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Original Article

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Childhood adversity and adolescent epigenetic age acceleration: the role of adolescent sleep health

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Abstract

Study Objectives: We investigated how a dimension of early life adversity (ELA), capturing threat in the home, relates to later epigenetic age acceleration in adolescence through sleep (duration, efficiency, and timing) to empirically test theoretical models suggesting the importance of sleep as a key mechanism linking ELA with poor health outcomes and to expand the limited literature on sleep and epigenetic aging among youth.

Methods: We utilized data from 861 participants in the Future of Families and Child Wellbeing Study who participated in the actigraphy substudy at age 15. Sleep variables used were average total sleep time (TST), sleep efficiency (SE), and sleep onset timing. Home threat was determined at ages 3, 5, and 9 from parent reports on the Child Conflict Tactics Scale, and epigenetic aging was measured through DNA methylation analyses of saliva samples collected at age 15.

Results: Higher levels of childhood home threat exposure were associated with less adolescent TST, lower SE, and later sleep onset timing. Adolescent SE and timing were associated with a faster pace of aging and epigenetic age acceleration. SE and timing mediated the link between childhood home threat exposure and adolescent epigenetic aging.

Conclusions: Epigenetic embedding of childhood threat exposure in the home may occur through adversity-related sleep disturbances in adolescence. Findings warrant greater attention to pediatric sleep health in theoretical models of biological embedding of adversity and point to sleep health improvement as a potential way to prevent adversity-related epigenetic age acceleration. *This paper is part of the Genetic and other Molecular Underpinnings of Sleep, Sleep Disorders, and Circadian Rhythms Including Translational Approaches collection.*

Key words: early adversity; sleep health; epigenetic aging

Statement of Significance

This study brings together two largely disparate bodies of literature: epigenetics of early life adversity and epigenetics of sleep. Findings advance knowledge on how adversity impacts different aspects of sleep (duration, efficiency, and timing), as well as biological aging. These findings offer potential pathways for mitigating long-term health risks associated with childhood adversity.

Introduction

Early life adversity, which has been conceptualized in many different ways, is common and associated with poor outcomes across the lifespan. For example, according to a recent meta-analysis [1], half of the adult population in the United States report experiencing at least one adverse childhood experience (ACE), and 16% report four or more. ACEs include experiences of child abuse and neglect as well as broader household dysfunction, like substance use problems and parental incarceration. Since the original ACE study [2], research has consistently shown robust associations between ACEs and a wide range of negative physical and mental health outcomes, including many major causes of death [3]. These findings underscore early adversity as a major public health concern and priority [4].

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One of the reasons that early life adversity is linked with these poor long-term health outcomes is that the physiological stress caused by early adversity can be so pervasive that it becomes biologically embedded [5]. This occurs when responses to stress alter biological functions, which can happen across multiple systems, leading to long-lasting changes in physiology. Biological embedding via epigenetic changes is one promising molecular mechanism involved in stress physiology and downstream health consequences [6]. Briefly, epigenetic modifications to the genome allow for altered gene expression and chromatin conformation, but do not change the DNA sequence and thus permit elaboration of the genome beyond what is determined by DNA base coding. The most highly studied and best characterized epigenetic modification in humans, DNA methylation (DNAm), primarily involves a direct covalent, chemical modification of a cytosine base lying sequentially adjacent to a guanine base (CpG), which may associate with subsequent gene transcription [7].

An area of recent substantial growth in biological embedding and epigenetics is the use of epigenetic "clocks" based on DNAm of CpG sites that closely track biological aging processes [8, 9]. Epigenetic clocks have emerged as accurate estimators of aging in healthy children and adults. Aging faster epigenetically than expected chronologically is known as epigenetic age acceleration. Increased epigenetic age acceleration shows critical associations with early life adversity and, in turn, poor health outcomes [9]. Hogan et al. [10] found that early adversity characterized by home threat (e.g. physical or emotional abuse) predicted epigenetic age acceleration across adolescence, which, in turn, was associated with higher levels of psychopathology in the Future of Families and Child Wellbeing Study (FFCWS). Similarly, Chang and colleagues [11] found that childhood physical and emotional aggression at home was associated with accelerated epigenetic aging in the FFCWS. A greater understanding of the mechanisms underlying associations between early life adversity and epigenetic aging would provide targets for intervention that could help mitigate poor health outcomes and improve long-term trajectories among individuals exposed to adversity. A mechanism that could link adversity to epigenetic changes is stress-related disruption to pediatric sleep health.

Early life adversity and sleep

Researchers have estimated that approximately half of all children in the United States experience sleep problems, with this number growing as high as 70% during the transition to adolescence, which is characterized by physiological (e.g. delayed circadian phase) and socio-contextual (e.g. school start times) developmental shifts that affect sleep–wake regulation [12–16]. For example, adolescents' biological shift to later sleep timing paired with early school start times can increase their risk for insufficient sleep and circadian misalignment. Experiences of adversity likely compound existing risk for sleep and circadian disruption among adolescents, as a growing body of literature demonstrates that youth who have experienced adversity have a heightened risk for impaired sleep. Indeed, previous work using the FFCWS found that ACEs occurring earlier in childhood were associated with greater social jetlag, longer TST during weekends (potentially indicating a greater need for stress recovery), and greater insomnia symptoms at age 15 [17]; however, findings were limited to self-report measures and did not include objective assessments of sleep behaviors (e.g. actigraphy)—limitations that are consistent in the broader literature [18, 19].

Sleep disturbances, like early adversity, are associated with poor health outcomes across the lifespan, and both appear to affect health via many of the same neurobiological mechanisms (e.g. disrupted regulation systems, hyperarousal) [20]. For example, research across rodent models and human youth and adults has shown that sleep deficiencies can result in increased pro-inflammatory cytokines, oxidative stress, and cortisol circadian rhythm disruption [21–24]. Importantly, these systems are all vital to stress regulation, are implicated in the pathogenesis of stress-related psychiatric disorders [25], and are integrally intertwined with chronobiology (e.g. circadian rhythms) [22, 26]. As a result of these connections between early life adversity and sleep, as well as the links between these factors and health, sleep disturbances are proposed to be an important mechanism connecting early experiences of adversity to poorer health outcomes in the long term [20]. Despite this evidence, the two bodies of literature on early adversity and epigenetics and on sleep and epigenetics remain comparatively disjointed, requiring greater exploration.

Sleep and epigenetic aging

Like with early life adversity, there is evidence that poorer sleep health has epigenetic consequences—although this area has received less attention to date [27]. Across species, there is growing evidence that sleep disturbances are tied to epigenetic modifications to the genome [28]. Among human adults, for example, previous studies have found associations between insomnia symptoms, shorter sleep duration, poorer sleep efficiency, and epigenetic aging, particularly pace of aging and age acceleration [29, 30]. However, research on the connection between sleep and DNAm across childhood and adolescence is limited and mixed. For example, Koopman-Verhoeff et al. [31] found that DNAm patterns of individual CpG clusters were associated with shorter actigraphy-based sleep duration in childhood. However, this relationship was not observed with subjectively assessed sleep, which is consistent with other studies that have failed to find links between subjective assessments of sleep and epigenetic aging among youth [32], though Koopman-Verhoeff and colleagues did not test epigenetic aging specifically. These findings underscore the importance of including objective sleep measurement tools in studies involving epigenetic aging. One recent study found that objectively assessed sleep initiation in adolescents was associated with altered young adult DNAm in genes previously identified in adult Genome-Wide Association Studies of sleep and circadian phenotype [33]. Only one study has examined the association between objectively assessed sleep and epigenetic aging in adolescence. Banker and colleagues [34, 35] used a cluster analysis method that included physical activity to provide initial evidence for an association between later sleep timing and accelerated epigenetic aging.

The current study

Despite growing evidence that pediatric sleep health is disrupted by early adversity and that both adversity and sleep deficiencies are biologically embedded via epigenetic changes, particularly epigenetic age acceleration, no previous investigations have connected these two research areas. In the current study, we used data from the FFCWS to evaluate three domains of actigraphy-measured sleep (i.e. sleep duration, efficiency, and timing) as mediators of the association between early life adversity (captured as a threat in the home), and epigenetic age acceleration. This builds on prior work in the FFCWS showing links between early life adversity and epigenetic age acceleration [10], and between early life adversity and subjective

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measures of sleep [17]. Furthermore, it provides an empirical evaluation of theoretical models suggesting that sleep is a crucial mechanism linking early life adversity to poorer health outcomes [20], and expands the nascent sleep–epigenetics literature, particularly as it relates to youth.

Methods

Participants

Data for the current study are from the FFCWS—a prospective longitudinal birth-cohort study [36] of 4898 children born between 1998 and 2000 in 20 large U.S. cities. Participating families were recruited at child's birth (1998–2000) and included married and nonmarried parents, with nonmarital births oversampled at a rate of 3:1. Families were surveyed at approximately the child's birth and ages 1, 3, 5, 9, 15, and 22 years. In the present study, we examined a subset of FFCWS participants ($n = 861$) who participated in the actigraphy substudy and had at least 2 days of valid actigraphy data at age 15. Table 1 includes complete sociodemographic details of the FFCWS subsample used in the current study.

Measures

Home threat.

A latent variable was created to represent home threat at ages 3, 5, and 9 using the Parent–Child Conflict Tactics Scale (CTS-PC) based on previous studies using FFCWS data [10, 37]. Home threat was defined as being exposed to physical and/or emotional abuse by a primary caregiver. Occurrences of physical ("hit child on bottom with a hard object") and emotional ("said you would send child away or would kick child out of the house") abuse within the last year were reported by primary caregivers. Three items per category were included in the measure, and each item was rated on a 7-point Likert scale ranging from "0—never happened" to "6—more than 20 times." The factor score of a global childhood home threat factor was extracted, representing home threat experiences across ages 3, 5, and 9, using similar items across waves. See Hogan et al. [10] for complete details.

Sleep.

Sleep variables were derived from wrist actigraphy devices (Actiwatch Spectrum; Philips-Respironics, Murrysville, PA) worn on the nondominant hand for 1 week. Staff at the Sleep, Health, and Society Collaboratory at Penn State retrieved actigraphy data in 30-second epochs using Philips Actiware software version 6.0.4. Multiple trained scorers determined cut-points for sleep and validity of days following a validated algorithm [38]. See Mathew et al. [39] for complete details on scoring procedures. We used the following sleep variables computed by the Sleep, Health, and Society Collaboratory and made publicly available: total sleep time (TST), sleep maintenance efficiency, and sleep onset timing.

Table 1. Descriptive statistics of study participants

Variable	*n*		%
Child sex (reported by caregiver at baseline)			
Male	406		47.2
Female	455		52.8
Child race and ethnicity (self-report at year 15)			
Black/African American (non-Hispanic/Latino)	383		44.5
Hispanic/Latino	218		25.3
Multiracial (non-Hispanic/Latino)	49		5.7
Other (non-Hispanic/Latino)	24		2.8
White (non-Hispanic/Latino)	143		16.6
Missing	44		5.1
Mother's education at birth			
No high school diploma	268		31.1
High school or equivalent	275		31.9
Some college	226		26.3
College or graduate degree	90		10.5
Missing	2		0.2
	Mean	***SD***	**Range**
Poverty ratio (year 1)	2.34	2.47	0.00–12.30
Chronological age (year 15)	15.42	0.51	14.67–17.84
Home threat (years 3, 5, 9)	0.013	0.44	−1.13–1.51
Total 24-hour sleep time (year 15)	7.41	0.92	4.76–11.66
Sleep maintenance efficiency (year 15)	90.71	2.95	75.86–96.80
Sleep onset start midnight centered (year 15)	0.51	1.69	−7.51–6.31
BEC proportion (year 15)	0.28	0.16	0.03–0.93
Dunedin PACE (Year 15)	1.27	0.17	0.87–1.79
PedBE epigenetic age acceleration (year 15)	−0.01	0.85	−2.31–4.01

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TOTAL SLEEP TIME.

The average total number of minutes of sleep a participant experienced in a 24-hour cut-point day, including nighttime sleep and any naps. This was converted to an hour metric to improve model estimation. A total 24-hour sleep duration was used for analyses that included naps, given the prevalence of napping in adolescence and the potential restorative effects of naps on epigenetic aging that may buffer the impact of inadequate nighttime sleep. The use of 24-hour TST is also consistent with other foundational work in this sample, including sleep data [40].

SLEEP MAINTENANCE EFFICIENCY.

The percentage of time spent asleep between nighttime sleep onset and offset. Higher values indicate better sleep quality.

SLEEP ONSET TIMING.

Nighttime sleep onset time is defined as the last 30-second epoch of >10 activity counts followed by at least 5 consecutive epochs of activity counts ≤10. Sleep onset time is midnight centered, with values of 0 equaling midnight.

Epigenetic aging.

The FFCWS survey subcontractor, Westat Inc., arranged the sample collection. Westat interviewers used the Oragene DNA Self-Collection kits (OGR-500) (DNA Genotek Inc) to collect child saliva samples during in-home visits for children at ages 9 and 15. Available samples ($n = 3945$) were assayed using methylation arrays (Infinium Human Methylation 450K and Infinium Methylation EPIC; Illumina) according to the manufacturer's protocol. Samples were excluded if the ENmix R package quality control procedure identified samples as having outlier methylation or bisulfite conversion values or if the sex predicted from the methylation data differed from the recorded sex. Additionally, the cell-type proportion in each saliva sample was estimated using the Houseman algorithm implemented in the *estimateLC* function in the *ewastools* package, using the children's saliva reference panel [41]. Two DNA methylation-based methods were used to estimate epigenetic aging.

DUNEDINPACE.

The DunedinPACE pace of aging [42], previously employed in pediatric saliva samples [9, 43], was examined for an epigenetic pace of aging. A value of one in this measure indicates the estimated epigenetic age and chronological age were equivalent, with a greater value indicating epigenetic age acceleration in comparison to chronological age. The development of this DNA methylation biomarker differs from age-focused epigenetic estimators in that it is rooted in the dynamics of health and phenotypes supporting successful biological aging processes [42, 44], including being trained on within-individual decline in 19 indicators of organ–system integrity spanning 2 decades in the Dunedin Study [42]. The FFCWS has two DunedinPACE measures, and the current study used the most updated method (poam45).

PEDBE EPIGENETIC AGE ACCELERATION.

Analyses estimating DNA methylation age acceleration in children were conducted using the Pediatric Buccal Epigenetic Clock (PedBE) [45], a clock trained in oral tissue to estimate biological age in children within an error of less than 4 months using 95 sites across the epigenome. PedBE was measured by the residuals of a linear mixed effect model with maximum likelihood estimation of predicted PedBE age on reported chronological age, accounting for predicted buccal epithelial cell proportion (as recommended by the authors of the tool) [45] and a random effect of individual (both years 9 and 15 were included). This was completed in R (4.3.1) with the nlme package. Buccal epithelial cell proportion was estimated using the EpiDISH [46] package and accounted for during epigenetic age acceleration calculation due to the association of this cell type and age.

DEMOGRAPHIC CHARACTERISTICS.

At the child's birth, the mother reported household income and houshold size, which were used to calculate their poverty ratio. The poverty ratio is calculated as the ratio of total household income to the official poverty thresholds designated by the U.S. Census Bureau. A value of 1 indicates a family is at the poverty level, a value below indicates a family is below the poverty line, and a value above 1 indicates a family is above the poverty line (e.g. 2.0 means that a family income is 200% of the federal poverty level). The mother reported the sex of the focal child at birth, and the child self-reported their racial identity at age 15.

Statistical analysis plan

A path analysis model was conducted using Mplus [47], applying Full Information Maximum Likelihood for any missing data, and maximum likelihood estimation with robust standard errors (MLR) was used to adjust for possible non-normality. The following fit statistics were employed to evaluate model fit: chi-square, $\chi 2$: $p > .05$ excellent, comparative fit index (CFI > 0.90 acceptable > 0.95 excellent), root-mean-square error of approximation (RMSEA < 0.08 acceptable < 0.05 excellent), and the standardized root-mean-square residual (SRMR < 0.08 acceptable < 0.05 excellent) [48]. The latent factor score of home threat across ages 3, 5, and 9 was the primary predictor in models. Year 15 TST, sleep maintenance efficiency, and sleep onset timing served as the simultaneous mediators. As such, the covariance between each sleep mediator was accounted for in the model, allowing for examining specific associations with each sleep parameter. Year 15 Dunedin pace of aging and PedBE epigenetic age acceleration served as simultaneous outcome variables, also allowing for accounting for their covariation. Youth sex, year 1 family poverty ratio, and buccal epithelial (BEC) proportion were included as covariates. Youth self-report race and ethnicity and year 9 epigenetic variables were included as auxiliary variables. The model indirect command in Mplus was used to obtain bootstrap standard errors for indirect effects. Sensitivity analyses examined the robustness of findings to summer-based actigraphy assessment, nighttime sleep not including naps instead of total 24-hour sleep time, the number of valid actigraphy days, quadratic effects, and multiple testing correction.

Results

Preliminary analyses

Table 1 and Figure 1 depict the distribution of the primary study variables. On average, adolescents had insufficient 24-hour total sleep duration, sleep maintenance efficiency of ~90% (not including sleep onset latency), and sleep onset timing around midnight. In the current sample, 56% of adolescents had at least one nap during the observation period, the average daily number of naps was.19 ($SD = 0.24$), and the average nap duration was 22.85

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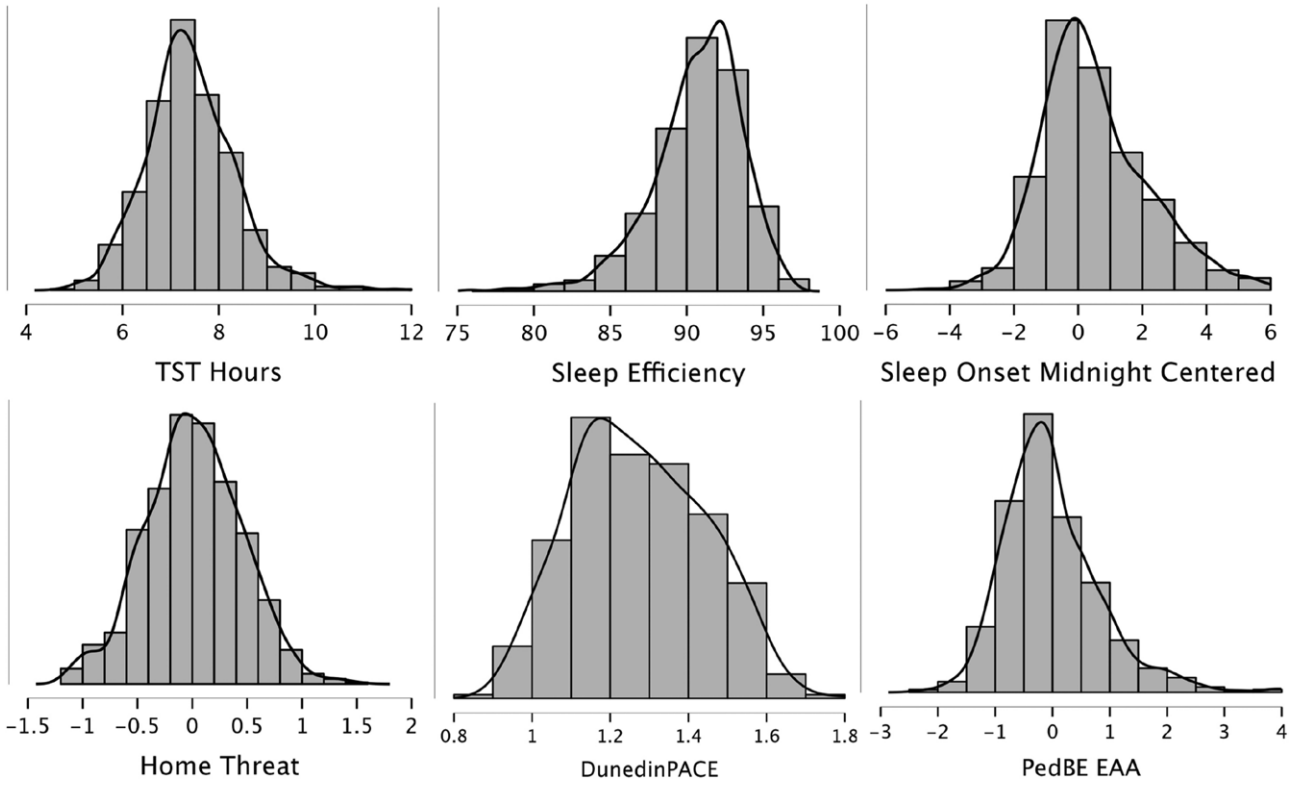

Figure 1. Density histogram plots of primary study variables.

minutes (*SD* = 32.09). Furthermore, adolescents demonstrated an accelerated epigenetic pace of aging and an age-consistent PedBE epigenetic clock. However, substantial variability was present across all primary variables, with sleep health parameters ranging from severe deficiencies to healthy levels and epigenetic aging ranging from decelerated to accelerated epigenetic aging. The correlation heatmap of core study variables is depicted in Figure 2. Overall, bivariate associations suggested that childhood home threat was negatively correlated with sleep duration, efficiency, and timing but not epigenetic aging. Further, bivariate results suggest lower sleep efficiency and later timing, but not sleep duration, were correlated with accelerated epigenetic aging. For covariates, the BEC proportion was positively correlated with both epigenetic outcomes, and the family poverty ratio was negatively correlated with the pace of aging. Overall, bivariate associations were generally in the expected direction and supported primary models.

Primary analyses

Complete results are reported in Table 2, and a simplified mediation model is depicted in Figure 3. The model fit was excellent, $\chi^2(6) = 9.42$, $p = .151$, RMSEA = 0.026 [0.000, 0.056], CFI = 0.996, SRMR = 0.018. Regarding covariates, girls had longer TST, earlier sleep onset timing, and faster epigenetic pace of aging. Living closer to the poverty line during childhood was associated with later sleep timing and a faster pace of aging in adolescence. Greater estimated BEC type proportion was associated with a faster pace of aging and accelerated epigenetic clock. Regarding the primary mediation associations, higher levels of childhood home threat were associated with less TST, lower sleep maintenance efficiency, and later sleep onset timing. Lower sleep efficiency and later sleep onset timing were associated with a faster pace of aging and pediatric epigenetic age acceleration. TST was not associated with epigenetic aging. The total indirect mediation effect of childhood home threat on adolescent epigenetic aging through sleep efficiency and sleep timing was significant for Dunedin pace of aging and PedBE accelerated epigenetic aging. For pace of aging, 50% of the total effect of childhood home threat was mediated by sleep disruption. For PedBE accelerated epigenetic aging, 18.75% of the total effect was mediated. Overall, findings support sleep efficiency and onset timing mediating the effects of childhood home threat on adolescent epigenetic aging.

Sensitivity analysis

Though details on whether the actigraphy assessment happened during a week when adolescents were attending regular school hours were not available, we created a conservative summer assessment variable based on whether the actigraphy assessment occurred in July or August. Adolescents who did the actigraphy assessment during summer had longer TST, lower sleep efficiency, and later sleep onset timing. When summer assessment was introduced as a covariate into the primary model, associations between home threat and sleep health parameters were similar to the uncorrected model except for sleep efficiency, which was attenuated to $p = .064$ due to increased standard errors. Summer actigraphy timing was not associated with epigenetic outcomes. Next, we examined if differential effects were found when using nighttime sleep duration compared to total 24-hour sleep time (including naps). The strength of the association between higher home threat and shorter nighttime sleep duration ($b = -0.27$, $p < .001$) increased, but sleep duration remained not associated with epigenetic outcomes. Furthermore, for all sleep health variables, we explored possible quadratic effects and found no support for adding nonlinear effects to models.

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Figure 2. Heatmap correlation matrix of primary study variables. TST = total sleep time; BEC = buccal epithelial proportion; EAA = epigenetic age acceleration

For primary models, we included participants if they had at least 2 valid days of actigraphy. For sensitivity analyses, we added the number of valid days into the model as a covariate. For those with 2 or more days, the number of valid days was not associated with TST, sleep maintenance efficiency, or sleep onset time, and all primary models associated remained unchanged with the inclusion of the number of valid days as a covariate.

Finally, given the number of covariates and multiple mediators and outcomes, we applied the Benjamini–Hochberg method to adjust for multiple tests. We found that all *p*-values <.04 had a high confidence of FDR 0.05, whereas *p*-values ≤.05 had a moderate confidence of FDR 0.10. Thus, home threat was a high-confidence predictor of later sleep timing but only a moderate confidence predictor of sleep efficiency and duration. Furthermore, sleep efficiency and later sleep onset timing were high-confidence predictors of DunedinPACE, whereas only sleep efficiency was a high-confidence predictor of PedBE epigenetic age acceleration.

Discussion

The current study used data from a longitudinal birth cohort to evaluate whether three domains of sleep health (i.e. sleep duration, efficiency, and timing) mediated the association between childhood home threat exposure (i.e. physical and emotional abuse) and adolescent epigenetic age acceleration. Overall, findings indicate that adolescent sleep efficiency and sleep onset timing mediated the relationship between childhood home threat exposure and epigenetic aging acceleration.

Findings from the current study provide support for the detrimental impact of early adversity characterized by home-based threat exposure on adolescent sleep health. These results are consistent with prior work showing that childhood adversity is associated with increased subjectively assessed sleep disturbances in FFCWS [17] and other longitudinal cohorts [49–51], as well as actigraphy-assessed sleep duration, efficiency, and timing [52]. Furthermore, findings showing home-based threat exposure negatively impacting youth sleep are consistent with previous work showing that negative or hostile (e.g. yelling, physical punishment) parenting behaviors are longitudinally associated with subjectively assessed youth sleep problems [53] and actigraphy-assessed sleep efficiency [54]. Overall, our findings are consistent with the sleep-related hyperarousal theoretical model of how home-based adversity may heighten physiological arousal or make it challenging to downregulate physiological stress, resulting in later sleep timing, lower sleep quality, and less TST [20, 55]. Future research will benefit from multiple waves of home-based adversity or stress, physiological pre-sleep arousal (e.g. HR activity), and actigraphy-based sleep health to better disentangle mechanisms or examine bidirectional effects.

To our knowledge, this is the first study to provide evidence that multiple aspects of actigraphy-assessed sleep are associated with accelerated epigenetic aging in adolescence. We found that later sleep timing and lower sleep efficiency were associated with

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Table 2. Primary path analysis model results

	b	*B*	*B* 95% CI	*p*
DV: total 24-hour sleep time				
Home threat	−0.13	−0.06	−0.13 to 0.00	.056
Poverty ratio	−0.02	−0.05	−0.10 to 0.01	.105
Sex	0.40	0.22	0.15 to 0.28	<.001
DV: sleep efficiency				
Home threat	−0.46	−0.07	−0.14 to 0.00	.049
Poverty ratio	0.07	0.06	−0.01 to 0.12	.061
Sex	0.27	0.05	−0.02 to 0.11	.189
DV: sleep onset timing				
Home threat	0.40	0.10	0.04 to 0.17	.003
Poverty ratio	−0.06	−0.09	−0.15 to −0.04	.001
Sex	−0.44	−0.13	−0.20 to −0.06	<.001
DV: DunedinPACE				
Home threat	0.01	0.04	−0.01 to 0.08	.109
Poverty ratio	−0.01	−0.09	−0.13 to −0.05	<.001
Sex	0.05	0.14	0.09 to 0.19	<.001
Buccal epithelial cell proportion	0.80	0.77	0.75 to 0.80	<.001
TST	−0.01	−0.01	−0.06 to 0.05	.797
Sleep maintenance efficiency	−0.01	−0.11	−0.16 to −0.06	<.001
Sleep onset timing	0.01	0.08	0.03 to 0.12	.001
DV: PedBE epigenetic age acceleration				
Home Threat	0.13	0.07	0.01 to 0.14	.042
Poverty ratio	−0.01	−0.04	−0.09 to 0.02	.242
Sex	0.06	0.04	−0.03 to 0.10	.299
Buccal epithelial cell proportion	2.49	0.48	0.41 to 0.55	<.001
TST	−0.05	−0.05	−0.12 to 0.02	.175
Sleep maintenance efficiency	−0.03	−0.09	−0.15 to −0.02	.011
Sleep onset timing	0.03	0.07	0.01 to 0.13	.048
Covariances				
Home threat with poverty ratio	−0.13	−0.12	−0.18 to −0.06	<.001
TST with efficiency	0.24	0.09	0.02 to 0.16	.009
TST with sleep onset timing	−0.16	−0.11	−0.18 to −0.03	.004
Efficiency with sleep onset timing	0.06	0.01	−0.06 to 0.08	.735
DunedinPACE with PedBE EAA	0.01	0.09	0.01 to 0.18	.032
Indirect effects				
DunedinPACE IND home threat	0.01	0.02	0.01 to 0.03	.006
PedBE IND home threat	0.03	0.01	0.01 to 0.02	.030

Model fit: $\chi^2(6) = 9.42$, $p = .151$, RMSEA = 0.026 [0.000, 0.056], CFI = 0.996, SRMR = 0.018.

greater epigenetic age acceleration and a faster pace of aging. Though no previous studies have examined these links in adolescence, Larson and colleagues [33] found that objectively assessed sleep onset timing in adolescents was associated with young adult DNAm in genes previously identified in adult GWAS of sleep and circadian phenotype. Our findings on sleep timing and quality suggest that examining sleep health domains beyond sleep duration may be vital in exploring the connection between sleep and epigenetic changes.

Importantly, the current study did not find support for an association between TST and accelerated epigenetic aging. This null finding is inconsistent with Carskadon and colleagues [29], who found that short and irregular sleep, assessed via daily diary among emerging adults, may be associated with accelerated epigenetic aging. Further, Koopman-Verhoeff et al. [31] found one DNAm module associated with actigraphy-assessed sleep duration but no support for sleep timing (assessed by sleep midpoint), though they did not examine epigenetic age acceleration. However, null results for TST in the context of significant results for later sleep timing are consistent with the only other study to examine actigraphy-assessed sleep and epigenetic age acceleration in adolescence [34]. Banker and colleagues [34] examined clusters based on sleep duration, sleep timing, and physical activity. They found support for later sleep timing (combined with low physical activity) being associated with more accelerated epigenetic aging in Mexican adolescents. The current findings, combined with those of Banker and colleagues, support sleep timing as important to consider for understanding how sleep impacts biological embedding via epigenetic changes. Additionally, the null association for TST may suggest the possibility of moderators, and future research could explore theory-driven a priori moderation models, such as youth sex, given recent findings that

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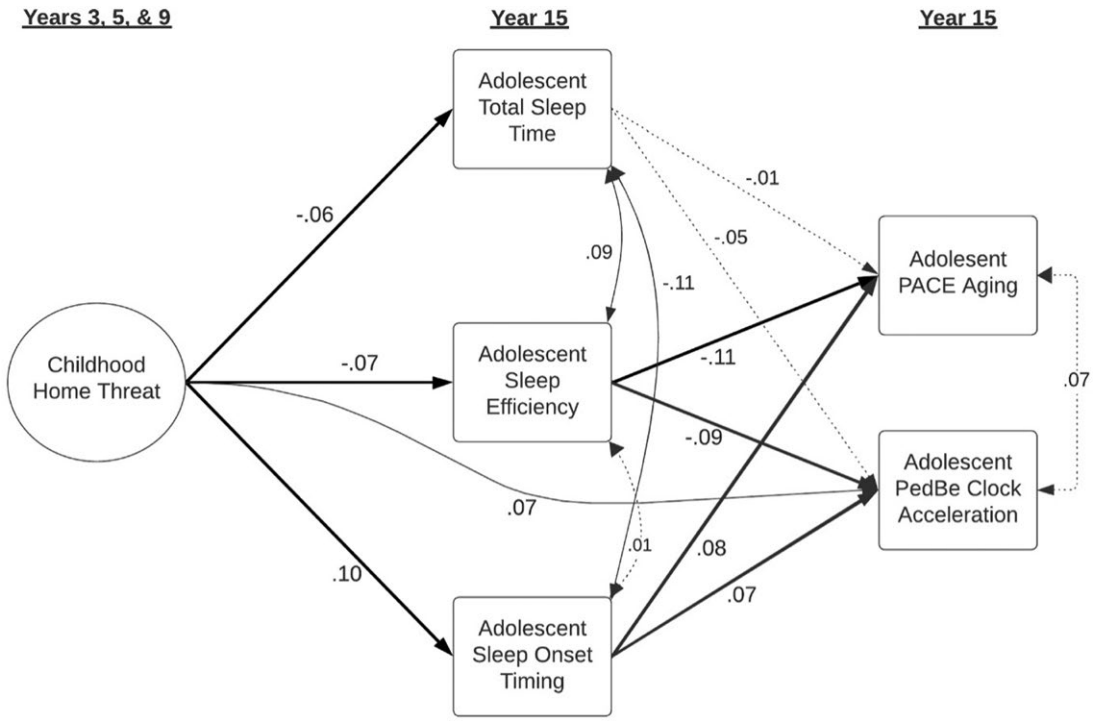

Figure 3. Simplified path analysis model results. Child sex at birth, family poverty ratio at year 1, and buccal epithelial (BEC) proportion are included as covariates in the model but are not depicted above. Solid lines are $p < .05$, and dotted lines are $p \geq .06$. Standardized beta coefficients are depicted. Total sleep time is 24-hour sleep includes naps. The complete results are in Table 2.

short sleep duration was associated with accelerated GrimAge, an alternative epigenetic clock, in females only [56]. Future research will also benefit from multiple waves of actigraphy and DNAm along with a more extended period of sleep assessment to explore potential mechanisms or alternative explanations, such as sleep irregularity [29], sleep debt [57, 58], social jetlag [17], chronotype [59], disruption of circadian-related physiological systems (e.g. hypothalamic–pituitary–adrenal axis [20]), or misalignment between central and peripheral clocks [60].

The current study was the first to examine sleep disruption as a mechanism linking early childhood adversity and adolescent biological embedding via epigenetic age acceleration. Findings in the current study supported sleep timing and quality as mediators for the longitudinal association between home threat exposure and Dunedin pace of aging and pediatric epigenetic age acceleration, with the greatest support for sleep efficiency or the combined mediation effect of both sleep health parameters. Furthermore, findings were robust to controlling for family poverty level, child sex, timing of actigraphy assessment, and adjusting for multiple tests. Though limited by sleep and epigenetic aging being assessed at the same wave (year 15), these results provide preliminary support for sleep as a mechanism for adversity-related biological embedding and long-term health trajectories. Findings warrant greater attention to pediatric sleep health in theoretical models of biological embedding of adversity and point to future directions in improving sleep health to potentially prevent adversity-related epigenetic age acceleration.

The current study has notable strengths and some limitations that would benefit from future research. This study featured a longitudinal design that allowed the exploration of directions of associations, which has been a limitation in past research. However, the single wave of actigraphy-based sleep assessment limited our ability to examine the bidirectional or alternative direction of effects between adversity and sleep and between sleep and epigenetic outcomes. Thus, actigraphy-based sleep before home threat exposure and three longitudinal waves of both sleep and DNAm are needed for more robust causal inferences. Additionally, future research studies that assess all constructs at each wave could explore both moderation and mediation models to examine competing hypotheses of sleep disruption as a mechanism versus a buffer or amplification of childhood adversity's impact on biological embedding. Alternatively, future research could benefit from experimental designs that improve sleep health and examine downstream impacts on epigenetic age acceleration. In the area of parenting, emerging evidence suggests enhancing family health and parent–child interaction may have a preventative effect on epigenetic age acceleration [61, 62] or pace of aging [63] among youth with heightened levels of adversity. Thus, future studies could explore how experimentally enhancing pediatric sleep health could result in reduced epigenetic age acceleration.

Another strength is its multimodal approach, which utilizes parent-report, actigraphy-assessed sleep health, and DNAm-based biomarkers of aging, therefore increasing confidence in associations observed due to removing potential method-effect confounding. Additionally, the current study included a large racially and economically diverse sample of youth across the United States. Research on social epigenomics has predominately focused on White European-ancestry adults. In contrast, social epigenetic research involving U.S. racial and ethnic minority populations and other populations experiencing health disparities (e.g. low socioeconomic status) remained limited, substantially limiting advancements being applied toward understanding or eliminating health disparities [64]. Findings from the current study suggest potential future research directions for connecting largely separate literature on the biological embedding of health disparities via epigenetic changes [64] and the causes and consequences of sleep health disparities [65, 66]. Research on

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family or community-level intervention or prevention programs that simultaneously support family health (e.g. parenting, parental well-being) and adolescent sleep health may be particularly advantageous future directions for potentially preventing accelerated epigenetic aging.

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Author contributions

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Data Availability

Data used for this manuscript were from The Future of Families and Child Wellbeing study and can be accessed through https://ffcws.princeton.edu/.

References

1. Madigan S, Deneault AA, Racine N, *et al*. Adverse childhood experiences: a meta-analysis of prevalence and moderators among half a million adults in 206 studies. *World Psychiatry*. 2023;**22**(3):463–471. doi:10.1002/wps.21122
2. Felitti VJ, Anda RF, Nordenberg D, *et al*. Relationship of childhood abuse and household dysfunction to many of the leading causes of death in adults: the Adverse Childhood Experiences (ACE) Study. *Am J Prev Med*. 1998;**14**(4):245–258. doi:10.1016/s0749-3797(98)00017-8
3. Petruccelli K, Davis J, Berman T. Adverse childhood experiences and associated health outcomes: a systematic review and meta-analysis. *Child Abuse Negl*. 2019;**97**:104127. doi:10.1016/j.chiabu.2019.104127
4. Gervin DW, Holland KM, Ottley PG, Holmes GM, Niolon PH, Mercy JA. Centers for disease control and prevention investments in adverse childhood experience prevention efforts. *Am J Prev Med*. 2022;**62**(6):S1–S5. doi:10.1016/j.amepre.2021.11.014
5. Hertzman C. Putting the concept of biological embedding in historical perspective. *Proc Natl Acad Sci USA*. 2012;**109**(Suppl_2):17160–17167. doi:10.1073/pnas.1202203109
6. Aristizabal MJ, Anreiter I, Halldorsdottir T, *et al*. Biological embedding of experience: a primer on epigenetics. *Proc Natl Acad Sci USA*. 2020;**117**(38):23261–23269. doi:10.1073/pnas.1820838116
7. Boyce WT, Kobor MS. Development and the epigenome: the 'synapse' of gene–environment interplay. *Dev Sci*. 2015;**18**(1):1–23. doi:10.1111/desc.12282
8. Horvath S. DNA methylation age of human tissues and cell types. *Genome Biol*. 2013;**14**(10):3156. doi:10.1186/gb-2013-14-10-r115
9. Raffington L, Tanksley PT, Vinnik L, *et al*. Associations of DNA-methylation measures of biological aging with social disparities in child and adolescent mental health. *Clin Psychol Sci*. 2023;**12**:551–562. doi:10.1177/21677026231186802
10. Hogan CM, Merrill SM, Hernandez Valencia E, *et al*. The impact of early life adversity on peripubertal accelerated epigenetic aging and psychopathology. *J Am Acad Child Adolesc Psychiatry*. 2024; (in press). doi:10.1016/j.jaac.2024.04.019
11. Chang OD, Meier HCS, Maguire-Jack K, Davis-Kean P, Mitchell C. Childhood maltreatment and longitudinal epigenetic aging: NIMHD social epigenomics program. *JAMA Netw Open*. 2024;**7**(7):e2421877. doi:10.1001/jamanetworkopen.2024.21877
12. Crowley SJ, Wolfson AR, Tarokh L, Carskadon MA. An update on adolescent sleep: new evidence informing the perfect storm model. *J Adolesc*. 2018;**67**(1):55–65. doi:10.1016/j.adolescence.2018.06.001
13. Carskadon MA. Sleep in adolescents: the perfect storm. *Pediatr Clin North Am*. 2011;**58**(3):637–647. doi:10.1016/j.pcl.2011.03.003
14. Crowley SJ, Acebo C, Carskadon MA. Sleep, circadian rhythms, and delayed phase in adolescence. *Sleep Med*. 2007;**8**(6):602–612. doi:10.1016/j.sleep.2006.12.002
15. Hirshkowitz M, Whiton K, Albert SM, *et al*. National Sleep Foundation's updated sleep duration recommendations: final report. *Sleep Health*. 2015;**1**(4):233–243. doi:10.1016/j.sleh.2015.10.004
16. Wheaton AG, Jones SE, Cooper AC, Croft JB. Short sleep duration among middle school and high school students—United States, 2015. *MMWR Morb Mortal Wkly Rep*. 2018;**67**(3):85–90. doi:10.15585/mmwr.mm6703a1
17. Rojo-Wissar DM, Sosnowski DW, Ingram MM, *et al*. Associations of adverse childhood experiences with adolescent total sleep time, social jetlag, and insomnia symptoms. *Sleep Med*. 2021;**88**:104–115. doi:10.1016/j.sleep.2021.10.019

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18. Brown SM, Rodriguez KE, Smith AD, Ricker A, Williamson AA. Associations between childhood maltreatment and behavioral sleep disturbances across the lifespan: a systematic review. *Sleep Med Rev.* 2022;**64**:101621. doi:10.1016/j.smrv.2022.101621
19. Schønning V, Sivertsen B, Hysing M, Dovran A, Askeland KG. Childhood maltreatment and sleep in children and adolescents: a systematic review and meta-analysis. *Sleep Med Rev.* 2022;**63**:101617. doi:10.1016/j.smrv.2022.101617
20. Fuligni AJ, Chiang JJ, Tottenham N. Sleep disturbance and the long-term impact of early adversity. *Neurosci Biobehav Rev.* 2021;**126**:304–313. doi:10.1016/j.neubiorev.2021.03.021
21. El-Sheikh M, Buckhalt JA, Cummings EM, Keller P. Sleep disruptions and emotional insecurity are pathways of risk for children. 2007. https://acamh.onlinelibrary.wiley.com/doi/full/10.1111/j.1469-7610.2006.01604.x Accessed April 8, 2022.
22. McEwen BS, Karatsoreos IN. Sleep deprivation and circadian disruption. *Sleep Med Clin.* 2015;**10**(1):1–10. doi:10.1016/j.jsmc.2014.11.007
23. Ordway MR, Condon EM, Basile Ibrahim B, *et al*. A systematic review of the association between sleep health and stress biomarkers in children. *Sleep Med Rev.* 2021;**59**:101494. doi:10.1016/j.smrv.2021.101494
24. Zhang J, Paksarian D, Lamers F, Hickie IB, He J, Merikangas KR. Sleep patterns and mental health correlates in US adolescents. *J Pediatr.* 2017;**182**:137–143. doi:10.1016/j.jpeds.2016.11.007
25. Doom JR, Gunnar MR. Stress physiology and developmental psychopathology: past, present, and future. *Dev Psychopathol.* 2013;**25**(4 Pt 2):1359–1373. doi:10.1017/S0954579413000667
26. Martire VL, Caruso D, Palagini L, Zoccoli G, Bastianini S. Stress & sleep: a relationship lasting a lifetime. *Neurosci Biobehav Rev.* 2020;**117**:65–77. doi:10.1016/j.neubiorev.2019.08.024
27. Carskadon MA, Barker DH. Editorial perspective: adolescents' fragile sleep—shining light on a time of risk to mental health. *J Child Psychol Psychiatry.* 2020;**61**(10):1058–1060. doi:10.1111/jcpp.13275
28. Huang H, Zhu Y, Eliot MN, *et al*. Combining human epigenetics and sleep studies in *Caenorhabditis elegans*: a cross-species approach for finding conserved genes regulating sleep. *Sleep.* 2017;**40**(6). doi:10.1093/sleep/zsx063
29. Carskadon MA, Chappell KR, Barker DH, *et al*. A pilot prospective study of sleep patterns and DNA methylation-characterized epigenetic aging in young adults. *BMC Res Notes.* 2019;**12**(1):583. doi:10.1186/s13104-019-4633-1
30. Kusters CDJ, Klopack ET, Crimmins EM, Seeman TE, Cole S, Carroll JE. Short sleep and insomnia are associated with accelerated epigenetic age. *Psychosom Med.* 2023;**86**:453–462. doi:10.1097/PSY.0000000000001243
31. Koopman-Verhoeff ME, Mulder RH, Saletin JM, *et al*. Genome-wide DNA methylation patterns associated with sleep and mental health in children: a population-based study. *J Child Psychol Psychiatry.* 2020;**61**(10):1061–1069. doi:10.1111/jcpp.13252
32. Sammallahti S, Koopman-Verhoeff ME, Binter AC, *et al*. Longitudinal associations of DNA methylation and sleep in children: a meta-analysis. *Clin Epigenetics.* 2022;**14**(1):83. doi:10.1186/s13148-022-01298-4
33. Larsen M, He F, Kawasawa YI, *et al*. Objective and subjective measures of sleep initiation are differentially associated with DNA methylation in adolescents. *Clin Epigenetics.* 2023;**15**(1):136. doi:10.1186/s13148-023-01553-2
34. Banker M, Jansen EC, Goodrich JM, *et al*. Associations between sleep and physical activity behavior clusters and epigenetic age acceleration in Mexican adolescents. *Med Sci Sports Exerc.* 2023;**56**:2173–2183. doi:10.1249/mss.0000000000003498
35. Jansen EC, Dolinoy DC, O'Brien LM, *et al*. Sleep duration and fragmentation in relation to leukocyte DNA methylation in adolescents. *Sleep.* 2019;**42**(9). doi:10.1093/sleep/zsz121
36. Reichman NE, Teitler JO, Garfinkel I, McLanahan SS. Fragile families: sample and design. *Child Youth Serv Rev.* 2001;**23**(4):303–326. doi:10.1016/s0190-7409(01)00141-4
37. Sisitsky M, Hare M, DiMarzio K, Gallat A, Magariño L, Parent J. Associations between early life adversity and youth psychobiological outcomes: dimensional and person-centered approaches. *Res Child Adolesc Psychopathol.* 2023;**51**:1789–1800. doi:10.1007/s10802-023-01064-x
38. Marino M, Li Y, Rueschman MN, *et al*. Measuring sleep: accuracy, sensitivity, and specificity of wrist actigraphy compared to polysomnography. *Sleep.* 2013;**36**(11):1747–1755. doi:10.5665/sleep.3142
39. Mathew GM, Reichenberger DA, Master L, Buxton OM, Chang AM, Hale L. Actigraphic sleep dimensions and associations with academic functioning among adolescents. *Sleep.* 2024;**47**(7). doi:10.1093/sleep/zsae062
40. Nahmod NG, Lee S, Master L, Chang AM, Hale L, Buxton OM. Later high school start times associated with longer actigraphic sleep duration in adolescents. *Sleep.* 2019;**42**(2). doi:10.1093/sleep/zsy212
41. Middleton LYM, Dou J, Fisher J, *et al*. Saliva cell type DNA methylation reference panel for epidemiological studies in children. *Epigenetics.* 2022;**17**(2):161–177. doi:10.1080/15592294.2021.1890874
42. Belsky DW, Caspi A, Corcoran DL, *et al*. DunedinPACE, a DNA methylation biomarker of the pace of aging. Deelen J, Tyler JK, Suderman M, Deelen J, eds. *eLife.* 2022;**11**:e73420. doi:10.7554/eLife.73420
43. Raffington L, Belsky DW, Kothari M, Malanchini M, Tucker-Drob EM, Harden KP. Socioeconomic disadvantage and the pace of biological aging in children. *Pediatrics.* 2021;**147**(6):e2020024406. doi:10.1542/peds.2020-024406
44. Oblak L, van der Zaag J, Higgins-Chen AT, Levine ME, Boks MP. A systematic review of biological, social and environmental factors associated with epigenetic clock acceleration. *Ageing Res Rev.* 2021;**69**:101348. doi:10.1016/j.arr.2021.101348
45. McEwen LM, O'Donnell KJ, McGill MG, *et al*. The PedBE clock accurately estimates DNA methylation age in pediatric buccal cells. *Proc Natl Acad Sci USA.* 2020;**117**(38):23329–23335. doi:10.1073/pnas.1820843116
46. Zheng SC, Breeze CE, Beck S, *et al*. EpiDISH web server: epigenetic dissection of intra-sample-heterogeneity with online GUI. *Bioinformatics.* 2019;**36**(6):1950–1951. doi:10.1093/bioinformatics/btz833
47. Muthén BO. Latent variable modeling in heterogeneous populations. *Psychometrika.* 1989;**54**(4):557–585. doi:10.1007/bf02296397
48. Hu L, Bentler PM. Cutoff criteria for fit indexes in covariance structure analysis: conventional criteria versus new alternatives. *Struct Equ Model Multidiscip J.* 1999;**6**(1):1–55. doi:10.1080/10705519909540118
49. April-Sanders A, Duarte CS, Wang S, *et al*. Childhood adversity and sleep disturbances: longitudinal results in Puerto Rican children. *Int J Behav Med.* 2021;**28**(1):107–115. doi:10.1007/s12529-020-09873-w
50. McPhie ML, Weiss JA, Wekerle C. Psychological distress as a mediator of the relationship between childhood

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maltreatment and sleep quality in adolescence: results from the Maltreatment and Adolescent Pathways (MAP) Longitudinal Study. *Child Abuse Negl.* 2014;**38**(12):2044–2052. doi:10.1016/j.chiabu.2014.07.009

51. Uy JP, Gotlib IH. Associations among early life adversity, sleep disturbances, and depressive symptoms in adolescent females and males: a longitudinal investigation. *J Child Psychol Psychiatry.* 2024;**65**(8):1037–1046. doi:10.1111/jcpp.13942
52. Spilsbury JC, Babineau DC, Frame J, Juhas K, Rork K. Association between children's exposure to a violent event and objectively and subjectively measured sleep characteristics: a pilot longitudinal study. *J Sleep Res.* 2014;**23**(5):585–594. doi:10.1111/jsr.12162
53. Acosta J, Parent J, DiMarzio K, McMakin DL, McKee LG, Dale CF. Longitudinal associations between parenting practices and youth sleep problems. *J Dev Behav Pediatr.* 2021;**42**(9):751–760. doi:10.1097/DBP.0000000000000953
54. Kelly RJ, Marks BT, El-Sheikh M. Longitudinal relations between parent–child conflict and children's adjustment: the role of children's sleep. *J Abnorm Child Psychol.* 2014;**42**(7):1175–1185. doi:10.1007/s10802-014-9863-z
55. Pfaff A, Jud A, Schlarb A. Systematic review on the association between sleep-related hyperarousal and child maltreatment. *Sleep Med.* 2021;**84**:219–226. doi:10.1016/j.sleep.2021.05.041
56. Goering M, Tiwari HK, Patki A, Espinoza CN, Knight DC, Mrug S. Examining health behaviors as mechanisms linking earlier pubertal timing with accelerated epigenetic aging in late adolescence. *J Youth Adolesc.* 2024; (in press). doi:10.1007/s10964-024-02096-2
57. Shen L, Wiley JF, Bei B. Perceived daily sleep need and sleep debt in adolescents: associations with daily affect over school and vacation periods. *Sleep.* 2021;**44**(12). doi:10.1093/sleep/zsab190
58. Van Dongen HPA, Rogers NL, Dinges DF. Sleep debt: theoretical and empirical issues. *Sleep Biol Rhythms.* 2003;**1**(1):5–13. doi:10.1046/j.1446-9235.2003.00006.x
59. Carskadon MA, Acebo C, Richardson GS, Tate BA, Seifer R. An approach to studying circadian rhythms of adolescent humans. *J Biol Rhythms.* 1997;**12**(3):278–289. doi:10.1177/074873049701200309
60. Oster H, Challet E, Ott V, *et al*. The functional and clinical significance of the 24-hour rhythm of circulating glucocorticoids. *Endocr Rev.* 2017;**38**(1):3–45. doi:10.1210/er.2015-1080
61. Sullivan ADW, Bozack AK, Cardenas A, *et al*. Parenting practices may buffer the impact of adversity on epigenetic age acceleration among young children with developmental delays. *Psychol Sci.* 2023;**34**(10):1173–1185. doi:10.1177/09567976231194221
62. Sullivan ADW, Merrill SM, Konwar C, *et al*. Intervening after trauma: child–parent psychotherapy treatment is associated with lower pediatric epigenetic age acceleration. *Psychol Sci.* 2024;**35**:1062–1073. doi:10.1177/09567976241260247
63. Merrill SM, Hogan C, Bozack AK, *et al*. Telehealth parenting program and salivary epigenetic biomarkers in preschool children with developmental delay: NIMHD social epigenomics program. *JAMA Netw Open.* 2024;**7**(7):e2424815. doi:10.1001/jamanetworkopen.2024.24815
64. Gillman AS, Pérez-Stable EJ, Das R. Advancing health disparities science through social epigenomics research. *JAMA Netw Open.* 2024;**7**(7):e2428992. doi:10.1001/jamanetworkopen.2024.28992
65. Jackson CL, Walker JR, Brown MK, Das R, Jones NL. A workshop report on the causes and consequences of sleep health disparities. *Sleep.* 2020;**43**(8). doi:10.1093/sleep/zsaa037
66. Jean-Louis G, Grandner MA, Seixas AA. Social determinants and health disparities affecting sleep. *Lancet Neurol.* 2022;**21**(10):864–865. doi:10.1016/S1474-4422(22)00347-7

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