Sleep patterns in male juvenile monkeys are influenced by gestational iron deprivation and monoamine oxidase A genotype

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Abstract

Individual differences in sleep patterns of children may have developmental origins. In the present study, two factors known to influence behavioural development, monoamine oxidase A (MAOA) genotype and prenatal Fe-deficient (ID) diet, were examined for their influences on sleep patterns in juvenile rhesus monkeys. Sleep patterns were assessed based on a threshold for inactivity as recorded by activity monitors. Pregnant monkeys were fed diets containing either 100 parts per million (ppm) Fe (Fe sufficient, IS) or 10 ppm Fe (ID). At 3–4 months of age, male offspring were genotyped for polymorphisms of the MAOA gene that lead to high or low transcription. At 1 and 2 years of age, sleep patterns were assessed. Several parameters of sleep architecture changed with age. At 1 year of age, monkeys with the low-MAOA genotype demonstrated a trend towards more sleep episodes at night compared with those with the high-MAOA genotype. When monkeys reached 2 years of age, prenatal ID reversed this trend; ID in the low-MAOA group resulted in sleep fragmentation, more awakenings at night and more sleep episodes during the day when compared with prenatal IS in this genotype. The ability to consolidate sleep during the dark cycle was disrupted by prenatal ID, specifically in monkeys with the low-MAOA genotype.

Key words: Sleep; Non-human primates; Prenatal iron deprivation; Monoamine oxidase A genotype

Sleep in primates, including humans, is characterised by a consolidated sleep phase during the dark cycle(1,2). Sleep locations protected from predators have been seen as the origin of this pattern, which contrasts with intermittent sleep periods, peaking in frequency according to the diurnal cycle, in rodents.

Disruption of the consolidated sleep pattern is the basis of common sleep disorders in humans, including delayed onset of sleep, waking during sleep, inability to resume sleep and daytime sleepiness(3). Non-human primates, including rhesus monkeys, have been established as valuable models for human sleep based on observation, activity monitoring and electroencephalography(4–6).

Although environmental factors and disease state are becoming known through research as sources for sleep disruption, a developmental origin for sleep regulation variability is less studied. In the present study, we assessed the influence of prenatal Fe deficiency (ID) on sleep patterns in rhesus monkeys aged 1 and 2 years, approximately equivalent developmentally to children aged 4 and 8 years. ID is the most common single-nutrient deficiency worldwide, with pregnant women and infants being the most affected. The Center for Disease Control reports that 33.8% of pregnant women in the USA develop anaemia (http://www.cdc.gov/pednss/pnss tables), with the highest frequency being observed in the third trimester. Because of the prolonged period of third-trimester fetal brain development in primates, monkeys, rather than rodents, are the more appropriate models for studying the consequences of third-trimester ID in children. To develop a model of third-trimester ID, their dams were fed a low-Fe diet in utero(7).

An additional variable in the present study was genotyping for monoamine oxidase A (MAOA) polymorphisms (high or low expression of the enzyme MAOA). A recent study has linked MAOA polymorphisms to daytime sleepiness, a possible reflection of sleep fragmentation, in humans(8). Similar MAOA polymorphisms occur in monkeys and have previously been shown to interact with prenatal ID to influence behaviour in social and cognitive tests in this cohort of monkeys(9,10). Both ID(11) and MAOA polymorphisms(12–14) influence monoamine neurotransmitter systems in the brain. We hypothesised that these two factors could interact during fetal brain development to produce long-term changes in sleep patterns.

Abbreviations: CNPRC, California National Primate Research Center; ID, Fe deficiency; IS, Fe sufficiency; MAOA, monoamine oxidase A; VGL, Veterinary Genetics Laboratory; VNTR, variable-number tandem repeats.

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Methods

Compliance with animal research guidelines

Animal husbandry was performed in accordance with the Guide for the Care and Use of Laboratory Animals of the National Research Council. All protocols were approved before implementation by the UC Davis Institutional Animal Care and Use Committee. The California National Primate Research Center (CNPRC) is accredited by the Association for Assessment and Accreditation of Laboratory Animal Care. Animal husbandry and veterinary medicine procedures were performed by specialised staff with advanced training in these areas.

Subjects, diets and genotyping

Pregnant rhesus (Macaca mulatta) dams were included in the study after screening for reproductive history. Experimental groups were balanced for dam age, weight and parity, but were otherwise randomly constructed. Pregnant dams were pair-housed in double cages (120 X 65 X 79 cm) in a cage room separate from the rest of the colony. They were fed the experimental diets twice a day in premeasured amounts, and water was available ad libitum from an automated system. Their care included daily cleaning of drop pans, twice daily feeding, biweekly cage changes to freshly sterilised cages, automatically controlled light cycles (lights on from 06:00 to 18:00 hours), and temperature control (20–25°C) and monitoring. Monkeys were observed each morning for health signs and referred to veterinarians for treatment if needed. An individual medical record was maintained for each animal. Monkey dams were time-mated and fed an ID (10 parts per million) or an Fe-sufficient (100 parts per million, £ pair-housed in double cages (120 X 65 X 79 cm) in a cage environment had a daily 12 h light cycle (lights on from 06:00 to 18.00 hours). The actimeter links to the computer to transfer data to ActiTrac software that provides measures of the onset, duration and level of each active and inactive period. An inactive period is defined as a 2 min period (epoch) for which that epoch and the epochs preceding and following it average to be below a software-defined activity threshold of 18 counts/2 min. This threshold has been validated as a measure of sleep in children, but not in monkeys. However, studies in monkeys show a good agreement between actimeter and electroencephalography indices of sleep.

Activity monitoring

Actimeters (ActiTrac, IM Systems) that record movement were placed on the back of a specially designed vest that the monkeys wore in their home cages for 48h. The home cage environment had a daily 12 h light cycle (lights on from 06:00 to 18.00 hours). The actimeter links to the computer to transfer data to ActiTrac software that provides measures of the onset, duration and level of each active and inactive period. An inactive period is defined as a 2 min period (epoch) for which that epoch and the epochs preceding and following it average to be below a software-defined activity threshold of 18 counts/2 min. This threshold has been validated as a measure of sleep in children, but not in monkeys. However, studies in monkeys show a good agreement between actimeter and electroencephalography indices of sleep.

Statistics and power estimates

Selected parameters were analysed with two-way ANOVA (genotype and ID diet) including the interaction (JMP, SAS Institute, Inc.). Planned comparisons were made to assess the effect of ID diet within genotype. Potential covariates (body weight, cage location, etc.) were screened for relevance to the sleep parameters, but none were significant. Datasets were screened for normal distribution before analysis.

Group sizes of 10 per diet group were selected for the present study based on behavioural effect sizes in a previous cohort. The effect sizes for the diet X genotype interaction could not be estimated. The effect size for our apical variable, the sleep fragmentation index, comparing the ID and IS groups with the low-MAOA genotype was d = 1.74. Small-sample, non-human primate studies can detect smaller
effects compared with human studies due to strict environmental control and subject selection.

Results

Diet and genotype did not influence the growth or health of the test cohort as shown in Fig. S2 (available online). At night, about 55% of the time was spent in the sleep (inactive) state at both ages. During the day, monkeys were inactive less than 5% of the time, on average. The pattern of day–night activity as recorded by actimeters is shown in Fig. S3 (available online).

The time spent sleeping at night did not change with age in the test cohort as a whole (Fig. 1(a)), but older monkeys took longer to fall asleep after the onset of the dark period ($F_{1,19}=9.72$, $P=0.006$; Fig. 1(b)) and had lower activity levels during the day ($F_{1,19}=8.44$, $P=0.009$; Fig. 1(c)) compared with younger monkeys.

At 1 year of age, statistical trends suggested that low-MAOA monkeys slept more at night compared with high-MAOA monkeys in terms of more total inactive (sleep) time ($F_{1,15}=3.35$, $P=0.059$; Fig. 2(a) and (b)). In addition, low-MAOA monkeys were more active when they were awake at night ($F_{1,15}=8.15$, $P=0.009$; Fig. 2(c)). Neither diet nor genotype influenced time to fall asleep, number of awakenings or time awake at night, or daytime sleep periods (data not shown).

At 2 years of age, the trend towards greater sleep at night in low-MAOA monkeys appeared to be reversed by ID. Awakenings at night were more frequent in low-MAOA ID monkeys than in low-MAOA IS monkeys (interaction $F_{1,15}=6.35$, $P=0.023$, low-MAOA ID > IS, $P=0.048$; Fig. 3(a)). Conversely, low-MAOA ID monkeys had more frequent sleep episodes during the day (interaction $F_{1,15}=11.69$, $P=0.004$; low-MAOA ID > IS, $P=0.008$; Fig. 3(b)). A significant interaction was also found for total sleep time during the day ($F_{1,15}=5.69$, $P=0.031$), but no post hoc tests were significant. The pattern of means under the IS condition for both these endpoints suggested a difference between high-MAOA IS and low-MAOA IS monkeys. Specifically low-MAOA monkeys with adequate prenatal Fe supply had fewer nighttime awakenings (low-MAOA IS < high-MAOA IS, $P=0.133$) and fewer daytime sleep episodes (low-MAOA IS < high-MAOA IS, $P=0.008$) compared with their high-MAOA counterparts, but this pattern was reversed by prenatal ID, suggesting a fragmentation of the consolidated sleep pattern. A fragmentation index (number of awakenings at night + number of sleep episodes during the day) showed a MAOA × ID interaction ($F_{1,15}=9.03$, $P=0.01$, low-MAOA IS < high-MAOA IS, $P=0.004$).
**Discussion**

Research indicates that children differ widely in their sleep patterns. Although environmental conditions can be significant predictors, sleep patterns have trait-like stability across childhood. Biological origins of trait-like sleep patterns may lie in genetics and/or early developmental influences. The present study suggests that MAOA polymorphisms and prenatal ID may play a role in the establishment of individual differences in sleep patterns.

The effect of prenatal ID on later sleep patterns has not been studied in children. The best-known association between ID and sleep has to do with treatment of restless leg syndrome with Fe, which is effective in children as well as in adults. The levels of ferritin, an index of Fe status, were lower in the children who responded to Fe therapy for restless legs. Establishing direct links between the present study and the literature on restless leg syndrome and ID is difficult because (1) the test cohort of the present study was not ID, (2) MAOA levels were not measured in these studies, (3) MAOA inhibition via nigrostriatal dopamine pathways, which are known to be influenced by ID, could also be explored in children.

Rodent studies have shown that Fe levels in brain regions follow a diurnal pattern that is disrupted in ID. ID also disrupts diurnal patterns of monoamine neurotransmitter systems. MAOA levels were not measured in these studies, but indices of dopamine metabolism suggested an impact on the activity of this enzyme, which could provide a biological basis for the ID x MAOA interaction identified in the present study. As anticipated, MAOA polymorphisms have been shown to influence monoamine neurotransmitters as reflected in cerebrospinal fluid (CSF). Polymorphisms of the serotonin transporter gene, which also affect the levels of dopamine, as well as of serotonin, in the brain, have recently been shown to influence sleep patterns in adolescents.

### Fig. 3. Effects of the monoamine oxidase A (MAOA) x iron deficiency (ID) interaction on sleep patterns and activity levels in 2-year-old male rhesus monkeys.

<table>
<thead>
<tr>
<th>Group</th>
<th>No. of awakenings at night</th>
<th>No. of sleep episodes during the day</th>
<th>Fragmentation index</th>
</tr>
</thead>
<tbody>
<tr>
<td>High-MAOA x ID</td>
<td>20 (±5)</td>
<td>2 (±0.5)</td>
<td>20 (±5)</td>
</tr>
<tr>
<td>High-MAOA x IS</td>
<td>30 (±5)</td>
<td>3 (±0.5)</td>
<td>30 (±5)</td>
</tr>
<tr>
<td>Low-MAOA x ID</td>
<td>30 (±5)</td>
<td>3 (±0.5)</td>
<td>30 (±5)</td>
</tr>
<tr>
<td>Low-MAOA x IS</td>
<td>40 (±5)</td>
<td>4 (±0.5)</td>
<td>40 (±5)</td>
</tr>
</tbody>
</table>

*Low-MAOA ID monkeys exhibited significantly higher number of awakenings compared with low-MAOA iron-sufficient (IS) monkeys (P = 0.048). †The low-MAOA ID group had more sleep episodes during the day compared with the low-MAOA IS group (P = 0.08). ‡Low-MAOA ID monkeys exhibited more fragmented sleep compared with low-MAOA IS monkeys (P = 0.0244).
Recently, a study in college students has linked low-MAOA polymorphisms to lower daytime sleepiness as assessed with a questionnaire\(^{(6)}\). This result, based on subjective reports of sleepiness, is generally consistent with the pattern of less daytime sleep in the control (IS) low-MAOA group compared with the control high-MAOA group in the present study (Fig. 3(b)). However, if the low-MAOA infants were Fe deprived as fetuses, the number of daytime sleep episodes increased dramatically.

The interaction pattern of means for sleep parameters suggests that ID differentially affected the two genotypes, but did not cause abnormal sleep. Although sleep fragmentation abnormalities can reach a level that signals sleep disorder, in the present study, the greater fragmentation in the low-MAOA ID v. IS monkeys did not lead to a level of fragmentation outside that observed in high-MAOA IS subjects. MAOA is X-linked so that high- and low-MAOA polymorphisms as determinants of MAOA transcription are clearly determined in males, but vary widely depending on allele combinations in females. Furthermore, the allele distribution of high- and low-transcribing polymorphisms in the human population is approximately 60/40, high-/low-MAOA, so that both polymorphisms are ‘normal’. Thus, this interaction between MAOA gene transcription and fetal ID is more accurately identified as relevant to individual differences in sleep patterns than to sleep pathology. That said, this interaction in juveniles might be exaggerated in neonates or during ageing when sleep patterns are more volatile and sensitive to disruption.

Supplementary material

To view supplementary material for this article, please visit http://dx.doi.org/10.1017/S0007114514002451

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The authors’ contributions are as follows: M. S. G. designed the study and wrote the manuscript; C. E. H. conducted the experimental procedures, developed the actimeter protocols and reviewed the manuscript.

The authors declare no conflicts of interest.

References


