Does Sleep Play a Role in Memory Consolidation? A Comparative Test

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Abstract

Sleep is a pervasive characteristic of mammalian species, yet its purpose remains obscure. It is often proposed that ‘sleep is for the brain’, a view that is supported by experimental studies showing that sleep improves cognitive processes such as memory consolidation. Some comparative studies have also reported that mammalian sleep durations are higher among more encephalized species. However, no study has assessed the relationship between sleep and the brain structures that are implicated in specific cognitive processes across species. The hippocampus, neocortex and amygdala are important for memory consolidation and learning and are also in a highly activated state during sleep. We therefore investigated the evolutionary relationship between mammalian sleep and the size of these brain structures using phylogenetic comparative methods. We found that evolutionary increases in the size of the amygdala are associated with corresponding increases in NREM sleep durations. These results are consistent with the hypothesis that NREM sleep is functionally linked with specializations of the amygdala, including perhaps memory processing.

Introduction

It has been suggested that sleep is of particular importance to brain processes such as memory consolidation and learning [1–4]. Experimental studies have supported this ‘memory consolidation’ hypothesis of sleep function by showing that sleep-deprived human and animal subjects perform poorly in learning tasks when compared to individuals that are well rested [2,5]. However, the approach and conclusions of these studies are often criticized, due to the stress associated with sleep deprivation experiments [6,7] and because memory consolidation can also occur in the absence of sleep.

The comparative study of sleep variation offers a complementary approach to investigating potential adaptive functions of sleep [8,9] and most comparative research has focused on sleep durations. The importance of sleep times is reflected in the observation that when sleep deprived, experimental human and animal subjects exhibit a ‘sleep rebound’ proportional to the amount of sleep lost [10], indicating that the amount of sleep, or of some specific component of sleep, is physiologically relevant. Previous comparative studies have suggested that the great interspecific variation in sleep durations observed in mammals may reflect either functional benefits or ecological constraints, or both [e.g. 9,11,12–15]. Recent analyses on mammalian sleep durations have reported a positive relationship between rapid-eye-movement (REM) sleep and mammalian whole brain volume, which has been taken as support for a cognitive function of sleep [8,12 but see 11]. While these reports are consistent with a memory related function of sleep, the brain is a complex organ, and comparative evidence suggests that functionally specific regions have changed in size independently of whole brain size [16]. Measures of total brain size or of encephalization are therefore too coarse to substantiate the idea of a functional association between sleep and specific cognitive processes. A potentially more targeted approach is to examine sleep parameters in relation to specific brain regions that play a role in memory consolidation.

Ecologically-imposed needs for increased memory capacity should be reflected by an increase in the size of brain structures that are responsible for memory processing and consolidation [17]. For example, spatial memory is important in animals that hoard food because it improves their ability to retrieve stored food at a later time, which in turn enhances fitness. The hippocampus is one of the most important brain structures involved in spatial memory processing and memory retention, and studies in birds have shown that hippocampal volumes and hippocampal neuron numbers are higher in species and populations that cache food relative to those that do not exhibit such behaviour [17–19]. Similarly, if sleep serves a specific function with regard to memory consolidation and learning, we expect that greater memory-related demands result in a greater need for sleep. Those brain structures that are devoted to memory processing and learning therefore should be positively associated with sleep durations.

Many brain regions are involved in the diverse aspects of memory formation, but those hypothesised to have prominent roles in forming adaptively relevant associations in mammals include the hippocampus, amygdala and neocortex [17,20–24]. During sleep a variety of brain structures are in a highly activated state, including those specifically linked to memory consolidation and learning.

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Materials and Methods

We constructed a dataset of mammalian sleep durations (REM and NREM sleep times in hours/day) from an exhaustive search of the published literature [29; data available at http://www.bu.edu/phylogeny/index.html]. In previous analyses of this dataset we found that when sleep was recorded for less than 12 hours, sleep times were significantly underestimated, and that EEG studies tended to have lower estimates of sleep durations relative to non-EEG behavioural studies [11]. We thus restricted our analyses to studies that recorded sleep durations with EEG equipment for at least 12 hours. We excluded monotremes and aquatic mammals because their peculiar sleep architecture may not be comparable to that of terrestrial mammals [9,30].

We extracted data on overall brain volume and the total volumes of individual brain components from a paper that employed uniform measurement procedures across species [31]. Data on neocortical and hippocampal volumes were available for 14 species in our sleep dataset, and data on amygdalar volumes for 15 species. Our final dataset comprised eight primates, one tree shrew, three ‘insectivores’, and two rodents (see Appendix S1). All variables were log-transformed to achieve normality.

Because closely related species tend to exhibit similar sleep durations [11], we implemented statistical methods that explicitly incorporate phylogeny to account for the lack of statistical independence in the data due to common ancestry [32–35]. Specifically we used the program BayesTraits [36,37] to perform a multiple regression analysis with the method of phylogenetic generalized least squares (PGLS). PGLS converts the phylogeny into a variance-covariance matrix of species relationships, which is then used to weight the parameters of regression analysis estimated with maximum likelihood [ML, 36,37]. We based our tests on the mammalian phylogenetic tree by Bininda-Emonds et al. [38] with updated branch lengths [39].

For each brain structure volume we calculated the volume of the remaining brain as a log-transformed difference from total brain volume, and used these volumes to account for the scaling of brain components with total brain volume [40]. We used ‘the rest of the brain’ for each individual structure instead of total brain volume when controlling for scaling effects because total brain volume includes the volume of the structure of interest. Our procedure thus ensured that the brain structure of interest was not represented on the X and Y axes simultaneously. REM and NREM sleep times were tested against each structure volume and corresponding volume of the remaining brain with multiple regression in PGLS. This allowed us to control for both phylogenetic relatedness of species and for scaling effects. We controlled for multiple testing using the false discovery rate test [FDR, 41,42]. All tests were two-tailed with \( \alpha = 0.05 \).

Results

After controlling for scaling effects, NREM sleep increased with amygdalar volume (amygdala: \( t_{10} = 4.60, p = 0.001 \), rest of the brain: \( t_{10} = -4.74, p<0.001, \) model-\( R^2 = 0.70 \); Figure 1) while the correlations with neocortex and hippocampus volumes were not significant (neocortex: \( t_{11} = -0.77, p = 0.458 \), rest of the brain: \( t_{11} = 0.65, p = 0.527, \) model-\( R^2 = 0.06 \); hippocampus: \( t_{11} = 1.89, p = 0.086, \) rest of the brain: \( t_{11} = -1.93, p = 0.080, \) model-\( R^2 = 0.26 \)). We found no significant association between REM sleep durations and any of the brain structures we used (amygdala: \( t_{10} = 1.27, p = 0.232 \), rest of the brain: \( t_{10} = -1.39, p = 0.195, \) model-\( R^2 = 0.16 \); neocortex: \( t_{11} = -1.71, p = 0.115, \) rest of the brain: \( t_{11} = 1.53, p = 0.153, \) model-\( R^2 = 0.22 \); hippocampus: \( t_{11} = 0.11, p = 0.918, \) rest of the brain: \( t_{11} = -0.26, p = 0.793, \) model-\( R^2 = 0.02 \)). After controlling for multiple testing, NREM sleep remained significantly correlated with amygdalar volume (FDR estimated threshold of significance: \( \alpha = 0.008 \)).

Discussion

We found that evolutionary increases in NREM sleep durations were correlated with evolutionary increases in the size of the amygdala, and this effect was independent of both scaling effects and phylogeny. We found no evidence of positive relationships between REM sleep and brain structures implicated in memory consolidation and learning. The hippocampus showed a tendency to increase with NREM sleep, although this relationship was not statistically significant (\( p<0.09 \)). Sample sizes are however

Figure 1. NREM sleep time and amygdala. NREM sleep durations increase with relative amygdalar volumes after accounting for scaling effects [(NREM sleep time) = 1.50 + 0.66 * (amygdala volumes) – 0.45 * (rest of the brain); see text]. The plot shows relative amygdalar volumes, which were calculated with a phylogenetically corrected regression of amygdalar volumes on the rest of the brain, using ML in PGLS (see methods). Species number: (1) Microcebus murinus, (2) Rattus norvegicus, (3) Nannospalax ehrenbergii, (4) Tupai a glis, (5) Callithrix jacchus, (6) Pan troglodytes, (7) Saimiri sciureus, (8) Papio hamadryas, (9) Erythrocebus patas, (10) Macaca mulatta, (11) Tenrec ecaudatus, (12) Erinaceus europaeus, (13) Aotus trivirgatus.
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recognized in the mammalian neocortex.