders, 1982).

Though circadian phenomena of the honeybee have been well investigated from several points of view, the molecular mechanisms underlying the circadian rhythm have not been revealed. But recently Toma et al. (2000) reported the cloning of the *per* cDNA in *A. mellifera* (GenBank: AF159569) and the circadian change in *per* mRNA levels in the brain. In the present study we report the rhythms shown by individuals of *A. cerana japonica*, which is endemic in Japan and shows ecological characteristics different from *A. mellifera* (Sasaki, 1999). In order to investigate the molecular mechanism underlying the circadian system of *A. cerana*, we cloned cDNAs showing a homology to *per* genes identified by the alignment of seven insect *per* sequences (Reppert et al., 1994) and preferential codon usage for *Apis* was applied. Three primers were successfully used: two sense primers F1 (5′-TG[TG][CT][TAG][AT][CT][TC][AG][GT]-AT[GC][AT][GA][TC][GG]-3′) and F2 (5′-CTGG GATACTC[AG][CT][GC][AG][GC]-3′) and one antisense primer R1 (5′-ATT[AG]TA TT[AG][TT][GA]-3′). The heads of workers were obtained and frozen immediately in liquid nitrogen. Total RNA was extracted from the heads by the acid guanidinium isothiocyanate phenol-chloroform (AGPC) method (Isoguen, Nippon gene, Toyama, Japan). Reverse transcription of total RNA from the bee heads was performed by using 5 μg total RNA and 25 units of avian myeloblastosis virus reverse transcriptase (AMV reverse transcriptase first-strand cDNA synthesis kit; Life Sciences, Inc., St. Petersburg, FL), in a 25 μl cDNA reaction mixture. One μl of the cDNA was amplified with 1.5 units of Taq DNA polymerase (Takara Shuzo, Kyoto, Japan) using primers F1 and R1 on a DNA thermal cycler model 9600 (Perkin Elmer). The PCR parameters were 30 sec template denaturation at 95°C, 1 min primer annealing at 55°C, 2 min primer extension at 72°C for 30 cycles. The products of this PCR were further amplified using a second set of oligonucleotide primers F2 and R1. The PCR parameters were the same as those of the first PCR. The final PCR products were electrophoresed on 0.7% agarose gels, purified by the glass powder method (AGC-001K DNA PREP, Diaaytron, Tokyo, Japan), and were cloned into pGEM-T easy vector (Promega Co., Madison, WI) for sequencing. The sequencing reactions were carried out by the cycle sequencing method with an ABI-373 automatic DNA sequencer (Applied Biosystems) according to the manufacturer’s protocol. All sequences were determined in both directions.

The 3′-terminal portion of *per* cDNA was cloned by the 3′-RACE (rapid amplification of cDNA ends) method. Seven μg of total RNA was reverse-transcribed (Superscript II RNase H+ Reverse Transcriptase, Life Technologies) using 3′-primer TAP1 (5′-GGCCAC- GCGTGGACTAATATATTTTTTTTTTTTTTTTTTTTTTTTTTTTTT-3′). The resulting cDNA was amplified using the anchor primer AP1 (5′-GGC CACGCGTGGACTAGTAGTAC-3′) and primer F3 (5′-AGGACCTCGGGT-CCTTTGATG-3′). The PCR parameters were 30 sec template denaturation at 95°C, 1 min primer annealing at 55°C, 2 min primer extension at 72°C for 30 cycles. The products of this PCR were further amplified using a second set of primers TAP1 and F4 (5′-CAGCACAGCGTGATGGTGGG-3′). The amplified 2.3 kb fragment was purified, and cloned into the pGEM-T easy vector.

The 5′-terminal portion of *per* cDNA was cloned by the 5′-
RACE method (5′RACE System for Rapid Amplification of cDNA Ends Version 2.0, Gibco BRL, Gaithersburg, MD) using primer GSP1 (5′-TGCTTCACTGTACATGACCGA-3′), GSP2 (5′-ATATCAGGATTGCGACCTTTC-3′) and nested GSP (5′-ATCCGTGTTGACCTACGAC-3′).

Finally, the complete cDNA coding sequences of per (consisting of two types α and β; see the materials and methods) were amplified from the bee head cDNA using two primers F5′ (5′-AGACAGTGTTGGATTCAACCGG-3′; -58 to -36, the first nucleotide A of the start codon was numbered +1) and R5′ (5′-AA ACAAGCCCTTGCAACCTG-3′; +3418 to +3437 [of type α]), which were based on the sequences obtained by 5′- and 3′-RACE, respectively.

Total RNA was prepared from the heads of A. mellifera foragers (Australian strain) and cloning of partial fragments of the per cDNA was performed according to the methods described above. To carry out PCR, two primers were designed on the basis of the decided sequence of cerana: one is sense primer R0 (5′-CTGGTGGTTACTGCTCAACCTGT-3′) and antisense primer FS (5′-GTTGTAATTTGAAGTGTGTTA-3′), which are located in the C2 region (Reppert, 1994). PCR, cloning and sequencing were carried out as described above.

Southern blotting analysis of genomic DNA

The cDNA probe of 786 bp was generated with primer R0 (5′-CTGGTGGTTACTGCTCAACCTGT-3′) and the primer FS (5′-GTTGTAATTTGAAGTGTGTTA-3′), which are located in C2 region (Reppert et al., 1994), by PCR amplification using subcloned cDNA (type α) as the template. Probes were labeled with random primers and klenow fragment of E. coli DNA polymerase using a random prime labeling kit (Amersham Pharmacia Biotech, Piscataway, NJ) to obtain fluorescein-labeled DNA probes.

Total genomic DNA was isolated from muscles of A. cerana workers according to the standard method. DNA was digested with EcoRI and HindIII and aliquots of ~2 µg were separated on 1% agarose gels, transferred onto nylon membranes (Hybond-N+, Amersham Pharmacia Biotech), and immobilized by UV cross-linking. Hybridization and detection were performed according to the protocol supplied with the detection kit (RPNS510; Amersham Pharmacia Biotech) with slight modifications. Membrane-bound digested DNA was hybridized with the detection kit (RPN3510; Amersham Pharmacia Biotech) with stringent washes, the membranes were incubated with blocking agent and then with anti-fluorescin-AP. The chemiluminescence of the hybridizing band was detected using an ECL instant camera (Amersham Pharmacia Biotech).

Isolation of mRNA and one step RT-PCR

Brains including optic lobes of five foragers were dissected out carefully at Zeitgeber time (ZT) 21:00 during the scotophase of LD 12:12 (Fig. 7), collected together and analysed immediately. mRNA was isolated from the brains using a mRNA purification kit (Amersham Pharmacia Biotech); the procedures included disruption by the guanidium isothiocyanate method and selective isolation of mRNA by oligo(dT)-cellulose chromatography. The polyadenylated mRNA was eluted with 200 µl of 10 mM Tris-HCl (pH 7.5) containing 1 mM EDTA. After DNase treatment of the elution mRNA was precipitated by adding 70% ethanol, collected by centrifugation and finally redissolved in 40 µl of DEPC-treated water.

One-step RT-PCR was performed using a kit purchased from QIAGEN (Chatsworth, CA) according to manufacturer’s protocol. The reaction mixture (50 µl) contained reverse transcriptase, Taq DNA polymerase, dNTP mixtures (400 µM of each dNTP), 0.6 µM oligonucleotide primers, 2.5 mM MgCl2, RNase inhibitor (10 units) and 1 µl of mRNA solution obtained by the method described above. First, reverse transcription reaction was performed at 50°C for 30 min, then the mixture was incubated at 95°C for 15 min to activate Taq DNA polymerase, and PCR amplifications were carried out. The PCR parameters were 1 min template denaturation at 94°C, 1 min primer annealing at 50°C, 1 min primer extension at 72°C for 30 cycles.

Selective analysis of the expression of per (α) was performed with primers R0 and F1′ (5′-CTGTAACAGGGATTGCGATCC-3′) and that of total per (α+β) was with R0 and F2′ (5′-CTGGGTTGACAGTTTGGCCT-3′), respectively (Fig. 4). The sequence of F1′ is based on the additional 24 bp stretch in the type α cDNA, and R0 and F2′ are based on sequences common to both types. The amplified ca. 0.7 kb fragment was purified, cloned into the pGEM-T easy vector, and sequenced.

As an internal control, a partial DNA fragment (362 bp in length) of the cerana cytoskeletal actin sequence was amplified by RT-PCR in which primers 1S (5′-GAATGGCACTGCTACATCC-3′) and 3A (5′-GAATTTCAAGCAGCAATCCATC-3′) were used. We cloned and sequenced the amplified DNA fragments and confirmed that they were cytoplasmic actin sequences: five nucleotide differences among the 362 bp sequence were found between the actin genes of cerana and mellifera.

Quantitative RT-PCR assay for period mRNA.

To detect the change in per mRNA level using a single brain of the honeybee, a quantitative RT-PCR analysis was established according to the methods reported previously (Nakayama et al., 1992; Nakamura et al., 1996) with slight modifications. Isolation of mRNA from the brain of foragers and RT-PCR method are performed as described above. After defined cycles of PCR for the analysis of per and cytoskeletal actin mRNA, 5 µl from a 50 µl reaction mixture was electrophoresed on a 1% agarose gel and amplified bands were detected by ethidium bromide staining. The intensity of the ethidium bromide fluorescence of each band was measured by the CCD imaging system (EDAS120, Kodak Digital Science, Eastman Kodak Company, New York). The PCR cycle-intensity curves are plotted on a semi-logarithmic graphs (Fig. 6). For estimation of the amount (a) of the template and the efficiency (b) of amplification in each PCR, regression line was fitted to the linear portion of the curve: the quantitative determination of target mRNA was performed before PCR products reached a plateau (Nakayama et al., 1992). The amount of per mRNA was normalized with that of actin mRNA (Fig. 7).

RESULTS

Activity rhythms of individual foragers

Walking locomotor rhythms of the foragers were investigated to determine the existence of a circadian system in A. cerana. The locomotor activity of individual forager honeybees was monitored using infrared actographs. Honeybees were entrained under a LD 12:12 photoperiodic regime at constant temperature and a typical record is shown in Fig. 1A. Under LD 12:12, activity is concentrated to the later part of the photophase. The onsets of activity were found at the beginning of the photophase and clear offsets occurred at light-off on most days. Foragers could be entrained under LD 16:8 and LD 8:16, and they also showed same tendency of predominant activity in the later part of the photophase (data not shown).

Circadian free-running rhythm was observed under DD-condition with free-running period (τ) shorter than 24 hr (Fig.1B and C). Circadian periods were measured first under LL condition and then after transition to DD condition. Some bees showed a free-running rhythm under LL and DD, and typical record is shown in Fig. 1D. The free-running mode, which was recognized clearly by tracing the shifts of offset times, changed.
discretely with no transitional phase after the LL to DD transition. The free-running periods ($\tau$) were found to be 24.4±0.1 hr (mean±SD, n=8) in LL and 23.1±0.1 hr (n=5) in DD with small deviations, respectively. Moore and Rankin (1985) reported that $\tau$-LL and $\tau$-DD of locomotor activity of $A. mellifera$ was 24.8 hr and 22.0 hr, respectively.

Cloning of per cDNA

To clone a period homolog from $A. cerana japonica$, we performed PCR with cDNA derived from the bee heads as the template. We made degenerate primers based on the conserved sequences revealed by the alignment of period amino acid sequences of several of insect species (Reppert et al.,...
of the donor site (Norton, 1994) was found at the 5’ terminal part of the 3’ terminal portion of the sequence (TCCCTTGTTACAG; a pyrimidine-rich region followed by dinucleotide AG) at the 3’ terminal portion of the stretch. These observations suggested that the two types of the cerana per sequence resulted from alternative splicing of the per mRNA precursor.

Using primers based on the nucleotide sequences common to both types of the cDNAs, we cloned the 5’- and 3’-portions of per cDNA by 5’- and 3’-RACE (Rapid Amplification of cDNA Ends) methods, respectively. To determine whether these RACE products were actually parts of a single transcript, PCR was performed using primers corresponding to the sequences of the 5’ terminal portion of the 24-bp region that was lacking in type β. However, no possible donor site (Norton, 1994) was found at the 5’ terminal part of the cDNA by 5’- and 3’-RACE (Rapid Amplification of cDNA Ends) methods, respectively. To determine whether these RACE products were actually parts of a single transcript, PCR was performed using primers corresponding to the sequences of the 5’- and 3’-untranslated regions (UTR) obtained by RACE (see the materials and methods). We amplified two DNA fragments of 3506 bp (GenBank: AB-048825) and 3482 bp (AB048826), corresponding to types α and β, respectively. The full-length cDNAs of the types α and β contained open reading frames (ORFs) encoding putative proteins of 1124 and 1116 amino acids, respectively. The estimated molecular masses for the types α and β proteins were 124,479 and 123,613, respectively. The amino acid sequences of the two proteins were identical except for a 8 amino acid stretch, corresponding to the 24-bp region described above, present or absent in the type α and β proteins, respectively (Fig. 2).

The first methionine of the encoded proteins was followed by another methionine, and the surrounding sequences of the codons for both methionines showed Kozak consensus sequences for the initiation of translation (Kozak, 1987). A protein databases search with the deduced amino acid sequences for the initiation of translation (Kozak, 1987). A protein databases search with the deduced amino acid sequences of the two proteins, which is present as a single copy, and suggested that types α and β are expressed from the same locus. We found that digestion of the genomic DNA with EcoRI and HindIII was followed by hybridization with per cDNA-specific probe. Southern blot analysis of digested genomic DNA revealed a single hybridization band in each lane (Fig. 3). This result indicated that the per gene of A. cerana is present as a single copy, and suggested that types α and β are expressed from the same locus. We found that digestion of the genomic DNA of mellifera by HindIII followed by hybridization using the same probe also gave a single band of the same size as cerana (data not shown). This suggested that per genes of cerana and mellifera have a similar structure.

Transcription of per in the brain
To investigate transcription of the per gene, RT-PCR analysis was performed using mRNA isolated from brains of foragers. When we used primers R0 and FI which is designed for regions of 681 base in length. Primers RO and FD, based on common sequence in types α and β, similar but slightly larger size of fragments were amplified (lane 3). Cloning and sequencing of the fragments revealed that these consisted of two types of α (753 base) and β (729 base) fragment (Fig. 4). Transcription of the cytoplasmic actin
Fig. 2. Alignment of the C2 region of the Period proteins from A. cerana determined in this study, A. mellifera (AF159569), P. americana (U12772), D. melanogaster (AF033029), M. domestica (AH007818), A. pernyi (U12769) and L. cuprina (Y19108). A partial sequence (AB050744) of A. mellifera obtained in this study is also included as A. mellifera*. Identical amino acids are indicated by asterisks. The PAS domains are enclosed by the square brackets. The PAS-A (A) and PAS-B (B) repeats, and the PAC (C; Ponting and Aravind, 1997) domain are boxed in gray. The CLD is underlined. The sites of the perL, perO1 and perS mutations in Drosophila and corresponding amino acids of other insects are shown in reverse contrast. The 8-amino acid peptide regions of A. cerana and A. mellifera determined in this study, which are lacking in type β cDNA, are boxed.
**Fig. 3.** Southern blotting analysis of the *per* gene of *A. cerana*. The *cerana* genomic DNA digested with *EcoRI* and *HindIII* was electrophoresed and hybridized with *A. cerana per* specific probe. The sizes of markers are indicated at the left.

**Fig. 4.** Schematic drawing of selective PCR for the amplification of type α and total (α+β) of *per*. To amplify the type α and total (α+β), a set of primers R0 and FI, and that of R0 and FD was used, respectively. See the text in detail.

**Fig. 5.** RT-PCR of *per* and actin fragments using mRNA isolated from brains of *A. cerana*. PCR products were separated on 1% agarose gel. The gel was stained by ethidium bromide. Lane 1 (actin); lane 2 (*per*, type α: primers RO-FI); lane 3 (total *per*, types α and β: primers RO-FD). The sizes of markers (lane M) are indicated at the left.
The cytoplasmic actin mRNA levels were almost the same between the samples collected at ZT 9 and ZT 21, whereas the mRNA levels of type α and total (α+β) were high at ZT 21 compared to ZT 9. The efficiencies of amplification in the PCR for type α and total (α+β) were found to be almost same (1.49–1.51); this allowed the comparison between the levels of type α and total (α+β).

Fig. 7 shows the daily changes of per mRNA levels in the brain of the bee kept under LD 12:12 photoperiodic regime. The levels of per (α) and total (α+β) were high during the dark-period compared to the light-period. They increased steeply...
not from reverse transcription of a premature transcript. Use of another 3' splice site, which is predicted to be located immediately upstream of the 24-bp region on the genome, probably results in the production of type $\alpha$. On the other hand, use of the 3' splice site found in the 24-bp region should give rise to the type $\beta$ by skipping the 24-bp region. The type $\alpha$ cDNA encodes a protein with an additional 8-amino acid stretch just upstream of the highly conserved "short period domain", to which many mutations affecting the period length were mapped (Baylies et al., 1992). This 8-amino acid stretch could not be aligned with the $\per$ sequences from any other insect species (Fig. 2).

Colot et al. (1988) identified 6 interspersed blocks of conserved regions C1 to C6 by comparison of the $\per$ sequences of three species of Drosophila. The cerana $\per$ protein sequence also showed significant conservation in the C1, C2 and C3 blocks (alignment of C2 blocks is shown in Fig. 2). Identity of the amino acid sequences in the C1, C2 and C3 blocks between A. cerana (type $\beta$) and Drosophila melanogaster were 38.0, 44.8 and 50.0%, respectively. On the other hand, C4, C5 and C6 blocks are less well conserved in A. cerana. We could not align these C-terminal regions between cerana and any Drosophila species, except for a few short stretches of 10–15 amino acids. This overall pattern of conservation, higher conservation in C1-3 and lower in the C-terminal half is also observed in other nondipteran insects such as A. peryyi (Reppert et al., 1994) and P. americana (data not shown; GenBank: U12772). In addition, we found no significant conservation in the C-terminal region among various insects suggests that this region may not be critical in the central clock mechanism. In contrast to the N-terminal half regions, the functions of the C-terminal half blocks of $\per$ protein are not well understood. It is tempting to speculate that the diverged C-terminal sequences of $\per$ might be involved in the temporal regulation of behaviors characteristic of each insect group.

In the N-terminal half of the cerana $\per$ sequence, we detected motifs and domains thought to be important for the central clock mechanisms with high identity to Drosophila sequences. Especially, the PAS, CLD and short period domains detected motifs and domains thought to be important for the $\per$ gene expression by Per protein. These are assumed to be critical regulatory steps in the generation of self-sustaining daily oscillations. Thus, the higher degrees of conservation found in these domains indicated that the cerana $\per$ period is a true structural and likely a functional ortholog of the Drosophila $\per$ gene.

The RT-PCR followed by sequencing the DNA fragments, which were amplified using primers of R0 and FD, indicated that both types $\alpha$ and $\beta$ of $\per$ mRNA are expressed in the brains of A. cerana. Moreover, the level of $\per$ mRNA in the brain showed robust daily change under a LD cycle as re-

**Table 1. Temporal change in the ratio between type $\alpha$ and $\beta$ transcript**

<table>
<thead>
<tr>
<th>Arbitrary unit of $\per$</th>
<th>Number of subclone</th>
</tr>
</thead>
<tbody>
<tr>
<td>Type $\alpha$ : Total ($\alpha+\beta$)</td>
<td>Type $\alpha$ : Type $\beta$ Total</td>
</tr>
<tr>
<td>ZT 6:00</td>
<td>0.40</td>
</tr>
<tr>
<td>ZT 9:00</td>
<td>0.45</td>
</tr>
<tr>
<td>ZT 18:00</td>
<td>3.1</td>
</tr>
<tr>
<td>ZT 21:00</td>
<td>2.6</td>
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</table>

The levels of $\per$ transcripts at ZT 6:00, 9:00, 18:00 and 21:00 in Fig. 7 were represented as arbitrary unit. *--**: significantly different (Fisher’s exact probability test: $p<0.01$).

at the beginning of the dark period, and then decreased gradually. The level of total $\per$ transcript was higher than that of type $\alpha$ at any time, and the ratio between the levels of type $\alpha$ and total ($\alpha+\beta$) changed by time (Fig. 7 and Table 1). In addition the peak-to-trough ratios in the two graphs are different. These observations suggest that the ratio between the abundance of the two types changed by time in LD cycle.

To confirm the change of the ratio in $\per$ transcripts directly, we cloned and sequenced the products (corresponding to the band of lane 3 in Fig. 5) of RT-PCR using primers R0 and FD. The results show that the ratio of type $\alpha$ clones to type $\beta$ clones was significantly different between the light- and dark-period (Table 1). The ratio of type $\alpha$ clones to total ($\alpha+\beta$) clones was low (5–13%) at the light-period (ZT 6 and ZT 9), and it increased to 57–63% at the dark-period (ZT 18 and ZT 21). These observations coincided with the results of RT-PCR assay (Table 1).

**DISCUSSIONS**

The foragers of A. cerana exhibit circadian locomotor rhythm which is entrained by light-dark cycles with activity largely concentrated to the late photophase (Fig. 1A). This daily rhythm pattern resembles that reported in A. mellifera (Moore and Rankin, 1993). Isolated A. cerana showed a short life-span as described for A. mellifera (Moore and Rankin, 1985), and almost all died within two weeks or so. During the experimental period in this study, however, the honeybees showed overt rhythms with free-running periods that were longer than 24 hr in LL and shorter than 24 hr in DD. The free-running period changed discretely without any transitional phase after LL to DD transition (Fig. 1D). These are the first observations indicating that A. cerana possesses a circadian clock as well as A. mellifera. As a first step to investigate the molecular mechanism underlying the biological clock of the honeybees, we cloned the $\per$ cDNA from A. cerana.

The cerana $\per$ cDNA sequence showed the highest degree of conservation to mellifera $\per$. Furthermore, we demonstrated that the $\per$ cDNAs consist of two types ($\alpha$ and $\beta$) in A. cerana, and that this is also the case in A. mellifera. The type $\alpha$ and $\beta$ were different only in a 24-bp nucleotide sequence present only in type $\alpha$. A consensus motif for the 3' splice site was found in this 24-bp nucleotide sequence, although no possible 5' splice site was found, indicating that the two types of cDNA resulted from alternative splicing and

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ported in other insects (Hardin et al., 1990; Sauman and Reppert, 1996). Phase relationships of the daily change of *per* (type α and total) mRNA abundance are similar to that reported in *A. mellifera* (Toma et al., 2000). These observations, together with the sequence data, supports the idea that the *cerana per* is a functional ortholog of the clock gene *period*.

We found that the ratio between the abundance of two types α and β changed by time in LD cycle (Fig. 7 and Table 1). In *Drosophila*, the *per* gene generates two types of transcripts by alternative splicing (Cheng et al., 1998). These two types differ only in the presence (type A) or absence (type B') of an alternative intron in the 3' untranslated region. Splicing of this intron was enhanced at low temperatures, and a mechanism that allows the preferential daytime activity of flies on cold days was proposed (Majercak et al., 1999). It is interesting to examine whether environmental and ontogenetic factors affect the levels of the two types transcripts in *A. cerana*. Further investigation of the *per* in *A. cerana* is currently underway in our laboratory to reveal the molecular mechanism underlying the circadian rhythm in this species.

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