Regulation of amyloid-β dynamics and pathology by the circadian clock

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Nighttime restlessness and daytime drowsiness are common and early symptoms of Alzheimer’s Disease (AD). This symptomology implicates dysfunctional biological timing in AD, indicative of a faulty circadian system. Accordingly, neurological changes in the volume and cell number within the suprachiasmatic nucleus (SCN), the central locus of the circadian system, are observed in postmortem AD tissue and correlate with circadian rhythm degradation (Swaab et al., 1985; Zhou et al., 1995; Harper et al., 2008; Wang et al., 2015). Although circadian dysfunction has long been considered a consequence of AD-related neurodegeneration, it has more recently been hypothesized as a potential contributor to the pathogenesis of AD (Maywood et al., 2006; Hastings and Goedert, 2013; Musiek and Holtzman, 2016). This idea is strongly supported by epidemiological studies showing that a loss of robust circadian activity rhythms or sleep fragmentation in cognitively normal people is associated with increased risk of developing dementia (Tranah et al., 2011; Lim et al., 2013). However, it remains unclear whether or how the circadian system influences AD pathogenesis.

Amyloid plaques composed of aggregated amyloid-β (Aβ) peptides are a defining pathological feature of AD. Identifying factors that influence the accumulation of Aβ peptide is critical toward enhancing our understanding of AD pathogenesis. Normally, soluble Aβ peptide levels exhibit robust daily oscillations in mouse hippocampal interstitial fluid (ISF), as measured by in vivo cerebral microdialysis, as well as in human cerebrospinal fluid (Kang et al., 2009; Huang et al., 2012; Roh et al., 2012). These oscillations show a clear 24-h period, persist in constant dim lighting conditions (Kang et al., 2009), and are in phase with known circadian rhythms in activity, suggesting that Aβ rhythms in the brain may be controlled by the circadian system. Although it is well established that the circadian clock regulates the timing of periods of wakefulness and inactivity as well as many other rhythmic processes in the brain (Toh et al., 2001; Laposky et al., 2005), the role of the circadian system in controlling Aβ dynamics and amyloid plaque deposition remains unknown.

The mammalian circadian system is organized hierarchically, with the central “master” circadian clock in the SCN of the hypothalamus synchronizing subsidiary peripheral clocks distributed throughout the brain and body to coordinate physiology and behavior rhythms within a 24-h period (Mohawk et al., 2012). The central clock in the SCN and peripheral clocks in cells throughout the body use similar core molecular components composed of transcriptional–translational feedback loops to drive clock-controlled gene expression in a tissue-specific manner. At the molecular level, the positive transcriptional limb composed of the transcription factor BMAL1 (also known as aryl hydrocarbon nuclear translocator-like [ARNTL]) in com-
plex with circadian locomotor output cycles kaput (CLO CK) or neuronal PAS-containing protein 2 (NPAS2) drives circadian transcription of clock-controlled genes including repressor Period (Per) and Cryptochrome (Cry) genes that comprise the negative regulatory limb of the circadian molecular clock. Deletion of Bmal1 renders the circadian molecular clock dysfunctional in any given tissue including the SCN, and it prevents clock-mediated transcriptional regulation (Bunger et al., 2000). Mice with global Bmal1 deletion have complete loss of circadian function both in terms of SCN-driven central rhythms such as activity and temperature as well as cellular transcriptional rhythms across tissues. However, targeted deletion of Bmal1 within brain regions outside of the SCN disrupts local cellular circadian clock function and gene transcription without disturbing SCN-driven central rhythms (Mieda and Sakurai, 2011; Musiek et al., 2013). Thus, tissue-specific deletion of clock function can be used to evaluate the contribution of peripheral (local) versus central circadian clock function on Aβ dynamics in vivo. In this study, we determine whether the circadian clock controls Aβ oscillations in the hippocampus and impacts amyloid plaque deposition in vivo by using both tissue-specific and global Bmal1 deletion in a mouse model of β-amyloidosis. Furthermore, we interrogate the relative contributions of the central SCN-driven circadian clock and that of the local clocks of the brain to Aβ dynamics and plaque pathology.

RESULTS AND DISCUSSION
Hippocampus-specific Bmal1 deletion does not alter ISF Aβ rhythms
Because the circadian clock machinery within the hippocampus can regulate local gene expression, we first sought to determine whether the local hippocampal circadian clock is required for daily oscillations of ISF Aβ by examining the effect of targeted Bmal1 deletion in the hippocampus in a mouse model of β-amyloidosis. We used the APPPS1–21 transgenic model, which expresses the human amyloid precursor protein (APP) gene bearing the KM670/671NL “Swedish” mutations as well as human presenilin 1 bearing an AD-associated L166P mutation (Radda et al., 2006). We chose this particular AD mouse model because these mice exhibit early onset of amyloid plaques beginning at 2 mo of age. Using young mice (≤4 mo old) eliminates any age-related changes in the mouse’s intrinsic circadian system. Also, this AD mouse model is one of the few on a pure C57BL/6 background, thereby minimizing any strain-dependent effects on circadian behaviors. We found that 3–4-mo-old APPPS1–21 mice do not have any apparent abnormalities in circadian rhythms of behavior or basal clock gene expression (Fig. S1), and thus all circadian dysfunction observed in subsequent experiments was induced by our manipulations of Bmal1 in this system. Moreover, we observed close correlation between a classical circadian behavior assay involving wheel-running behavior and rhythms in core body temperature, allowing us to use core body temperature for circadian behavioral rhythms in subsequent experiments. To achieve localized deletion of Bmal1 within the hippocampus, we performed intrahippocampal injection of an adenovassociated virus (AAV8) expressing either Cre–internal ribosome entry site (IRES)–GFP or a GFP control construct in 3-wk-old APPPS1–21 mice bearing two floxed Bmal1 alleles (Bmal1<sup>fl/fl</sup>APPS1–21; Storch et al., 2007). Because amyloid plaque deposition can influence soluble Aβ dynamics (Roh et al., 2012), microdialysis was performed before 2 mo of age, which marks the appearance of amyloid plaque pathology, in all experiments. At 5 wk of age, microdialysis probes were placed directly into the region of viral vector injection, ensuring that Bmal1 was deleted in the hippocampal tissue directly surrounding the microdialysis probe (Fig. 1, A–D). After a 2-wk recovery from surgery, ISF Aβ levels were measured in freely moving mice for ≤4 d under 12-h:12-h light/dark (L:D) conditions (Kang et al., 2009). Hippocampus-specific Bmal1 deletion had no effect on the hippocampal daily oscillations of ISF Aβ, suggesting that the local core circadian clock within the hippocampus is not required for daily Aβ oscillations (Fig. 1, E and f).

Bmal1 deletion throughout the brain but with sparing of the SCN leaves ISF Aβ rhythms intact
We next sought to more thoroughly distinguish the effect of peripheral circadian clocks from those of the central clock on ISF Aβ oscillations. Because oscillation in Aβ levels may depend of peripheral circadian clocks in other brain regions that innervate the hippocampus, we examined whether Bmal1 deletion throughout the entire brain but with sparing of the SCN would impact hippocampal ISF Aβ rhythms. We used Nestin-Cre<sup>−/−</sup>Bmal1<sup>fl/fl</sup> mice, which have Bmal1 deleted in neurons and astrocytes throughout the brain but with unperturbed BMAL1 expression in the SCN (Chen et al., 2007). These mice have intact core body temperatures and rest–activity rhythms (Fig. 2, B and D; Musiek et al., 2013). However, we have previously shown that these mice lack of circadian clock gene transcription in the cerebral cortex and develop astroglis due to the loss of local Bmal1, effects which are independent of the central clock (Fig. S2 A; Musiek et al., 2013). We examined the effects of brain-specific clock disruption but with intact SCN-mediated rhythms on hippocampal ISF Aβ rhythms by generating Nestin-Cre<sup>−/−</sup>Bmal1<sup>fl/fl</sup>APPS1–21 mice (referred to as Nes–Bmal1 KO;APP). We observed that daily oscillations in hippocampal ISF Aβ in Nes–Bmal1 KO;APP mice were similar to those seen in Cre<sup>−/−</sup>;APP littermate controls, though the small peak in Aβ levels observed immediately after lights off was slightly blunted (Fig. 2, E and F). These results again show minimal involvement of extra-SCN local cellular clocks of the brain in ISF Aβ rhythms and suggest that these rhythms are mediated by the central clock in the SCN and transmitted to the hippocampus.
Local Bmal1 deletion in the brain with sparing of the SCN modestly increases fibrillar but not total amyloid plaque burden

We next used Nes–Bmal1 KO;APP mice to examine the effect of brain-specific clock disruption but with sparing of the SCN on amyloid plaque pathology. At 4 mo of age, Cre−, Bmal1<sup>−/−</sup>; APPPS1–21 (Cre−;APP) mice accumulate mild amyloid plaque pathology in the hippocampus similar to that observed in standard APPPS1–21 mice. Nes–Bmal1 KO;APP littermate mice showed no increase in total amyloid plaque burden within the hippocampus compared with Cre−;APP littermates as assessed by Aβ<sub>1-42</sub> antibody staining (Fig. 2, G and H). However, there was a modest but clear trend toward an increase specifically in fibrillar amyloid plaque burden, quantified by staining with the congophilic dye X34, in the hippocampus of Nes–Bmal1 KO;APP mice (P = 0.06 by two-tailed t test, and P = 0.03 by one-tailed t test). Thus, mice with deletion of Bmal1 throughout the extra-SCN brain but with intact central circadian rhythms had relatively normal hippocampal ISF Aβ oscillations, and they showed no change in total plaque levels but did show a small increase in hippocampal fibrillar plaque burden. Collectively, these data indicate that local peripheral clocks do not strongly influence Aβ oscillations or overall plaque deposition in the hippocampus but that local Bmal1 deletion may promote the formation of fibrillar Aβ plaques.

Global Bmal1 deletion causes loss of ISF Aβ rhythms in the hippocampus and markedly increases amyloid plaque burden

Finally, we examined the effect of whole-organism circadian disruption, including the SCN, on hippocampal ISF Aβ dynamics and plaque deposition. We were unable to cross APP PS1–21 mice to standard global Bmal1 KO mice because of poor viability. However, we were able to measure endogenous murine ISF Aβ (as opposed to human Aβ in the APPPS1–21 models) by microdialysis in standard Bmal1 KO mice, which have global Bmal1 deletion and have dysfunctional central and peripheral clocks as well as fragmented activity and core body temperature circadian rhythms (Fig. 3, A and B; Burger et al., 2000). These experiments allowed us to evaluate the effect of global Bmal1 deletion on ISF Aβ dynamics, but because there is no human APPPS1 transgene, the levels of murine Aβ were
lower, and samples had to be pooled to detect Aβ, decreasing the sampling frequency. Despite these obstacles, we found that arrhythmic Bmal1 KO mice had severely diminished daily oscillations in hippocampal ISF Aβ, even under 12-h:12-h L:D conditions, as compared with WT littermates (Fig. 3 D). However, integrated levels of ISF Aβ over the 24-h circadian cycle were similar to WT littermate controls (Fig. 3 E), demonstrating that although Bmal1 deletion disrupts the day/night rhythms of Aβ (leading to higher levels during the light period and lower levels during the dark), it does not cause gross increases in Aβ levels. Thus, loss of central and peripheral rhythms caused by global Bmal1 deletion abrogates rhythmicity of ISF Aβ in the hippocampus.

Because standard global Bmal1 KO;APPPS1–21 mice were not viable in our hands and because mice do not develop amyloid plaques without a human APP transgene, we chose to examine the effects of global Bmal1 deletion on amyloid plaque deposition using a tamoxifen-inducible global Bmal1 KO mouse (CAG-CreERT2;Bmal1f/f, abbreviated as Bmal1 iKO), which could be bred onto an APPPS1–21 background. Bmal1 iKO mice were previously characterized and phenocopy standard Bmal1 KO mice as they become transcriptionally arrhythmic after tamoxifen treatment and develop astrogliosis (Yang et al., 2016). Indeed, tamoxifen treatment of Bmal1 iKO mice at 8 wk of age resulted in a nearly complete deletion of BMAL1 throughout the brain, including the SCN (Fig. 4, A and C), and led to a loss of circadian core body temperature rhythms (Fig. 4, B and D).

However, postnatal deletion of Bmal1 in these mice avoids the developmental pathologies and early mortality observed in standard Bmal1 KO mice (Yang et al., 2016). We generated CAG-CreERT2;Bmal1f/f;APP APPPS1–21 mice (abbreviated as Bmal1 iKO;APP) to evaluate the effect of circadian disruption...
on amyloid plaque deposition. Notably, Bmal1 iKO;APP mice were not amenable to ISF Aβ measurement as the tamoxifen regimen was toxic to mice <6 wk old and treatment after that age did not allow sufficient time to allow for surgery, recovery, and microdialysis before plaque accumulation had begun at 2 mo of age. We treated cohorts of Bmal1 iKO;APP mice and their Cre− littermate controls (Bmal1f/f;APPPS1-21 mice; both sexes) with tamoxifen for 5 d starting at 8 wk of age and collected tissues at 4 mo of age. Bmal1 iKO:APP mice accumulated significantly more hippocampal amyloid plaque burden, quantified either by Aβ antibody to assess total plaque load or by staining with the congophilic dye X34 to assess fibrillar plaque pathology (Fig. 4, E and F).

Thus, global disruption of circadian function by postnatal global Bmal1 deletion increases amyloid plaque deposition in the hippocampus. Collectively, our results show that global Bmal1 deletion abolishes behavior rhythms mediated by the central clock, disrupts local clock-mediated transcription, abrogates ISF Aβ rhythms, and increases amyloid plaque deposition in the hippocampus.

**Bmal1 regulates local apolipoprotein E (ApoE) expression in the brain**

To explore possible transcriptional mechanisms by which the circadian system regulates Aβ plaque deposition, we performed transcriptional analysis of a panel of genes with known functions related to Aβ production, clearance, or aggregation in cortex tissue from Nes-Bmal1 KO (which have intact central rhythms but local Bmal1 deletion) and Bmal1 iKO mice (which have disrupted central rhythms and local Bmal1 deletion) as well as Cre− controls. Expression of several Aβ-related genes were altered, and these changes were generally consistent between the two models, suggesting local transcriptional regulation by Bmal1 (Fig. S2 A). Among these, we observed significantly increased expression of Apoe in both mouse models, demonstrating that Apoe is regulated by local BMAL1 independent of the central clock. We examined Apoe expression in cortex tissue from Nes−Bmal1 KO mice across the circadian cycle. Apoe mRNA showed only a modest time-of-day variation in control mice and was increased at all time points in Nes−Bmal1 KO mice (Fig. S2 B). The human APOE genotype is major determinant of AD risk, and murine Apoe has been shown to potently promote amyloid plaque deposition, specifically fibrillar amyloid plaques (Holzman et al., 2000; Fagan et al., 2002; DeMattos et al., 2004; Kim et al., 2011). Thus, local Bmal1 deletion in the brain induces Apoe expression, providing one potential mechanism by which local Bmal1 deletion promotes fibrillar plaque formation. However, multiple BMAL1-controlled pathways may also contribute to this effect.

Our data demonstrate that the circadian system influences daily oscillations in hippocampal ISF Aβ and that disruption of circadian function promotes hippocampal amyloid plaque deposition in vivo. ISF Aβ oscillations do not require local cellular clock function in the hippocampus itself nor in other non-SCN brain regions but instead appear to depend on the central circadian clock within the SCN. Loss of local BMAL1 expression in the hippocampus with sparing of central rhythms in Nes-Bmal1KO; APP mice had minimal impact on overall amyloid plaque deposition, but it did promote fibrillar plaque accumulation, perhaps at least in part through direct regulation of Apoe. Global Bmal1-iKO;APP mice,
which have an arrhythmic central clock and local Bmal1 deletion, develop much more striking increases in plaque burden than Nes-Bmal1KO;APP mice, which have normal central rhythms but local Bmal1 deletion, showing that the increases in amyloid pathology cannot be fully explained by noncircadian effects of Bmal1 deletion and are likely caused by a combination of dysregulated SCN-mediated circadian control of Aβ oscillations and local alterations in Bmal1-mediated transcription. In total, our study suggests that the circadian system is critical for maintaining proper Aβ oscillations and Aβ homeostasis in the hippocampus and that circadian dysfunction may disrupt the normal temporal synchrony or feedback inhibition between Aβ production and systems involved in Aβ clearance and/or aggregation. As circadian rhythm dysfunction appears to precede cognitive impairment in AD (Tranah et al., 2011; Musiek et al., 2018), our findings highlight novel mechanisms linking early circadian dysfunction to accelerated amyloid plaque accumulation and provide evidence for an important influence of the circadian system on AD pathogenesis.

Fragmented circadian rhythms can be detected in normal aging as well as in preclinical AD (Musiek et al., 2018) and become more apparent in early symptomatic AD (Hatfield et al., 2004; Harper et al., 2005). Degeneration of the SCN has been described in AD and linked to circadian rhythm degradation (Swaab et al., 1985; Zhou et al., 1995; Harper et al., 2008; Wang et al., 2015). Altered Bmal1 expression or function has also been specifically associated with AD. Altered methylation of Bmal1 in AD has been proposed as a possible cause of circadian dysfunction (Cronin et al., 2017), whereas Aβ can reportedly induce BMAL1 degradation in an AD mouse model (Song et al., 2015). Finally, polymorphisms in Bmal1 are associated with increased AD risk in ApoE4-negative individuals (Chen et al., 2015). Thus, there is a strong biological rationale for modeling AD-related circadian dysfunction by disrupting Bmal1. However, Bmal1 regulates expression of transcripts which are nonrhythmic, suggesting that it serves noncircadian functions (Yu and Weaver, 2011; Yang et al., 2016). We have previously demonstrated that Bmal1 deletion can induce glial activation and oxidative damage in Nes-Bmal1KO mice, which have normal circadian rhythms and sleep timing, demonstrating that Bmal1 can exert critical local effects in the brain (Musiek et al., 2013). However, in this study, we did not see significant effects of local Bmal1 deletion on ISF Aβ dynamics or total plaque deposition, demonstrating that the effects of global Bmal1 deletion on hippocampal ISF Aβ and plaque burden are at least in part a result of disrupted central rhythms. Increased Apoe expression was observed in both Nes-Bmal1KO and Bmal1iKO mice, suggesting that loss of Bmal1 induces local Apoe expression independent of an effect on rhythms or sleep. It has been well established that APOE specifically promotes fibrillar amyloid plaque deposition, as APP transgenic mice lacking APOE have striking decreases in fibrillar plaque burden (Holtzman et al., 2000; Fagan et al., 2002; DeMattos et al., 2004; Kim et al., 2011).
Thus, the local tissue effect of Bmal1 deletion on Apoe levels could potentially explain the specific increase in fibrillar plaques in Nes-Bmal1 KO;APP mice. However, our data suggest that the combination of central clock dysfunction, which disrupts ISF Aβ rhythms, and local Bmal1 deletion, which increases local Apoe expression and may alter other pathways, leads to a striking increase in plaques observed in Bmal1 iKO;APP mice (see Fig. 4).

It is well established that sleep exerts a powerful influence on Aβ plaque pathology as sleep deprivation accelerates plaque deposition, whereas increasing sleep through inhibition of orexin signaling mitigates plaque accumulation (Kang et al., 2009; Roh et al., 2014). The central circadian clock of the SCN regulates the timing of sleep and thus could affect amyloid plaque deposition through a sleep-dependent mechanism. Our data show that this may be the case as Bmal1 iKO mice, which have fragmented sleep rhythms, have a greater increase in plaques than SCN-sparing brain-specific Nes-Bmal1 KO mice, which have normal sleep timing. However, this is not caused by sleep deprivation as global Bmal1 KO mice are known to have slightly increased total and slow-wave sleep (Laposky et al., 2005). Bmal1 KO mice do have arrhythmic sleep timing with loss of variation in sleep between the light and dark periods (Laposky et al., 2005), a pattern which resembles the sleep and wake fragmentation observed in AD patients, who often wake throughout the night and nap throughout the day (Witting et al., 1990; Satlin et al., 1995; Hatfield et al., 2004). This circadian fragmentation appears before symptom onset in AD (Tranah et al., 2011; Musiek et al., 2018), suggesting that it could exacerbate amyloid deposition in an early phase of AD pathogenesis. A clear implication of our findings is that therapies directly targeting the circadian system to normalize circadian timing, rather than just augmenting total sleep, may be beneficial in the prevention of AD.

Our study has some limitations. Our microdialysis experiments were performed in standard 12-h:12-h L:D conditions rather than constant darkness. Because Bmal1 iKO;APP mice developed increased plaques in L:D conditions, we concluded that it was critical to demonstrate that ISF Aβ oscillations were also disturbed in L:D, which is what we observed. Moreover, Bmal1 deletion causes arrhythmicity even in L:D conditions, making repetition of these experiments in constant darkness less critical. Direct lesioning of the SCN in APPPS1−21 mice to disrupt central rhythms without deleting local clock genes would provide complementary data to our study, though such experiments are fraught with difficulty as the SCN is small and surrounded by other hypothalamic nuclei, which can potentially also impact amyloid plaque development if accidently damaged. These studies could be pursued in the future. Monitoring of sleep by electroencephalography was not performed, though electroencephalography analysis of sleep has previously been performed in standard Bmal1 KO and Nes-Bmal1 KO mice and was found to be arrhythmic in the former and normal in the latter and correlated closely with actigraphy and body temperature rhythms in both models.

In summary, our data reveal the importance of circadian timing in the regulation of amyloid pathology. The circadian system orchestrates the synchrony between many physiological processes with the external environment and regulates gene transcription in various cell types throughout the brain. Our findings demonstrate a potential mechanistic link between circadian dysfunction and AD pathogenesis, suggesting that therapeutic efforts to optimize circadian timing may hold promise for AD prevention.

MATERIAL AND METHODS

Reagents and animals

The following antibodies were used: BMAL1 rabbit polyclonal (1:2,000; 2288; Novus Biologicals) and a monoclonal AP1-13 (1:1,000; HJ3.4) made in-house (Kang et al., 2009). Various salts and BSA were purchased from Sigma-Aldrich. Mice with germline deletion of Bmal1 (Bmal1−/−), Nestin-Cre+ (stock 03771), CAGERT2-Cre+ (stock 004453), and Bmal1f/f (stock 07668) mice were purchased from The Jackson Laboratory. APPPS1−21 mice were obtained from M. Jucker (University of Tübingen, Tübingen, Germany). Bmal1f/f or Bmal1f/f;APPPS1−21 mice were crossed with either tamoxifen-inducible universal (CAG-CreERT2) mice or with Nestin-Cre+/− mice to yield Bmal1f/f mice without Cre, Bmal1f/f; CAG-CreERT2+/− mice, and Bmal1f/f;Nestin-Cre+/− mice with or without a single copy of the APPPS1−21 transgene. All mice were maintained on a C57Bl/6 background. Both genders were used in all experiments. Mice were bred and housed in accordance with Washington University Animal Studies committee protocols. Mice were bred and group housed (unless otherwise stated) under 12-h:12-h L:D conditions with ad libitum access to food and water. Tamoxifen stock solution (25 mg/ml; T5648; Sigma-Aldrich) was prepared as previously described (Yang et al., 2012) and administered to 2-mo-old Bmal1f/f;CreERT2−APP PS1−21 mice seven times over 5 consecutive days at 100 µl per dose by oral gavage. The efficacy of Bmal1 excision 2 mo after the tamoxifen regimen was assessed by the levels of quantitative PCR (qPCR) transcripts and BMAL1 immunostaining within the hippocampus. Mice with a reduction of at least 75% BMAL1 immunoreactivity within the hippocampus or an at least 50% reduction in mRNA of Dbp, a BMAL1-controlled gene, met the criteria for further analysis. For circadian gene expression experiments, mice were housed in constant darkness for 24 h before and throughout harvest and were anesthetized in darkness before perfusion. Mice were perfused at 4-h intervals starting at 6:00 AM and ending 24 h later.

Stereotaxic injections

Stereotaxic guided surgeries were performed on isoflurane-anesthetized mice as previously described (Kress et al., 2013). In brief, AAV8 vectors expressing Cre-IRES-GFP or just GFP under the chicken β-actin promoter (AAV8-CBA-Cre-IRES-GFP or AAV8-CBA-GFP) were prepared by the
Microdialysis

Hippocampal in vivo Aβ microdialysis was performed as previously described (Kang et al., 2009; Roh et al., 2012). At ∼6 wk of age, AAV-injected Bmal1f/f;APPPS1-21, Bmal1f/f; Nestin-Cre+/−:APP/PS1-21, or germline Bmal1 KO mice (∼2–3 mo old) were implanted with a guide cannula for microdialysis in the left hippocampus (bregma, 3.1 mm, 2.5 mm lateral to midline, and 1.2 mm below the dura at a 12° angle) and recovered in their home cage for ∼2 wk. On the day microdialysis began, mice were tethered to a Basi Rattern System, and a microdialysis probe (2 mm; 38-kD molecular weight cutoff; BR style; BioAnalytical Systems) was inserted into the left hippocampus through the guide cannula and connected to a syringe pump (Stoelting). Artificial cerebrospinal fluid, pH 7.35, containing 1.3 mM CaCl2, 1.2 mM MgSO4, 3 mM KCl, 0.4 mM KH2PO4, 25 mM NaHCO3, 122 mM NaCl, and 0.15% BSA was continuously perfused through the microdialysis probe at a constant flow rate of 1 µl/min (for the detection of murine Aβ, the flow rate was adjusted to 0.5 µl/ min). After 3 d of habituation, hourly microdialysis samples were collected over 2–4 d (Cirrito et al., 2003; Kang et al., 2009). The mean daily ISF Aβ level was calculated over 2–3 d for each mouse. The rhythm amplitude of the daily ISF Aβ oscillation was determined using the circadian cosinor method (circadian.org/software.html). Data from probe placements outside of the hippocampal region or from mice that did not eat, drink, or move normally were discarded.

Circadian temperature rhythm

Thermochron iButtons (DS1921H) were used to continually record core body temperature rhythms every 15 min as previously described (Pilz et al., 2015). In brief, in anesthetized mice, a longitudinal abdominal incision was made, and the iButton was positioned within the intraperitoneal cavity. Incisions were closed with absorbable and nylon sutures. Mice were house individually in 12-h:12-h L:D conditions for 3–4 wk and then for 2–7 d in constant dark (DD) conditions before the retrieval of the iButton. Temperature values were imported into ClockLab Analysis (6.0.35; Actimetrics) to create actograms and L:D periodograms (χ2 method).

ELISA

Microdialysis samples were analyzed for Aβx-40 with a sandwich ELISA (Roh et al., 2012). In brief, a monoclonal Aβ antibody targeted against amino acids 35–40 (HJ2) was used to capture Aβx-40 peptide. A biotinylated central domain monoclonal antibody was then applied (HJ5.1). Assays were developed using Super Slow ELISA TMB after an incubation with streptavidin–poly-HRP40 (Fitzgerald). A Bio–Tek Synergy 2 plate reader was used to read the optical density at 650 nm. Samples were run in replicate, and replicates with a coefficient of variation >15% were discarded.

qPCR

For RNA isolation, frozen cortical tissue was homogenized in TRIzol (Invitrogen). Chloroform (1:5) was added, samples were agitated and centrifuged at 13,000 g for 15 min at 4°C, and then the chloroform layer was removed, diluted 1:1 in 70% ethanol, and purified using RNA purification columns and reagents (PureLink; Thermo Fisher Scientific). RNA was converted to complementary DNA via reverse transcription using the High-Capacity cDNA-RT kit (MultiScribe; Applied Biosystems) with 1 µg RNA per 20 µl reaction. Quantitative real-time PCR was then performed using proprietary TaqMan primers and reagents and an ABI StepOne qPCR machine (Thermo Fisher Scientific). All mRNA levels were normalized to β-actin (Actb) mRNA levels.

Immunohistochemistry

Immunostaining was performed as previously described (Roh et al., 2012). In brief, mice were deeply anesthetized via i.p. pentobarbital followed by transcardial perfusion with ice-cold PBS containing 3,000 U/liter heparin for 3 min. The whole brain or only one hemisphere was fixed in 4% paraformaldehyde for 24 h (4°C) and then cryoprotected with 30% sucrose in PBS (4°C) for 48 h, and 50-µm serial coronal sections were cut on a freezing sliding microtome. For antibody staining, sections were incubated in PBS for 30 min at RT before blocking for 30 min in PBS containing 3% goat serum, 2% BSA, and 0.25% Triton X-100, and then they were incubated overnight in PBS plus 0.1% Triton X-100 with primary antibody and 1% goat serum at 4°C. Sections were then washed with PBS containing 0.1% Triton X-100 for 30 min followed by a 1-h RT incubation with fluorophore–conjugated secondary antibody (Alexa Fluor 488– or 568–conjugated anti–rabbit or anti–mouse) and then washed. Nuclei were visualized with DAPI (Invitrogen) in PBS for 30 min at RT, and then sections were washed for 15 min in PBS and mounted on a coverslip using either Fluoromount (Sigma-Aldrich) or ProLong Gold Antifade Mountant (Invitrogen). For X34 staining, sections were washed in PBS plus 0.10% Triton X-100 for 30 min and then incubated in staining media containing 60% PBS (vol/vol), 0.4% wheat, and 40% ethanol, 1:500 volume of 10 N NaOH, and 10 µM X34 for 20 min at RT. Sections were then washed for three time for 2 min each in 60% PBS (vol/vol) and 40% ethanol solution and then washed twice for 5 min each in PBS plus 0.10% Triton X-100. HJ3.4-stained sections were incubated with biotinylated secondary antibodies (Cell Signaling Technologies) and then with streptavidin–conjugated horseradish peroxidase (ABC kit; Vector Labs), and then were visualized with diaminobenzidine (Sigma-Aldrich). Sections were then
imaged with either an Eclipse 80i microscope (Nikon) with an Orca-Flash camera (4.0; Hamamatsu Photonics) using a MetaMorph (Molecular Devices) system or an A1Rs1 confocal system (Nikon; Washington University Center for Cellular Imaging). Images were adjusted in ImageJ (National Institutes of Health) or Photoshop (Adobe) for brightness, contrast, and pseudocoloring.

**Plaque burden quantification**

For plaque burden quantification, serial coronal sections (50 µm thick) were collected from the corpus callosum to caudal hippocampus. Approximately 3–4 sections (each separated by 300 µm) were stained with biotinylated HJ3.4 antibody to visualize Aβ-immunoreactive plaques or X34 dye to visualize fibrillary amyloid plaques. Sections were then imaged with either an Eclipse 80i microscope with an Orca-Flash 4.0 using the MetaMorph system or an Axioscan Z1 automated slide scanning system (ZEISS; Washington University Center for Cellular Imaging). Using a neurostereological method as described previously (Kang et al., 2009), the percent area for Cellular Imaging). Using a neurostereological method as described previously (Kang et al., 2009), the percent area was determined using the circadian cosinor method (Cosinor Software). Pilot studies to determine the variability in the observations in a group with bar graphs and the error of outcome measures and the effective size were used to estimate the number of observations necessary to test the null hypothesis. All graphical representations display the mean of the observations in a group with bar graphs and the error bars depicting SEM. Distribution-free statistical analyses were performed in Prism using the nonparametric Mann–Whitney rank comparison. The cutoff for significance was P < 0.05. The rhythm amplitude of the daily ISF Aβ oscillation was determined using the circadian cosinor method (Cosinor Software). A cosine transformation was applied to the time variable with 24 h circadian cycle for the daily temperature and ISF Aβ oscillation (nonlinear regression equation: y = baseline + amplitude * cos((frequency * x) + phase shift)) in Prism (Huang et al., 2012).

**Data analysis and statistics**

Graphical illustrations were constructed with Prism (7.0; GraphPad Software). Pilot studies to determine the variability of outcome measures and the effective size were used to estimate the number of observations necessary to test the null hypothesis. All graphical representations display the mean of the observations in a group with bar graphs and the error bars depicting SEM. Distribution-free statistical analyses were performed in Prism using the nonparametric Mann–Whitney rank comparison. The cutoff for significance was P < 0.05. The rhythm amplitude of the daily ISF Aβ oscillation was determined using the circadian cosinor method (Cosinor Software). A cosine transformation was applied to the time variable with 24 h circadian cycle for the daily temperature and ISF Aβ oscillation (nonlinear regression equation: y = baseline + amplitude * cos((frequency * x) + phase shift)) in Prism (Huang et al., 2012).

**Online supplemental material**

Fig. S1 shows temperature probe data, wheel running activity data, cortical clock gene expression data, and amyloid plaque quantification from 3–4-mo APPPS1-21 mice, demonstrating that these mice have moderate plaque burden but maintain normal circadian rhythms in both 12-h:12-h LD and DD conditions and have normal clock gene expression. Fig. S2 contains qPCR data quantifying 13 candidate transcripts known to be involved in Aβ metabolism in both Neurin-Bmal1 KO:APP and Bmal1 iKO:APP mice, revealing up-regulation of Apoe in both models.

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Author contributions: E.S. Musiek conducted the experiments, injections, surgeries, microdialysis, Aβ assays, data analysis, and imaging. E.S. Musiek developed the mouse lines and assisted with immunohistochemistry, qPCR, and imaging. F. Liao provided technical expertise with microdialysis and Aβ assays. J. Dimmity conducted the qPCR transcript analysis. M.R. Cedeno assisted with mouse breeding and immunohistochemistry. G.J. Kress, E.S. Musiek, and D.M. Holtzman designed the experiments. G.A. FitzGerald provided the original Nestin-Cre·β-Mal1 and CAG -Creαβ2·Bmal1(f/f) mice. G.J. Kress and E.S. Musiek prepared the manuscript with editorial assistance from D.M. Holtzman.

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