

# Clock genes and sleep

Dominic Landgraf · Anton Shostak · Henrik Oster

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**Abstract** In most species—from cyanobacteria to humans—endogenous clocks have evolved that drive 24-h rhythms of behavior and physiology. In mammals, these circadian rhythms are regulated by a hierarchical network of cellular oscillators controlled by a set of clock genes organized in a system of interlocked transcriptional feedback loops. One of the most prominent outputs of the circadian system is the synchronization of the sleep–wake cycle with external (day–) time. Clock genes also have a strong impact on many other biological functions, such as memory formation, energy metabolism, and immunity. Remarkably, large overlaps exist between clock gene and sleep (loss) mediated effects on these processes. This review summarizes sleep clock gene interactions for these three phenomena, highlighting potential mediators linking sleep and/or clock function to physiological output in an attempt to better understand the complexity of diurnal adaptation and its consequences for health and disease.

**Keywords** Circadian clock · Clock genes · Sleep · Metabolism · Immunity · Memory

## Introduction

Almost 40 years have passed since the first clock gene, *period*, was discovered by Ronald Konopka and Seymour

Benzer in a forward genetic screen on fruit flies [75]. Starting from this landmark finding, *N*-ethyl-*N*-nitrosourea (ENU) mutagenesis phenotypic screens became a powerful tool to unravel the genetic basis of circadian rhythms. In the mid-1990s, the first mammalian clock gene, circadian locomotor output cycles kaput (*Clock*), was identified and cloned by Martha Vitaterna in the lab of Joseph Takahashi [71, 156]. In mammals—as in most organisms studied so far—circadian rhythms are controlled by a set of clock genes forming a network of positive and negative autoregulatory feedback loops [57, 120]. These clock genes are expressed in most tissues. A circadian pacemaker located in the suprachiasmatic nuclei (SCN) of the hypothalamus is reset by external light stimuli and synchronizes peripheral oscillators throughout the body with each other and with the light–dark cycle via humoral, neuronal, and behavioral cues [120]. At its heart, the cellular circadian clockwork consists of a main (or core) and an auxiliary (or accessory) transcriptional-translational feedback loop (TTL; Fig. 1, left side). The former is composed of the positive components brain and muscle ARNT-like 1 (BMAL1 or ARNTL), CLOCK and neuronal PAS domain protein 2 (NPAS2), as well as the negative components CRYPTOCHROME 1/2 (CRY1/2) and PERIOD 1–3 (PER1–3). BMAL1, CLOCK, and NPAS2 are members of the basic helix–loop–helix (bHLH) *Per-Arnt-Sim* (PAS) family of transcription factors. In the SCN, CLOCK/NPAS2 and BMAL1 form heterodimers that bind to specific circadian E-box elements on the promoters of their targets, thereby activating *Cry* and *Per* transcription during the (subjective) day. In the late afternoon, PER and CRY protein levels reach a critical concentration and, now forming complexes themselves, translocate into the nucleus. There, they interact with CLOCK/NPAS2-BMAL1 and, by repressing the transcription of their own genes, form a negative feedback loop. Progressive degradation of negative

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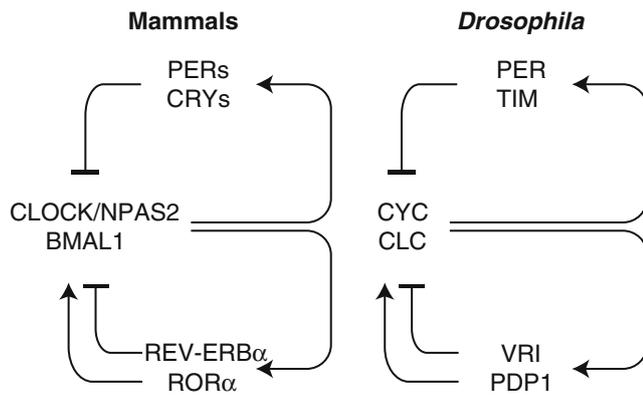
D. Landgraf and A. Shostak contributed equally to this work.

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D. Landgraf · A. Shostak · H. Oster (✉)  
Circadian Rhythms Group,  
Max Planck Institute for Biophysical Chemistry,  
Am Faßberg 11,  
37077 Göttingen, Germany  
e-mail: henrik.oster@mpibpc.mpg.de



**Fig. 1** Transcriptional-translational feedback loops regulate cellular circadian rhythms in mammals and flies. Both vertebrate and invertebrate clockworks are based on similar mechanistic concepts and share a number of genetic components. In mammals (*left*), a core loop is composed of PER and CRY proteins that inhibit their own transcription by inhibition of CLOCK (NPAS2)/BMAL1. An accessory loop involves REV-ERB $\alpha$  and ROR $\alpha$  that regulate *Bmal1* transcriptional rhythms. In *Drosophila* (*right*), CLK/CYC activate PER/TIM that feedback on CLK/CYC activity. VRI and PDP1 form an accessory loop that regulates *Clk* transcriptional rhythms

regulators towards the end of the subjective night starts a new cycle by the re-activation of *Per/Cry* transcription. Posttranscriptional modifications are heavily involved in clock oscillations and impart precision and robustness to the TTL. In particular, members of the casein kinase family (e.g., CKI $\epsilon$ , CKI $\delta$ ) are known to phosphorylate PER proteins at conserved residues and promote degradation, thereby delaying PER nuclear entry [48, 83]. The auxiliary loop comprises two genes of the orphan nuclear receptor family, *Rev-erba* (*Nr1d1*) and *Rora* (*Rora*). REV-ERB $\alpha$  and ROR $\alpha$  repress or activate, respectively, the transcription of genes with ROR elements in their promoters, such as *Bmal1* and *Npas2*. *Rev-erba* and *Rora* are considered to be dispensable for cellular rhythm generation, yet they were shown to regulate phasing and amplitude of clock gene expression rhythms [116, 127]. Further ancillary loops have been described. The CLOCK/NPAS2/BMAL1-regulated bHLH transcription factors DEC1 (BHLHE40) and DEC2 (BHLHE41) were shown to bind E-box elements and modulate CLOCK/NPAS2/BMAL1-driven circadian transcription [62, 124]. Another TTL involves the two transcription factors D-site albumin promoter binding protein and E4BP4 (NFIL3) that compete for binding of D-boxes, a third circadian regulatory DNA motif, at the promoters of *Per1-3*, *Rev-erba*, *Rora*, and various clock-controlled genes (CCGs) [90, 101]. Similarly, in *Drosophila*, CYCLE (CYC) and CLOCK (CLK), the orthologs of BMAL1 and CLOCK, form heterodimers and activate transcription of the circadian repressor genes *Timeless* (*Tim*) and *Period* (*Per*) via E-boxes (Fig. 1, right side). TIM is a substitute for mammalian CRYs as the major core TTL

inhibitor, whereas in the fly, CRY functions primarily as a photoreceptor and helps to synchronize the clock to the light–dark cycle [142]. TIM/PER complexes are transported to the nucleus to repress CYC/CLK-mediated transcription [56]. DOUBLETIME, a homolog of casein kinase I, phosphorylates PER, assigning it for sequestration via the proteasomal pathway [72, 117]. Similar to mammals, the fly clock contains at least one auxiliary loop consisting of VRILLE (VRI) and PAR-domain protein-1 (PDP1). The former inhibits, whereas the latter activates *Clk* transcription [26].

### Interaction between circadian and homeostatic sleep components

The current model predicts that sleep is regulated by two principle mechanisms [13, 27]. The first, termed *process c*, determines the appropriate timing of sleep. Nocturnal animals experience sleep mostly during the day, while diurnal species such as humans rest predominantly during the night. The SCN, as master circadian pacemaker, sends projections to important sleep regulatory nuclei such as the ventrolateral pre-optic area, the dorsomedial nucleus of the hypothalamus, and the hypocretin/orexin neurons of the lateral hypothalamus. Process c is complemented by a homeostatically controlled sleep drive, process s, which builds up an increased need for sleep in response to extended wake periods, independent of the time of day. So far, the anatomical substrate of process s remains elusive. Of note, sleep in mammals and birds is quantified primarily by electro-encephalography (EEG). In contrast, characterization of sleep in insects, where rhythm and homeostasis appear to be as robust as in mammals, relies mostly on measurements of rest/activity periods and arousal thresholds [60, 131]. SCN-lesioned rats and mice show disrupted sleep timing and consolidation, though the overall time spent asleep each day and the delta response to sleep deprivation remain uncompromised [67, 100, 147]. Previous studies conveyed on humans under forced desynchrony protocols demonstrated that slow wave activity was largely independent of internal circadian phase, though distribution of REM sleep and spindle activity in non-rapid eye movement (NREM) sleep correlated with body temperature rhythms [34]. At the same time, homeostatic sleep components can modify circadian pacemaker function. Sleep states affect activity of SCN neurons with decreasing firing rates during NREM phase and after sleep deprivation [30, 31]. Moreover, prolonged awaking effects the expression of clock genes in the cerebral cortex, upregulating both of *Per1* and *Per2* [161, 162]. This body of evidence suggests that the circadian clock regulates sleep–wake timing and opposes process s in order to gate consolidated bouts of sleep and waking.

## Clock genes and sleep timing

In humans, naturally occurring polymorphisms in clock genes correlate with early or late chronotype. A *PER3* gene length polymorphism is linked to extreme diurnal preferences [4]. The longer allele, which carries five repetitions (*PER3<sup>5/5</sup>*) of a variable number tandem repeat, is associated with early morning type, whereas the shorter allele (*PER3<sup>4/4</sup>*) correlates with eveningness and delayed sleep phase syndrome (DSPS). Recently, it was demonstrated that a polymorphism in the *PER3* promoter is also associated with DSPS [6]. Similar correlations of polymorphic alleles with diurnal preferences are observed for *PER1* and the 5'untranslated region of *PER2* [18, 19].

Circadian control of sleep can be better demonstrated on disorders associated with extremely shifted sleep–wake time. In familiar advanced sleep phase syndrome (FASPS), genetic studies identified mutations in the *PER2* (S662G) and *CKIδ* (T44A) genes in some families [148, 164]. Remarkably, both mutations affect an evolutionary conserved process, the phosphorylation of the PER2 protein by CKI. Xu et al. [164] have shown that a single amino acid substitution (T44A) in the human *CKIδ* protein decreases its enzymatic activity in vitro. The corresponding mutation, when reproduced in mice, causes a shortened circadian period length, which is consistent with symptoms of FASPS patients. Surprisingly, a miss-sense mutation in the same conserved residue of the *Drosophila* *CKI* ortholog *Dbt* leads to an increase in the free-running period [164], as

would be expected from DSPS patients. These findings highlight the different organization of circadian/sleep regulatory mechanisms in insects and mammals, despite the fact that individual components share a great similarity between vertebrate and invertebrate systems (see also Fig. 1). In another study, transgenic mice expressing human PER2 with the S662G mutation on a *Per2*-deficient background display a shorter period resembling humans with FASPS. Conversely, an aspartate substitution at the same residue (S662D), mimicking a constitutively phosphorylated state, correlates with a longer period [165].

## Clock genes and sleep homeostasis

A number of recent studies suggest that clock genes, besides regulating circadian sleep–wake timing, also contribute to sleep homeostatic control (reviewed in [47] and summarized in Table 1). Naylor et al. [105] demonstrated that mutations in *Clock* have effects on a variety of sleep–wake parameters in the mouse. *Clock* mutant animals show a reduction in total sleep time (around 2 h) under light/dark (LD) conditions, mostly due to reduced NREM sleep. In constant darkness (DD), homozygous mutants spend more time of their circadian cycle awake, mostly sacrificing NREM sleep, even when the results are normalized to their longer endogenous circadian period of 28.8 h. The response to sleep deprivation is also altered in these mice with decreased REM sleep rebounds, though the effects on

**Table 1** Clock gene mutant mice with sleep abnormalities

Mouse mutant	Circadian phenotype	Sleep phenotype					
		Sleep amount, light/dark phase	REM, light/dark phase	NREM, light/dark phase	Delta power in NREM, light/dark phase	Response to sleep deprivation	References
<i>Bmal1<sup>-/-</sup></i>	Arrhythmic	Normal/elevated	Normal/elevated	Normal/elevated	Elevated/reduced	Attenuated NREM/REM	[81]
<i>Npas2<sup>-/-</sup></i>	Short period	Normal/reduced	Normal/reduced	Normal/reduced	Normal/normal	Attenuated NREM, reduced delta power	[39, 46]
<i>Clock<sup>Δ19</sup></i>	Long period	Reduced/reduced	Normal/normal	Reduced/reduced	–	Attenuated REM	[105]
<i>Per1/2<sup>m/m</sup></i>	Arrhythmic	Reduced/normal	Normal/normal	Reduced/normal	Normal/normal	Increased delta power	[135]
<i>Cry1/2<sup>-/-</sup></i>	Arrhythmic	Normal/elevated	Reduced/elevated	Normal/elevated	Elevated/elevated	Attenuated NREM/REM, reduced delta power	[161]
<i>Dbp<sup>-/-</sup></i>	Short period	Normal/normal	Reduced/normal	Normal/normal	Normal/reduced	Attenuated REM	[45]
<i>Dec2<sup>P385R</sup></i>	Normal	Reduced/normal	Reduced/normal	Reduced/normal	Normal/normal	Attenuated NREM/REM, reduced delta power	[59]
<i>PK2<sup>-/-</sup></i>	Attenuated amplitude	Reduced/normal	Normal/elevated	Reduced/normal	Normal/normal	Attenuated NREM/REM, reduced delta power	[65]
<i>Vipr2<sup>-/-</sup></i>	Arrhythmic	Reduced/elevated	Reduced/elevated	Reduced/elevated	Normal/normal	–	[133]

NREM and total sleep are unchanged [105]. Gene association studies performed on two independent populations of humans report links between sequence variants of *CLOCK* and sleep duration [1]. In the clock machinery, *Npas2* acts as a functional paralog of *Clock*, yet their expression in the brain rarely overlaps [2, 50, 71]. Consistent with this, *Npas2*-deficient mice show about 25% reduction in NREM and REM sleep as well as reduced sleep consolidation [39]. Subjected to 8 h of prolonged waking, *Npas2* mutants display a smaller compensatory increase in NREM sleep and in delta activity [46].

*Bmal1*-deficient mice are to date the only reported mouse strain in which the deletion of a single gene totally disrupts circadian molecular and behavioral rhythms [17]. Consistent with their arrhythmic behavior, homozygous *Bmal1*<sup>-/-</sup> mice show attenuated sleep–wake rhythms and increased sleep fragmentation. In contrast to *Clock* mutants, *Bmal1*<sup>-/-</sup> animals exhibit longer REM and NREM periods under LD and DD conditions. Furthermore, during the light phase delta power is constantly high, indicating that these animals are persistently under elevated sleep pressure. Paradoxically, when actively sleep deprived, *Bmal1* mutants show an attenuated homeostatic response. This might be due to a lesser amount of sleep lost during sleep restriction when compared to wild-type animals [81].

Mice lacking both *Cry1* and *Cry2* genes are frequently used as a genetic model of circadian arrhythmicity [152, 157]. In *Cry1/2*<sup>-/-</sup> mice, sleep parameters do not differ between light and dark phases, indicating a non-circadian distribution of sleep. Both NREM sleep and EEG delta power are increased during the light phase, and *Cry1/2* mutants also show attenuated responses to sleep restriction [161]. Of note, single *Cry1* or *Cry2* knockouts do not display any significant differences in sleep parameters consistent with their—at least partially—redundant role in the circadian clock [162]. Similarly, *Per* gene mutations have only modest effects on sleep homeostasis. Studies done on both *Per1* and *Per2* single mutant mice reveal altered 24-h distribution of sleep but normal responses to sleep deprivation [76, 135, 162]. However, behaviorally arrhythmic *Per1/2* double mutant animals show decreased REM and NREM sleep periods during the light phase and moderately increased delta power after prolonged waking [135]. Remarkably, in rats, expression of *Per1* in the dorsomedial SCN was correlated with timing of REM sleep occurrence, pointing to a function of the central pacemaker itself in sleep architecture regulation [84]. In humans, the *PER3* gene also plays a role in sleep homeostasis. Individuals bearing the gene length variant *PER3*<sup>5/5</sup> show longer durations of NREM sleep bouts, higher delta power, and an exaggerated response to sleep deprivation [155].

In *Drosophila*, mutants of mammalian clock gene orthologs also exhibit profound changes in sleep homeostasis. In particular *clk<sup>rk</sup>*, *per<sup>01</sup>*, and *tim<sup>01</sup>* flies show increased sleep rebounds after 7, 9, and 12 h of sleep deprivation and recover 100% (compared to 30–40% in wild-type *Canton-S* flies) of sleep lost within 12 h [132]. In turn, more tremendous sleep rebound and even lethality in response to 12 h of sleep deprivation have been observed in *cyc<sup>01</sup>* mutants [132]. Interestingly, this phenotype differs between genders with stronger effects seen in females [61].

*Dbp* knockout mice were the first animal model investigated for the role of clock genes in sleep homeostasis [45]. In constant darkness, *Dbp*-deficient mice exhibit a slightly shorter free-running period and decreased overall activity [90]. On EEG recordings *Dbp* mutants show reduced REM sleep during the light phase as well as less delta power activity in the dark. After 6 h of sleep restriction, significantly attenuated REM responses are observed [45]. In a recent study, He and co-workers [59] found *DEC2* to regulate sleep length in humans. They identified a miss-sense mutation in the human *DEC2* gene that is associated with a sleep phenotype (6 vs. 8 h sleep duration in control subjects). When this point substitution is reproduced in mice, it decreases total sleep time via both REM and NREM without affecting circadian period [59]. A targeted deletion of *Dec2*, however, does only produce a mild sleep phenotype in mice [59]. Interestingly, in the fly homolog of *DEC2*, *CLOCKWORK ORANGE (CWO)* [87], the affected amino acid residue (P385) is not conserved, but flies expressing a mutant mouse *Dec2* show a similar sleep phenotype [59].

Of note, some of the genes known to mediate transcriptional output from the circadian clock machinery have also been implicated in sleep regulation. For instance, targeted deletion of *Prokineticin2 (Pk2)*, encoding a peptide secreted from the SCN and critical for the maintenance of robust circadian behavioral rhythms [24, 86], produces profound alterations in sleep homeostasis. *Pk2* mutants show a 20% reduction in total sleep time, mostly due to a decrease in NREM sleep in the light phase, whereas REM sleep is increased. Delta power and REM sleep rebound after sleep deprivation are also attenuated in these mice [65]. A recent study on the *VPAC2* subtype of the VIP receptor (*VIPR2*) implicated in the coupling of cellular oscillators within the SCN pacemaker demonstrates the significance of synchronization of electrical activity in SCN neurons on sleep regulation. Consistent with locomotor activity data, an attenuated diurnal rhythm of sleep and wakefulness is seen in *Vipr2*-deficient mice, although total sleep time and other homeostatic parameters are not affected [58, 133]. Interestingly, in flies, a disruption of the VIP analog neuropeptide pigment dispersing factor (*PDF*) increases sleep and causes reduced responsiveness to external stimuli [25]. Together,

these studies clearly show that circadian and homeostatic regulatory circuits show a high degree of interaction. It remains unclear, however, how this cross-talk is mediated at the molecular level and which neuronal circuits are involved.

### Clock genes and sleep-associated functions

Clock genes do not only influence sleep architecture and quality. They might also be involved in sleep and sleep-correlated functions within an organism [51]. In many cases, clock gene mutations and sleep disorders share the same symptoms and phenotypes. Sleep loss, for example, has been correlated to numerous metabolic symptoms, which are also observed in circadian clock-deficient animal models. Clock genes affect synaptic plasticity in learning and memory formation and modulate immune functions during the course of the day. In the same way, sleep—or the lack thereof—has a strong impact on these processes.

### Energy metabolism

The efficient regulation of energy homeostasis is an essential factor for an organism's survival. It comprises a range of different processes, including energy uptake (i.e. eating), storage (mostly as lipids, glycogen or tissue protein), and expenditure (energy usage for biosynthetic processes, heat production or locomotion). Energy is taken up in the form of macronutrients—carbohydrates, fat, or protein. In most species, nutrient ingestion follows a strict circadian rhythm, and several clock genes have been shown to be involved in the regulation of metabolic homeostasis. *Clock* mutant mice show blunted diurnal activity rhythms resulting in elevated food intake during the usual resting phase (day) and less ingestion during the active phase (night). These mice become hyperphagic and obese [151]. Another study showed that daytime high fat diet (HFD) in mice leads to a significant higher weight gain than nighttime HFD [3]. This is a possible explanation for the clock mutants' obese phenotype. Similarly, *Per2* mutant mice show arrhythmic feeding behavior and eat significantly more under (HFD) conditions. These effects are based on a decreased level of alpha melanocyte-stimulating hormone ( $\alpha$ -MSH), a well-known appetite suppressor, at the beginning of the light phase. Constant administration of  $\alpha$ -MSH to *Per2* mutants leads to reduced food uptake, revealing  $\alpha$ -MSH as a direct target of the clock gene *Per2*, independent of rhythmicity [167]. Interestingly, some of these effects are also seen after sleep restriction in rodents and in humans. In the latter, a restriction of sleep time to 4 h for only a few consecutive

nights is enough to significantly increase appetite [139, 140]. Rats that are kept awake for 2 weeks using the classic disc-over-water technique show hyperphagy—although they lose weight under these conditions [119]. Of note, a number of other animal studies failed to confirm an increase in food uptake in response to sleep restriction, indicating that small variations in experimental procedures may have a significant impact on these processes [9, 170]. A straight-forward mechanistic explanation for a sleep-loss-mediated increase in energy uptake remains elusive. It was suggested that a temporal deregulation of peripheral orexigenic and anorexigenic hormones could underlie this effect. The most promising candidates are the gastrointestinal peptide ghrelin [29, 73] and the adipokine leptin secreted by white adipocytes [89]. In humans as well as in animals, sleep restriction or total sleep deprivation cause significant decreases in circulating leptin and increased ghrelin, thus promoting appetite and hunger [11, 44, 140, 145]. Human leptin plasma levels are partially dependent on meal time [128] and also on the circadian time and sleep state. Under un-stressed and constant feeding conditions, leptin shows a marked nocturnal rise in humans [128]. When sleeping time is shifted by 8 h, leptin levels are differentially regulated by both the circadian system and sleep, resulting in a short period rhythm with peaks in the night and around mid-sleep phase [136]. In contrast, the diurnal expression of ghrelin seems not to be directly clock-regulated. Under ad libitum feeding conditions ghrelin shows a bimodal rhythm with peaks in the afternoon and towards the end of the dark phase in rats, correlating with gastric emptying and filling [103]. However, in humans, sleep triggers ghrelin release during night. Comparable to rats, humans also show a bimodal ghrelin rhythm with one peak in the afternoon and one peak during night. The peak during night is absent when test persons were sleep deprived [40]. Ghrelin signaling seems to have a strong influence on the circadian system. In cultured mouse brain slices containing the SCN, ghrelin administration increases firing rate of individual SCN neurons. Ghrelin receptor activation phase shifts SCN bioluminescence rhythms in culture and resets locomotor activity rhythms in intact mice [168]. Another agent connecting the circadian system, sleep, and food uptake is the neuropeptide orexin (or hypocretin/HCRT). Its two isoforms, orexin A and B, are exclusively expressed in neurons of the lateral hypothalamus. Both have potent wake-promoting effects and at the same time stimulate food intake [126]. Orexin release is circadian clock-controlled and *Hcrt* transcription rhythms are abolished in *Clock* mutant mice [151]. The SCN directly innervates orexigenic neurons [104]. Under starvation conditions, the sleep duration of rats is shortened [28], while sleep deprivation increases energy uptake [119]. The orexin system constitutes a potential candidate linking both processes.

Similar to food uptake, energy metabolism is influenced by the circadian system and sleep. Both sleep and clock disruptions have strong effects on glucose and lipid metabolism. Several clock gene mutant mouse strains show phenotypes resembling aspects of the type II diabetes pathology. The overexpression of mutant *Cry1* protein results in polydipsia, polyuria, and hyperglycemia [109]. *Clock* mutant mice show hyperglycemia and hypoinsulinemia [151]. Moreover, *Clock* mutant and *Bmal1*<sup>-/-</sup> mice exhibit impaired glucose liberation from the liver. Under HFD conditions, these mice show deficient insulin regulation and beta cell function in the pancreas [125]. A liver-specific deletion of *Bmal1* promotes hypoglycemia and deregulated expression of genes involved in glucose metabolism, such as phosphoenolpyruvate carboxykinase 1 (*Pck1*), glucokinase (*Gck*), and glucose-6-phosphate translocase 1 (*G6pt1/Slc37a4*) [79]. The fact that polymorphisms in the *Clock* gene are associated with metabolic syndrome in man and that several *Bmal1* haplotypes in rats are connected to type II diabetes underlines the connection between circadian genes and metabolism [130, 163]. CCG mutations can also cause diabetic symptoms. Nocturnin is a clock-controlled deadenylase involved in post-transcriptional regulation of gene expression. Loss of *Nocturnin* (*Cern14*) has strong effects on insulin sensitivity and glucose tolerance [53]. Other examples are the orphan nuclear receptor peroxisome proliferator-activated receptor  $\alpha$  (*Ppara*) and tumor necrosis factor alpha (TNF- $\alpha$ ) [54, 108]. Strikingly similar effects on metabolism have been attributed to sleep (or the lack thereof). The global trend towards shorter sleep times during the last decades was suggested as one of the factors underlying the alarming increase in the prevalence of the metabolic syndrome and type II diabetes [52, 106]. In line with this, poor sleep quality is a risk factor for type II diabetes [146]. Experimentally, restriction of sleep to 4 h per night for less than a week increases blood glucose levels while at the same time decreasing insulin sensitivity [139], suggesting that a chronic reduction of sleep time raises the risk of developing diabetes.

Other processes associated with clock gene function are lipid metabolism in adipocytes and energy expenditure in the muscles. *Clock* mutant mice suffer from hyperlipidemia [151], and *Bmal1* is necessary for adipocyte differentiation from mouse embryonic fibroblast cultures. Restoration of BMAL1-expression in *Bmal1*-deficient 3T3-L1 precursor cells rescues adipogenesis. A treatment with PPAR $\gamma$  ligands reconstitutes the differentiation potential of these cells. In addition, many other lipid metabolism-related genes, like *aP2*, *SREBP-1 $\alpha$* , and *perilipin*, are effected by *Bmal1* restoration, indicating that all these genes are direct targets of *Bmal1* [134]. Interestingly, *Bmal1*<sup>-/-</sup> mice exhibit no

alterations in body weight gain under a variety of diet conditions. However, a possible obesity phenotype in these animals might be confounded by their premature aging [74]. The *Bmal1* regulator ROR $\alpha$  promotes fatty acid oxidation via its targets, caveolin-3 and CPT-1, lipogenesis, and lipid storage in skeletal muscles [82], while *Nocturnin*-deficient mice show resistance to diet-induced obesity [53]. Although the molecular mechanisms are less well understood, several studies suggest that shortened sleep also has a strong influence on lipid metabolism. A chronic lack of sleep, either shortened sleep time or poor sleep quality, is a strong risk factor for obesity and the development of the metabolic syndrome [49, 69]. In a large longitudinal study on nurses, Patel et al. [112] observed a cross-sectional U-shaped association between sleep duration and body mass index (BMI) development over several years. It was suggested that sleep effects on lipid metabolism are mediated by endocrine factors, such as cortisol, prolactin, or insulin, as well as by sympathetic hyperactivity, which had previously been linked to obesity and insulin resistance. In this manner, sleep restriction represents a minor form of chronic stress, thus activating the *sympathicus* and elevating epinephrine and norepinephrine secretion from the adrenal medulla. In line with this, sympathetic activation and catecholamine administration inhibit leptin expression and secretion [137], increase free fatty acid levels [66], and decrease insulin sensitivity [94]. Restricted sleep and sleep deprivation elevate glucocorticoid levels [85], further promoting visceral fat deposition and insulin resistance [122].

Several endocrine factors have been suggested as potential modulators of clock and sleep regulated aspects of energy metabolism, including adrenal glucocorticoids, pituitary hormones, as well as the “night hormone” melatonin. In most mammals and birds, melatonin is produced in the pineal gland during the night. The pineal receives direct and indirect signals from the SCN and is, therefore, rhythmically locked to the circadian master clock. Bi-directional links have been described between melatonin production and the regulation of glucose metabolism. In diabetic Goto-Kakizaki (GK) rats, melatonin levels are significantly reduced, while melatonin receptor expression in the pancreas is increased [113]. In line with this, melatonin signaling has a strong influence on insulin secretion from the pancreatic beta cells [102].

### Neuronal plasticity

Clock gene–sleep interactions have also been reported in the context of neuronal plasticity and learning processes [51]. These include both short and long-term memory

(LTM) formation and recall. The latter is thought to depend primarily on hippocampal long-term potentiation (LTP), a form of synaptic plasticity [96]. LTP efficiency is time-of-day dependent in the hippocampus and in the SCN [10, 22, 107]. Several studies show that circadian core clock genes are involved in long-term memory formation. Mutations of *Npas2* cause impaired LTM in a fear conditioning paradigm [50]. Several clock output factors also have a role in memory formation. Inhibition of melatonin or deletion of the gene encoding the SCN-secreted peptide vasoactive intestinal polypeptide (VIP) disrupts memory formation [23, 159]. These phenotypes are often connected to cAMP signaling [158, 169]. MAPK phosphorylation and cAMP and CREB phosphorylation are clock gene controlled in the hippocampus. The nadir of these events corresponds to the time when the strongest learning deficits are observed and pharmacological inhibition of MAPK phosphorylation during a learning task impairs memory formation [41]. Like memory formation, memory recall is under direct influence of clock genes. *Cry1/2*<sup>-/-</sup> mice show normal spatial memory and perform well in simple avoidance tasks. They are, however, unable to efficiently learn in a more complex time–place context [153]. Similar findings were reported from *Per2* mutant animals [160]. In a food-rewarded hippocampus-dependent spatial memory task (eight-arm radial maze) [129], *Per1*<sup>-/-</sup> mice fail more frequently than wild-type littermates [70]. Various publications show strong influences of sleep on memory. For instance, individuals carrying homozygous *Per3*<sup>5/5</sup> alleles exhibit an interesting connection among their clock genotype, sleep, and regional brain response patterns to an executive task. In contrast to *PER3*<sup>4/4</sup> participants, sleep deprivation correlates to changes in brain activity only in *PER3*<sup>5/5</sup> participants [154].

Although the influence of sleep on memory processes has primarily been studied in a neurophysiological rather than in a molecular context, there are several common features of sleep and clock gene impact on memory processes. The hypothesis that sleep has a positive influence on memory formation is not new [68]. Numerous studies provide evidence that both declarative and procedural memory processes benefit from proper sleep [95, 138]. Even very short naps of a few minutes have been shown to improve declarative and procedural memory formation and recall [77, 78, 99, 150]. Re-entrainment of sleep patterns can restore cognitive functions either in transgenic mice carrying the Huntington's disease mutation [111] or in elderly patients showing symptoms of dementia [121]. However, until now, it is not fully clarified whether sleep has, like clock gene function, an influence on the formation of LTP. LTP can occur during REM sleep [15], and REM deprivation impairs LTP in the rat hippocampus [123].

On the other hand, REM deprivation does not necessary lead to disturbed memory formation [118]. Total sleep deprivation can lead to problems in learning [32], but this effect seems to be highly dependent on the subjects' general cognitive capacity [33]. In animals, current sleep deprivation protocols always include a certain stress component, which in itself can interfere with memory formation [63].

### Immune functions

Similar to the brain, the immune system acts as a bidirectional interface between the organism and its environment. From a more general perspective, it also functions in a very similar way in terms of detection of, reaction to, and memorization of information. Sleep has a strong influence on the immune system and vice versa [93]. Inflammation state affects sleep time and quality in animals and humans [16, 30, 38], while sleep restriction leads to higher mortality rates upon infection or sepsis [42, 43, 149]. Several immune parameters show circadian rhythmicity in the blood of humans and other mammals [80]. Clock gene expression is rhythmic in peripheral leukocytes [5]. Moreover, the secretion of important neuroendocrine immune modulators is under circadian as well as under sleep control. The activities of the hypothalamus pituitary adrenal (HPA) axis and the sympathetic nervous system, both stress activated, are influenced by the circadian system and sleep. In arrhythmic *Per2/Cry1* double mutant mice, HPA axis regulation is strongly affected. The responsiveness of the adrenal to adrenocorticotropin stimulation and, thus, the production of glucocorticoids are regulated by adrenocortical circadian clocks [110]. Humans show elevated cortisol and norepinephrine levels in response to sleep deprivation while epinephrine levels become arrhythmic [80]. These effects will likely give rise to changes observed in leukocyte production. For leukocytes, strong diurnal rhythms have been reported [14, 144], some of which seem to directly respond to cortisol secretion during night time and to epinephrine during the day [36, 37]. Moreover, sleep loss affects levels of lymphocytes, monocytes, natural killer (NK) cells, and T-cell proliferation in humans [12, 14, 35, 97]. Not only the appearance of immune cells is circadian as well as sleep-controlled but also the levels of several cytokines [93]. While interleukin (IL)-6 production seems to primarily depend on clock function, rhythmic TNF- $\alpha$ , IL-10, and IL-12 release from monocytes as well as IL-12 production by dendritic cells depend critically on sleep–wake conditions [80].

Circadian rhythm disruption has been shown to severely weaken the immune system. Mice exposed to four consecutive weekly 6-h phase advances of the light/dark

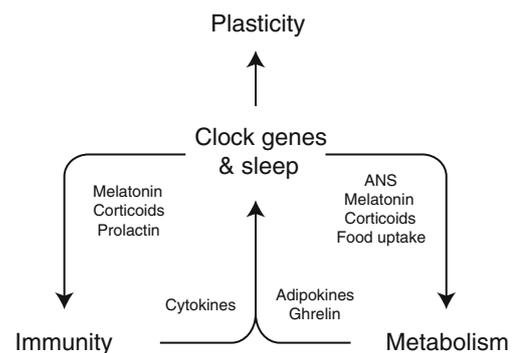
schedule (a repetitive jet lag paradigm) show increased mortality in response to lipopolysaccharide (LPS) injection [20]. Likewise, the clock gene *Per2* has been identified to play a direct role in the activation of macrophages by controlling the expression of interferon- $\gamma$  (IFN- $\gamma$ ), a macrophage activating factor, in the mouse spleen [7]. The same is true for the natural killer (NK) cell receptors LY49C and NKG2D [91]. NK cell-specific *knockdown* of *Per2* leads to decreased protein levels of the immune factors granzyme B and perforin in rats, but not of IFN- $\gamma$  [8]. Interestingly, LPS administration in *Per2*-deficient mice provokes attenuated immune responses and yields considerable higher survival rates than in wild-type animals [88]. *Bmal1*<sup>-/-</sup> mice show significantly reduced levels of B cells in peripheral blood, spleen and bone marrow [143]. *PER3*<sup>5/5</sup> individuals show elevated IL-6 concentrations compared to those with the *PER*<sup>4/4</sup> genotype [55]. As for metabolism, melatonin secretion might be one of the messengers linking sleep, circadian system, and immune function. Chemical inhibition of melatonin secretion leads to decreased antibody responses in mice. This effect is reversed by melatonin administration [92]. Melatonin further promotes the production of macrophage and granulocyte progenitor cells and affects the production of cytokines, such as IL-1, IL-2, IL-6, IL-12, TGF- $\beta$ , M-CSF, and TNF- $\alpha$  [141]. Vice versa, cytokines might have influence on clock gene expression. TNF- $\alpha$  and IL-1 $\beta$  suppress the expression of *Per1-3* and *Rev-erb $\alpha$*  in fibroblasts and liver of mice [21] in a p38 MAP kinase and calcium-dependent way [114]. This impairment of clock genes might lead to increased fatigue seen after infections.

Both sleep deprivation and clock mutations deregulate the production of pro-inflammatory cytokines, and low-grade systemic inflammation is a known pathological component of obesity and metabolic syndrome [64, 98]. Moreover, the production of IL-1 is increased in humans with self-reported poor sleep quality. Remarkably, this correlation of sleep debt and IL-1 levels does not apply for obese humans (BMI $\geq$ 30) [115]. Elderly people with metabolic syndrome and systemic inflammation show a higher risk of cognitive impairment compared with those without metabolic syndrome or with metabolic syndrome but without inflammation [166]. This leads to the suggestion of a direct connection between sleep, circadian clock genes, metabolism, cognition, and the immune system.

## Conclusions

Although it seems clear that sleep and clock genes have strong influences on various physiological processes, it is often technically difficult to disentangle clock gene,

circadian rhythm, and sleep-specific influences because of their mutual dependency and because only little so far is known about the underlying mechanisms and circuits (summarized in Fig. 2). While, in this paper, we have independently evaluated the impact of both processes, it is well conceivable that some of the physiological functions of one might be mediated via regulation of the other, i.e., sleep regulates clocks regulate physiology or clocks regulate sleep regulate physiology—and vice versa. While tremendous progress has been made in deciphering the molecular machinery of circadian clocks, little is still known of how different tissue oscillators communicate with each other to synchronize behavior and physiology. Even less understood are the processes underlying sleep. In fact, the tight interaction between clocks and sleep processes and the surprisingly strong effect that clock gene mutations have on both processes c and s might provide new inroads into mapping the sleep circuitry of the brain and into identifying molecular substrates of sleep within neuronal cells. With the advent of conditional genetics in mice and functional brain imaging techniques in humans, new tools have been developed to more specifically address these issues in the living organism. On the other hand, improved experimental paradigms need to be developed to resolve some of the conflicting findings from animal and human studies. The pathological long-term effects of the progressing sleeplessness and circadian desynchrony of modern societies will be in the focus of future research. A better understanding of the underlying mechanisms might well become a key for advanced therapeutic strategies against some of the most pressing health issues such as diabetes and neuropsychiatric disorders.



**Fig. 2** Interaction of sleep and clocks in the regulation of cognitive and physiological processes. A reciprocal interactivity exists between sleep and circadian clock function. Both neuronal and blood-borne factors have been proposed to mediate clock–sleep and sleep–physiology communication. On the other hand, peripheral humoral factors have been shown to provide feedback about the physiological state to sleep and clock regulatory circuits. The local regulation of physiology by tissue clocks may serve to integrate sleep state and timing signals at the cellular level. For details, see text

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