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The Epigenetic Clock at Birth: Associations With Maternal Antenatal Depression and Child Psychiatric Problems

RH = Epigenetic Clock and Development

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Clinical Guidance

Supplemental Material

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Abstract

Objective

Maternal antenatal depression may compromise the fetal developmental milieu and contribute to individual differences in aging and disease trajectories in later life. We evaluated the association between maternal antenatal depression and a novel biomarker of aging at birth, namely epigenetic gestational age (GA) based on fetal cord blood methylation data. We also examined if this biomarker prospectively predicts and mediates maternal effects on early childhood psychiatric problems.

Method

694 mothers from the PREDO Study provided information on history of depression diagnosed before pregnancy, 581 completed the Center for Epidemiological Studies Depression Scale throughout pregnancy, and 407 completed the Child Behavior Checklist at child’s age 3.7 (standard deviation(SD)=0.75) years. DNA methylation (DNAm) GA of fetal cord blood DNA was based on the methylation profile of 148 selected CpGs. Epigenetic GA was calculated as the arithmetic difference between DNAm GA and chronological GA and adjusted for chronological GA.

Results

Maternal history of depression diagnosed before pregnancy [Mean difference=-0.25 SD units, 95% Confidence Interval (95%CI) -0.46;-0.03)] and greater antenatal depressive symptoms (-0.08 SD unit per SD unit increase, 95%CI -0.16;-0.004) were associated with child’s lower epigenetic GA. Child’s lower epigenetic GA, in turn, prospectively predicted total and internalizing problems and partially mediated the effects of maternal antenatal depression on internalizing problems in boys.

Conclusion

Maternal antenatal depression is associated with lower epigenetic GA in offspring. This lower epigenetic GA seems to be associated with a developmental disadvantage for boys, who in early childhood show greater psychiatric problems.
Keywords: epigenetic clock, gestational age, cord blood, antenatal depression, childhood psychiatric problem

Introduction

Maternal depression complicates up to 20% of pregnancies. Depression not only hinders the health and well-being of the pregnant mother, but is also associated with adverse perinatal and developmental outcomes in her child. The adverse outcomes include prematurity and increased risks of poorer cognition and psychiatric problems later in life. Findings from these studies are compatible with the Developmental Origins of Health and Disease (DOHaD) framework, which suggests that in utero exposure to environmental adversities may alter the structure and function of developing cells, tissues, organs, and physiological feedback systems, leading to individual differences in aging and disease trajectories that persist throughout the lifespan.

Mounting evidence suggests that exposure to prenatal environmental adversity may be embedded in epigenetic alterations in the offspring, such as in DNA methylation (DNAm), which is characterized by the addition of a methyl group primarily to cytosine linked to guanine by phosphate (CpG) sites. DNAm can be used to generate aggregate markers of aging, such as the Hannum and the Horvath epigenetic age predictors. The Hannum age predictor is based on DNAm of 71 CpG sites in whole blood of 19 to 101-year-old individuals and the Horvath age predictor on DNAm of 353 CpG sites of multiple tissues of 0 to 100-year-old individuals. Both predictors are highly correlated with an individual’s chronological age (r’s >0.91). Having a higher DNAm age than chronological age, based on these molecular aging biomarkers, has been shown to predict disease trajectories and mortality more accurately than chronological age. However, it remains less clear if exposure to prenatal environmental adversity is associated with epigenetic gestational age (GA) at birth or how epigenetic GA is associated with developmental problems later in life.
A recent study demonstrated that a higher epigenetic GA (higher DNAm GA than chronological GA), based on the Horvath and the Hannum epigenetic age predictors of cord blood methylation data, was associated with maternal smoking during pregnancy and delivery by caesarean section.\textsuperscript{9} These predictors are, however, not well-suited for epigenetic age estimation at birth because their correlation with chronological GA is nearly zero.\textsuperscript{9} A recent study generated a novel epigenetic GA biomarker based on fetal umbilical cord blood or newborn blood spots,\textsuperscript{10} which showed a high correlation with ultrasound-based GA.\textsuperscript{10} This study demonstrated that lower epigenetic GA (lower DNAm GA than chronological GA) at birth was associated with maternal socio-economic disadvantage and low birth weight. We have extended these analyses by showing that lower epigenetic GA was associated with maternal insulin treated gestational diabetes mellitus in a previous pregnancy and Sjögren’s syndrome, and higher epigenetic GA with a maternal age of over 40 years at delivery, neonate’s lower 1-min Apgar score and female sex.\textsuperscript{11}

We are unaware of any previous studies that would have tested whether maternal antenatal depression and child psychiatric problems are associated with child’s epigenetic GA at birth. The current study sought to determine if maternal history of depression diagnosed before pregnancy and antenatal depressive symptoms were related to the child’s epigenetic GA at birth based on fetal cord blood DNAm data. We also tested if these conditions exerted additive effects on child’s epigenetic GA, as not all with a history of depression diagnosis report high antenatal depressive symptoms and \textit{vice versa},\textsuperscript{1} and if the effects of antenatal depressive symptoms were gestation-stage specific. Further, we tested if child’s epigenetic GA at birth predicted early childhood psychiatric problems, and if child’s epigenetic GA mediated the associations of maternal antenatal depression with child psychiatric problems. Finally, we tested if the associations were moderated by child’s sex, as sex biases exist in longevity and aging trajectories,\textsuperscript{12} epigenetic age based on the Horvath and the
Hannum epigenetic age predictors, epigenetic GA at birth, and prevalence and etiology of psychiatric problems. The effects of maternal stress exposure during pregnancy and particularly antenatal depression on offspring developmental outcomes have also shown sex-specificity. The evidence in humans has shown that maternal antenatal depression was associated with a higher risk of depression in the offspring at 18 years of age but only in girls. Yet, in one rodent study, maternal early pregnancy stress was associated with a depression-like behavioral phenotype in male but not in female offspring.

Method

Study population

The Prediction and Prevention of Preeclampsia and Intrauterine Growth Restriction (PREDOMI) Study comprises 1083 pregnant women and their singleton children born in 2006-2010 in Finland. The recruitment took place in consecutive order when these women attended their first ultrasound screening at 12-13 weeks of gestation in hospital maternity clinics of the study. Of the recruited women, 973 had 1 or more risk factors of pre-eclampsia and intrauterine growth restriction (IUGR), and 110 had no known risk factors.

In total, we had 814 fetal umbilical cord blood samples with full information on genome-wide methylation and genotype passing through quality control (see Figure S1, available online). Of this entire sample, data on maternal depression diagnosed before pregnancy was available for 694, on maternal antenatal depressive symptoms for 581, and on childhood psychiatric problems at child’s mean age of 3.7 years for 407. Table 1 describes the sample characteristics.
The Ethics Committees of the Helsinki and Uusimaa Hospital District and the participating hospitals approved the study protocol. Written informed consent was obtained from all participating women.

**Child DNA methylation, epigenetic and chronological GA at birth**

Fetal cord blood samples were collected according to standard procedures. DNA was extracted at the National Institute for Health and Welfare, Helsinki, Finland and the Institute for Molecular Medicine Finland, University of Helsinki, Finland. Methylation analyses were performed at the Max Planck Institute of Psychiatry in Munich, Germany. DNA was bisulphite-converted using the EZ-96 DNA Methylation kit (Zymo Research, Irvine, CA). Genome-wide methylation status of over 485,000 CpG sites was measured using the Infinium Human Methylation 450 BeadChip (Illumina Inc., San Diego, CA) according to the manufacturer’s protocol. The arrays were scanned using the iScan System (Illumina Inc., San Diego, CA). The quality control pipeline was set up using the R-package minfi. Samples with maternal blood contamination were excluded (N=9) according to the method described in. The final dataset contained 428,619 CpGs.

Methylation beta-values were normalized according to Horvath’s modified beta-mixture quantile (BMIQ) normalization.

DNAm GA was calculated as described in based on the methylation profile of 148 selected CpGs. Chronological GA was based on ultrasound scans and epigenetic GA was calculated as the arithmetic difference between DNAm GA and chronological GA and adjusted for chronological GA. Adjustment for chronological GA was necessary to remove the effect of chronological GA entirely (Pearson correlation between DNAm GA-GA arithmetic difference and GA r=-0.27, p<0.01).

**Child cord blood cell counts at birth**
To control for the potential effects of cell type heterogeneity in fetal umbilical cord blood, cord blood cell counts at birth were estimated for 7 cell types (nucleated red blood cells, granulocytes, monocytes, natural killer cells, B cells, CD4+ T cells, and CD8+ T cells) using the method of Bakulski et al., which is also incorporated in the R-package minfi.

Child genotyping and multi-dimensional scaling analysis
To control for the potential effects of population structure, genotyping was performed on Illumina Human Omni Express Exome Arrays (Illumina Inc., San Diego, CA). Only markers with a call rate of at least 98%, minor allele frequency of 1% and a p-value for deviation from Hardy-Weinberg-Equilibrium > 1 x 10^-6 were kept in the analysis. We performed multi-dimensional scaling (MDS) analysis on the identity by state matrix of quality-controlled genotypes. The first 2 MDS components depicted the population structure.

Maternal history of depression diagnosed before pregnancy and antenatal depressive symptoms
At between 12+0-13+6 weeks+days of gestation, the women answered the question “Have you ever been diagnosed by a physician with depression?” followed by a question on timing of the diagnosis; 76 women reported that the diagnosis occurred before pregnancy (3 women who did not specify timing were excluded). Of them, 12 indicated using antidepressant medication during the past year. 618 women reported no history of physician diagnosed depression and no antidepressant medication use in the past year (3 women who reported using antidepressants but no depression diagnosis were excluded).

Starting from 12+0-13+6 weeks+days of gestation each woman completed the 20 item Center for Epidemiological Studies Depression Scale (CES-D) for depressive symptoms over the previous 7
days biweekly up to 14 times until 38+0-39+6 weeks+days of gestation or delivery. On average, each woman filled in the CES-D 12.6 (SD=2.2) times; of the 581 women with CES-D data, 481 (82.8%) had less than 2 missing values. We used raw data to calculate trimester-specific means of the CES-D sum-scores to represent the level of depressive symptoms at each pregnancy trimester (one value at gestational weeks+days 12+0-13+6; mean of values between 14+0-27+6 gestational weeks+days; mean of values between 28+0-39+6 gestational weeks+days). We then calculated the mean of these three trimester-specific values, the trimester-weighted mean value, to represent the overall level of antenatal depressive symptoms.

**Child psychiatric problems**

When their children were 2.3 to 5.8 years old (Mean 3.7, SD 0.75), mothers completed the Child Behavior Checklist (CBCL 1½-5) on psychiatric problems. We calculated the total problems t-score based on the 99 problem items rated on a scale from 0 (not true) to 2 (very or often true). We also calculated internalizing and externalizing problems t-scores, two subscales of the total problems.

**Covariates**

All analyses were adjusted for child’s chronological GA, cord blood cell-type composition and the first two MDS components. Based on our previous findings in this cohort, we thereafter made adjustments for maternal age at delivery (≥40y/<40y), insulin-treated gestational diabetes mellitus in a previous pregnancy (yes/no), Sjögren’s syndrome (yes/no), neonate’s 1-min Apgar score (≤6/>6) and sex (girl/boy). In the analyses of child psychiatric problems, we made further adjustments for child’s age at follow-up (y) and maternal Beck Depression Inventory-II scores (BDI-II <14/BDI-II ≥14) reported at the child follow-up.
Statistical analyses

We studied the associations of maternal history of depression diagnosed before pregnancy and trimester-weighted mean of antenatal depressive symptoms with child epigenetic GA using linear regression analysis. We tested if these effects were additive by adding maternal depression diagnosis x trimester-weighted mean of antenatal depressive symptoms interaction term into regression equation following main effects of these variables. We examined gestation-stage-specific effects with generalized additive mixed models using reverse temporal model that treated the bi-weekly measures of antenatal depressive symptoms as the longitudinal dependent variable and child’s epigenetic GA as the time-invariant and gestation week as the time-varying independent continuous variables; time (gestation week) x epigenetic GA interaction tested if the effect was gestation-stage-specific. For all these analyses, depressive symptoms scores were square-root-transformed to attain normality; the symptom scores were further standardized to mean of 0 and SD of 1 to facilitate interpretation (for mixed models the SD scores were calculated using the grand mean of the biweekly CES-D sum-scores across 12-39 gestational weeks and its SD to retain within-time-variation).

As child’s CBCL psychiatric problems scores are not independent of each other, but rather represent a hierarchical structure, we first examined associations of child’s epigenetic GA with early childhood total problems and then examined associations with child’s internalizing and externalizing problems using linear regression analyses. Problem-scores were logarithm-transformed to obtain normality and standardized to facilitate interpretation. In our study the two CBCL subscales were highly intercorrelated (Pearson’s r=0.62, p<0.001), and together explained 95.3% of the variance in total problems. However, to decrease the likelihood of type 1 error, we tested the associations with the two subscales only if the higher level association was significant and report also Bonferroni-corrected confidence intervals (CI).
In testing whether the associations varied by sex, we entered sex x history of depression diagnosed before pregnancy/antenatal depressive symptoms interaction term into the regression equation with child epigenetic GA at birth as the outcome; and entered sex x child epigenetic GA at birth interaction into the regression equation with child psychiatric problems as the outcome.

Finally, we tested if child epigenetic GA at birth mediated the association between maternal antenatal depression and child psychiatric problems by using the PROCESS macro for SPSS. Mediation tests were conducted pending these variables were interrelated.

In order to validate our findings, we applied the bootstrapping method in all analyses. We used unrestricted random sampling method to generate 1000 samples, and 95% bootstrap CI (95% CI) using the normal distribution theory; to account for type 1 error in analyses on internalizing and externalizing problems we also used Bonferroni-corrected 95% CI (97.5% CI is significant at 95% CI after correction for two tests on subscales). Statistical analyses were performed using IBM SPSS 24.0 and SAS 9.4.

**Results**

Table 1 shows that the subsamples with data on maternal history of depression diagnosed before pregnancy (n=694), maternal antenatal depressive symptoms (n=581) and child psychiatric problems (n=407) did not differ from the entire sample in any of the studied characteristics, except that DNAm GA was higher in the subsample with child psychiatric problems data. Pearson correlations between DNAm GA and GA were 0.51 (p<0.001) in the entire sample, and 0.52 (p<0.001), 0.50 (p<0.001), and 0.47 (p<0.001) in the three subsamples of participants with data on
maternal history of depression diagnosed before pregnancy, data on maternal antenatal depressive symptoms and data on child psychiatric problems, respectively.

**Maternal antenatal depression and child’s epigenetic GA at birth**

Figure 1 shows that maternal history of depression diagnosed before pregnancy (Panel A; exclusion of antidepressant users (n=12) did not alter the finding, 95% CI -0.47; -0.01) and greater antenatal depressive symptoms (Panel B) were associated with lower epigenetic GA after adjusting for child’s chronological GA, fetal cord blood cell-types and 2 MDS components (Model 1). When adjusted further for the other covariates (Model 2), this latter association became non-significant (Figure 1).

Furthermore, we found that while child’s epigenetic GA was lower for children whose mothers had a depression diagnosis, clinically relevant antenatal depressive symptoms or both than for children whose mothers reported neither, the effects of maternal history of depression diagnosed before pregnancy and antenatal depressive symptoms were not additive [(see Figure S2, available online; women with a depression diagnosis before pregnancy had 3.61 times higher odds (95% CI 2.09;6.27) of clinically relevant antenatal depressive symptoms (trimester-weighted mean depressive symptoms score $\geq 16$) than those without the diagnosis].

There were no gestation-stage-specific effects of antenatal depressive symptoms on child’s epigenetic GA (see Figure S3, available online).

Finally, we tested if child’s sex moderated any of the associations. There were no significant sex x maternal depression diagnosis (95% CI -0.41;0.46 for interaction term) or sex x maternal depressive symptoms (95% CI -0.07;0.22 for interaction term) interactions on child’s epigenetic GA.
Child’s epigenetic GA at birth and psychiatric problems at 3.7 years

Table 2 shows that there were no significant associations between child’s epigenetic GA and psychiatric problems in the total sample. However, sex x epigenetic GA interactions were significant for total and internalizing problems (Table 2). In model 2, there was an interaction also on externalizing problems. The interaction between sex and epigenetic GA on internalizing problems remained significant after Bonferroni-correction for two conducted tests (Bonferroni-corrected 95% CI 0.02;0.48 and 0.01;0.46 in models 1-2, respectively), while that on externalizing problems in model 2 did not (Bonferroni-corrected 95% CI -0.02;0.43).

Table 2 shows that in boys but not in girls lower epigenetic GA at birth was significantly associated with greater total and internalizing problems. In neither boys nor in girls was epigenetic GA at birth significantly associated with externalizing problems (Table 2). Furthermore, Table S1 (available online) shows sample characteristics by sex and highlights that, on average, boys had significantly lower epigenetic GA at birth and higher total and externalizing problems scores than girls.

Associations between maternal antenatal depression and child’s psychiatric problems at 3.7 years: mediation via child’s epigenetic GA

The mediation analyses were conducted in boys as epigenetic GA was not associated with psychiatric problems in girls; and only on total and internalizing problems since they were predicted by child’s epigenetic GA (Table 2) and by maternal antenatal depression in boys (see Table S2, available online). Figure 2 shows that in boys, epigenetic GA partially mediated the association between antenatal depression and internalizing problems. Mediation was not significant on total problems (95% CI -0.001;0.14 for indirect effect).
Discussion

This study shows that maternal history of depression diagnosed before pregnancy and higher levels of antenatal depressive symptoms were significantly associated with child’s lower epigenetic GA at birth. The effects of these conditions were not additive and antenatal symptoms effects were not gestation-stage-specific. This study also shows that child’s lower epigenetic GA at birth prospectively predicted child’s total and internalizing problems in early childhood, however, only in boys. Also in boys, child’s epigenetic GA at birth partially mediated the association of maternal antenatal depression with child internalizing problems.

These findings may seem to contradict the findings in adult populations that have shown that higher, rather than lower epigenetic age, in comparison to chronological age, is associated with several negative health outcomes.\textsuperscript{8,25,26} That lower epigenetic age might indicate such an increased risk is, however, congruent with the DOHaD-concept: the risk for aging-related diseases and mental problems is increased in individuals exposed to prenatal environmental adversities, which are associated with lower birth weight, lower GA, and maternal depression during pregnancy.\textsuperscript{1,2} Since DNA methylation has been shown to undergo age-related changes,\textsuperscript{27} it remains possible that both lower and higher epigenetic GA signal risk. This risk may, however, depend on life stage. Future studies will need to evaluate this hypothesis and whether epigenetic GA at birth predicts other epigenetic age biomarkers in later life.

While we anticipated to find sex differences in the associations, it remains elusive why the associations with psychiatric problems were specific to boys. It has been suggested that sex differences in the ‘programming effects’ of prenatal stress may serve an adaptive, evolutionary purpose. In stressful environments, it may be more adaptive for females to be vigilant, alert and stress responsive to protect the young; this may become phenotypically apparent in depression and
anxiety. For males aggression and stress resistance may be more adaptive as they go out, explore new environments and compete with other males. These ‘adaptive’ phenotypes may become vulnerabilities when they no longer match the environments. The association we found with the internalizing phenotype in boys contradicts with the suggested evolutionarily adaptive male phenotype. It also contradicts with previous findings showing that maternal depression during pregnancy predicts depression specifically in girls. However, many studies suggest corresponding adverse effects of antenatal depression on offspring psychopathology in both sexes, and corresponding with our findings, a rodent study showed that maternal early pregnancy stress predicted a depression-like phenotype only in male offspring. Indeed, evidence exists suggesting that what might be phenotypically adaptive for males and females may be determined by a complex interaction of type, timing, severity, and chronicity of the prenatal stress exposure and the developmental stage of the offspring. Whether lower epigenetic GA in boys would also predict other outcomes or would become predictive of outcomes in girls in later life stages is the subject of ongoing studies. Furthermore, since we found that boys had lower epigenetic GA at birth and higher total and externalizing psychiatric problems in early childhood than girls, the sex differences in the associations of epigenetic GA and psychiatric problems may also possibly have resulted from a greater ability to detect such associations in boys. Yet, we found no sex differences in the levels of internalizing problems, but epigenetic GA and internalizing problems were also only associated in boys. The findings on the possible sex-specificity of the effects of prenatal stress on offspring developmental outcomes are inconclusive, and a consensus exists that further exploration of the potential sex-specificity of prenatal programming effects is needed.

The main study strength pertains to the well-characterized, ethnically homogenous cohort and prospective mother-child data. Chronological GA was based on ultrasound scans and we applied novel bioinformatics methods to account for any sample-contamination by maternal blood and for
the effects of cell type heterogeneity$^{18}$ and genetic population structure,$^{19}$ which are factors strongly influencing epigenetic profiles.$^{28}$ Furthermore, we validated our findings by using the bootstrap method and applied a hierarchically-structured analysis strategy when we examined child psychiatric problems to decrease the likelihood of false-positive findings. We also corrected these analyses for multiple testing, and the sex-interaction on internalizing problems remained significant. Yet, our novel findings must be interpreted with caution, and further studies are needed to confirm or refute them.

The limitations of our study relate to our recruitment strategy which was based on women’s risk factor status for preeclampsia and IUGR, ethnic homogeneity of our sample and one tissue type, precluding generalizations to groups that differ from ours and other tissues. Sample attrition limits the generalizability of our study findings, and the low number of mothers with depression diagnosis limited our statistical power to assess additive effects of depression before and during pregnancy. Also, the biological mechanisms driving the effects found remain unclear. During pregnancy these mechanisms may include depression related endocrine factors, neurotransmitters, and levels of inflammatory markers in the mother, fetus and placenta.$^{29}$ In fact, epigenetic age acceleration in adults may be driven by direct effects of glucocorticoids on DNA methylation.$^{30}$ The mechanisms involved after birth may include structural and functional immaturity of organs and problems in neonatal adaptation increasing vulnerability to developmental adversities. Maternal depression after pregnancy may also compromise the developing attachment bond. However, in our study, maternal depression parallel to rating the child did not account for the associations found between child epigenetic GA at birth and child psychiatric problems.

In summary, children of mothers with a history of depression diagnosed before pregnancy or with greater antenatal depressive symptoms display lower epigenetic GA at birth. This lower epigenetic
GA at birth seems to be associated with a developmental disadvantage for boys, who went on to display greater psychiatric problems in early childhood. Lower epigenetic GA actually partially mediated the effects of maternal depression on child outcome. Epigenetic GA at birth may hold potential for identifying, before the onset of psychiatric problems, at risk children thereby allowing for timely, personalized preventive interventions.
References


10. Knight AK, Craig JM, Theda C, et al. An epigenetic clock for gestational age at birth based


Table 1. Sample characteristics.

<table>
<thead>
<tr>
<th></th>
<th>Entire sample with fetal cord blood DNA methylation data (N=814)</th>
<th>Sample with fetal cord blood DNA methylation and maternal history of depression diagnosed before pregnancy data (N=694)</th>
<th>Sample with fetal cord blood DNA methylation and maternal antenatal depressive symptoms data (N=581)</th>
<th>Sample with fetal cord blood DNA methylation and child’s psychiatric problems in early childhood follow-up data (N=407)</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Child characteristics at birth</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Gestational age (weeks)</td>
<td>39.8(1.6) 31.0–42.7</td>
<td>39.8(1.6) 31.0–42.7</td>
<td>39.7(1.6) 31.0–42.7</td>
<td>39.8(1.5) 31.0–42.7</td>
</tr>
<tr>
<td>DNAm gestational age (weeks)</td>
<td>38.5(2.0) 28.5–47.1</td>
<td>38.5(2.0) 29.6–47.1</td>
<td>38.4(2.1) 28.5–47.1</td>
<td>38.6(2.0) 29.6–47.1</td>
</tr>
<tr>
<td>Epigenetic gestational age (DNAm gestational age – gestational age) (weeks)</td>
<td>-1.3(1.8) -10.6–7.0</td>
<td>-1.3(1.8) -10.1–7.0</td>
<td>-1.4(1.9) -10.6–7.0</td>
<td>-1.2(1.9) -8.0–7.0</td>
</tr>
<tr>
<td>Sex (boys)</td>
<td>430(52.8%)</td>
<td>365(52.6%)</td>
<td>299(51.5%)</td>
<td>212(47.9%)</td>
</tr>
</tbody>
</table>

Mean/N (SD/%) Range
1-min Apgar score ≤6  |  47(5.9%)  |  40(5.8%)  |  0.53  |  34(5.9%)  |  0.44  |  22(5.4%)  |  0.35  

**Maternal characteristics**

**History of depression**

diagnosed before pregnancy (yes)  |  76(11.0%)  |  76(11.0%)  |  1.00  |  62(11.3%)  |  0.29  |  49(12.9%)  |  0.11  

**Antenatal trimester-weighted mean CES-D score (0-60)**

|  | 11.5(6.5)  | 0.7–39.9  | 11.5(6.6)  | 0.7–39.9  | 0.61  | 11.5(6.5)  | 0.7–39.9  | 1.00  | 11.5(6.7)  | 0.7–39.9  | 0.86  

**Age over 40 years at delivery (yes)**

|  | 139(17.1%)  | 119(17.1%)  | 0.39  | 96(16.5%)  | 0.35  | 76(18.7%)  | 0.13  

**Insulin-treated gestational diabetes mellitus in previous pregnancy (yes)**

|  | 8(1.0%)  | 6(0.9%)  | 0.13  | 6(1.0%)  | 0.49  | 3(0.7%)  | 0.24  

**Sjögren’s syndrome (yes)**

|  | 11(1.4%)  | 8(1.2%)  | 0.20  | 9(1.5%)  | 0.36  | 7(1.7%)  | 0.28  

Note: DNAm refers to DNA methylation, CES-D to Center for Epidemiological Studies Depression Scale.

P1 refers to p-value comparing the sample with data on history of depression diagnosed before pregnancy (N=694), P2 on maternal antenatal depressive symptoms (N=581), and P3 on child’s psychiatric problems (N=407) with the entire sample (N=814).
Table 2. Associations between child’s epigenetic gestational age at birth and psychiatric problems at 3.7 years.

<table>
<thead>
<tr>
<th>Psychiatric problems in standard deviation units: (dependent outcome variable)</th>
<th>Epigenetic gestational age in standard deviation units (independent predictor variable)</th>
<th></th>
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<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>sex x epigenetic</td>
<td>gestational age main effect*</td>
<td>boys (n=212)</td>
<td>girls (n=195)</td>
<td>boys (n=212)</td>
<td>girls (n=195)</td>
<td>boys (n=212)</td>
<td>girls (n=195)</td>
</tr>
<tr>
<td></td>
<td>B*</td>
<td>95% Confidence Interval*</td>
<td>B*</td>
<td>95% Confidence Interval*</td>
<td>B</td>
<td>95% Confidence Interval</td>
<td>B</td>
</tr>
<tr>
<td>Total</td>
<td></td>
<td></td>
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</tr>
<tr>
<td>Model 1</td>
<td>-0.06</td>
<td>-0.17;0.05</td>
<td>0.04;0.44</td>
<td>-0.16</td>
<td>-0.31;-0.0003</td>
<td>0.08</td>
<td>-0.08;0.24</td>
</tr>
<tr>
<td>Model 2</td>
<td>-0.06</td>
<td>-0.16;0.05</td>
<td>0.06;0.44</td>
<td>-0.17</td>
<td>-0.32;-0.02</td>
<td>0.10</td>
<td>-0.06;0.26</td>
</tr>
<tr>
<td>Internalizing</td>
<td></td>
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<td></td>
</tr>
<tr>
<td>Model 1</td>
<td>-0.04</td>
<td>-0.15;0.08</td>
<td>0.05;0.46</td>
<td>-0.16</td>
<td>-0.31;0.001</td>
<td>0.13</td>
<td>-0.05;0.30</td>
</tr>
<tr>
<td>Model 2</td>
<td>-0.03</td>
<td>-0.15;0.08</td>
<td>0.03;0.43</td>
<td>-0.16</td>
<td>-0.31;-0.01</td>
<td>0.14</td>
<td>-0.04;0.31</td>
</tr>
<tr>
<td>Externalizing</td>
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<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Model 1</td>
<td>-0.06</td>
<td>-0.17;0.05</td>
<td>-0.01;0.39</td>
<td>-0.13</td>
<td>-0.29;0.02</td>
<td>0.06</td>
<td>-0.10;0.23</td>
</tr>
<tr>
<td>Model 2</td>
<td>-0.06</td>
<td>-0.17;0.05</td>
<td>0.01;0.40</td>
<td>-0.15</td>
<td>-0.30;0.01</td>
<td>0.08</td>
<td>-0.08;0.24</td>
</tr>
</tbody>
</table>
Note: B refers to unstandardized regression coefficient from linear regression analysis, indicating standard deviation change in problem scores per standard deviation change in epigenetic gestational age.

Model 1 is adjusted for child’s chronological gestational age, fetal cord blood cell counts, 2 multidimensional scaling components from genome-wide data, child’s sex (pooled analysis), and age at follow-up. Model 2 is adjusted for Model 1 covariates plus maternal age at delivery, insulin-treated gestational diabetes mellitus in previous pregnancy, Sjögren’s syndrome, maternal Beck Depression Inventory-II score parallel to child rating and child’s 1-minute Apgar score.

* Main effects in the total sample are tested without sex x epigenetic gestational age interaction term, while sex x epigenetic gestational age interactions are tested in the presence of main effects of these predictor variables.

**These confidence intervals pertain to the interaction term “sex x epigenetic gestational age” tested in the presence of main effects.
Figure legends

Figure 1. Maternal antenatal depression and child’s epigenetic gestational age at birth.

Note: Panel A: Means and 95% Confidence Intervals of child’s epigenetic gestational age in groups divided according to maternal history of depression diagnosed before pregnancy. The unstandardized regression coefficients (B) and 95% Confidence Intervals refer to mean differences in epigenetic gestational age between children of mothers with and without a history of depression diagnosed before pregnancy derived from linear regression analyses.

B= -0.25, 95% Confidence Interval -0.46;-0.03 (Model 1);
B= -0.24, 95% Confidence Interval -0.45;-0.02 (Model 2)

Panel B: A scatterplot with a regression line displaying the unstandardized regression coefficient (B) and 95% Confidence Intervals showing associations between maternal trimester-weighted mean antenatal depressive symptoms and child’s epigenetic gestational age.

B= -0.08, 95% Confidence Interval -0.16;-0.004 (Model 1);
B= -0.07, 95% Confidence Interval -0.15;0.004 (Model 2)

Panels A and B: Regression Model 1 is adjusted for child’s chronological gestational age at birth, fetal cord blood cell-type composition, and 2 multi-dimensional scaling components and Model 2 for Model 1 plus maternal age at delivery, insulin-treated gestational diabetes mellitus in previous pregnancy, Sjögren’s syndrome, child’s 1-minute Apgar score and sex. Figures display Model 1 adjustments.

Figure 2. Maternal antenatal depression partially acts via child’s epigenetic gestational age at birth on child’s psychiatric problems among boys.
Note: Mediation analyses showing that maternal antenatal depression (history of depression diagnosed before pregnancy or antenatal depressive symptoms) partially act via child’s epigenetic gestational age at birth to impact on child’s internalizing problems among boys. The numbers represent standardized regression coefficients ($\beta$) and 95% Confidence Intervals (95%CI). The associations are adjusted for child’s chronological GA at birth, fetal cord blood cell-type composition, 2 multi-dimensional scaling components, maternal age at delivery, insulin-treated gestational diabetes mellitus in previous pregnancy, Sjögren’s syndrome, Beck Depression Inventory-II scores parallel to child ratings, child’s 1-minute Apgar score and age at early childhood testing.

**Figure S1.** Flow chart of the Prediction and Prevention of Preeclampsia and Intruterine Growth Retardation (PREDO) study and sample attrition.

**Figure S2.** The lack of additive effects of maternal history of depression diagnosed before pregnancy and antenatal trimester-weighted mean Center for Epidemiological Studies Depression Scale (CES-D) score on child’s epigenetic gestational age at birth.

Note: 95% CI -0.31;0.61 (Model 1), 95% CI -0.32;0.60 (Model 2) for maternal history of depression diagnosed before pregnancy (yes vs. no) x antenatal trimester-weighted mean Center for Epidemiological Studies Depression Scale (CES-D) score (CES-D\(\geq\)16 vs. < 16) interaction; Mean difference=-0.18, 95% CI -0.34; -0.03 (Model 1), 95% CI -0.33;-0.02 (Model 2) for no diagnosis and CES-D<16 vs. other groups.

37 women who had antenatal depressive symptoms data did not have data on history of depression diagnosed before pregnancy; Model 1 is adjusted for child’s chronological GA at birth, fetal cord blood cell-type composition, and 2 multi-dimensional scaling components and Model 2 for Model 1 covariates plus maternal age at delivery, insulin-treated gestational diabetes mellitus in previous pregnancy, Sjögren’s syndrome, child’s 1-minute Apgar score and sex.

**Figure S3.** Associations between maternal antenatal depressive symptoms at different stages of pregnancy and child’s epigenetic gestational age.

Note: To test if the associations were gestation-stage specific we used generalized additive mixed models (reverse temporal model) that treated the bi-weekly measures of antenatal depressive symptoms as the longitudinal dependent variable and epigenetic gestational age as the time-invariant continuous variable and gestation week as the time-varying independent continuous variable; time (gestation week) x epigenetic gestational age interaction tested if the effect on bi-weekly antenatal depressive symptoms was gestation-stage specific. For display purposes regression lines are presented pooling the individual slopes for the 1st trimester (slopes at 12+0-13+6 weeks of gestation), 2nd trimester (mean of slopes between 14+0-27+6 gestational weeks) and 3rd trimester (mean of slopes between 28+0-39+6 gestational weeks).
Panel A

Maternal history of depression diagnosed before pregnancy

Panel B

Maternal antenatal trimester-weighted mean depressive symptoms score (Standard Deviation units)
Maternal antenatal depression

Indirect effect $\beta = 0.04$, 95% CI $0.001; 0.15$

$\beta = 0.37$, 95% CI $0.04; 0.70$

Child's Internalizing problems at age 3.7 years

Child's epigenetic gestational age at birth

$\beta = 0.33$, 95% CI $0.04; 0.64$
876 fetal cord blood DNA samples available for genome-wide methylation analysis using Infinium Human Methylation 450 BeadChip.

- 3 samples excluded: missing chronological gestational age data and an outlier with epigenetic gestational age >5 standard deviations.

834 fetal cord blood DNA samples full information on genome-wide methylation and DNAm gestational age was calculated.

- 694 with data on maternal history of depression diagnosed before pregnancy
- 581 with data on maternal antenatal depressive symptoms
- 407 with data on child psychiatric problems in early childhood follow-up

825 fetal cord blood DNA samples passed quality control procedures and had full information on genome-wide methylation.

- 42 samples excluded: duplicates, outliers in the median intensities, cross-hybridizing probes or probes containing SNPs and CpGs with a detection $P$-value $> 0.01$ in at least 50% of the samples, due to location on chromosome X or Y, or sex discrepancies.

817 fetal cord blood DNA samples valid information on genome-wide methylation and genotype data.

- 9 samples excluded: maternal blood contamination

814 fetal cord blood DNA samples with child epigenetic gestational age.

- 8 samples excluded: call rate below 98% and discrepancies between phenotypic and genotypic sex in genome-wide genotype data

- 3 samples excluded: missing chronological gestational age data and an outlier with epigenetic gestational age >5 standard deviations

8 samples excluded: maternal blood contamination.

- 834 fetalcordbloodDNA samples full information on genome-wide methylation and DNAm gestational age was calculated
Child’s epigenetic gestational age at birth (Standard Deviation units)

- n = 392
  - No diagnosis and CES-D < 16

- n = 90
  - No diagnosis and CES-D ≥ 16

- n = 34
  - Yes diagnosis and CES-D < 16

- n = 28
  - Yes diagnosis and CES-D ≥ 16
Time x child’s epigenetic gestational age interaction term 95% Confidence Interval -0.002; 0.002 (Model 1); 95% Confidence Interval -0.002; 0.002 (Model 2)
Table S1. Characteristics of the sample with data on child psychiatric problems in early childhood follow-up stratified by child’s sex (N=407).

<table>
<thead>
<tr>
<th>Child characteristics at birth and in early childhood:</th>
<th>Boys (N=212)</th>
<th>Girls (N=195)</th>
<th>P boys vs. girls</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mean/N (SD/%) Range</td>
<td>Mean/N (SD/%) Range</td>
<td>boys vs. girls</td>
<td></td>
</tr>
<tr>
<td>Gestational age (weeks)</td>
<td>39.8(1.5) 34.4–42.7</td>
<td>39.9(1.5) 31.0–42.0</td>
<td>0.74</td>
</tr>
<tr>
<td>DNAm gestational age (weeks)</td>
<td>38.3(2.0) 32.8–45.8</td>
<td>38.9(2.0) 29.6–47.1</td>
<td>0.003</td>
</tr>
<tr>
<td>Epigenetic gestational age (DNAm gestational age – gestational age) (weeks)</td>
<td>-1.5(2.0) -7.1–7.0</td>
<td>-0.9(1.7) -8.0–6.8</td>
<td>0.003</td>
</tr>
<tr>
<td>Age at follow-up (years)</td>
<td>3.7(0.8) 2.4–5.8</td>
<td>3.6(0.8) 2.3–5.8</td>
<td>0.63</td>
</tr>
<tr>
<td>1-min Apgar score ≤ 6 (yes)</td>
<td>12(5.7%)</td>
<td>10(5.1%)</td>
<td>0.49</td>
</tr>
</tbody>
</table>

Psychiatric problems:
- Total: 46.6(9.6) 28.0–74.0 vs. 44.4(7.9) 28.0–68.0, P = 0.010
- Internalizing: 45.3(9.0) 29.0–76.0 vs. 44.6(8.4) 29.0–70.0, P = 0.43
- Externalizing: 48.4(9.5) 28.0–83.0 vs. 45.3(7.8) 28.0–67.0, P <0.001

Maternal characteristics:
- History of depression diagnosed before pregnancy (yes): 31(15.5%) vs. 18(9.9%), P = 0.071
- Antenatal trimester-weighted mean score of CES-D (0-60): 11.7(6.7) 1.0–39.8 vs. 11.2(6.7) 0.7–35.3, P = 0.49
- Age over 40 years at: 42(19.8%) vs. 34(17.4%), P = 0.31
delivery (yes)

<table>
<thead>
<tr>
<th>Description</th>
<th>Yes (n)</th>
<th>No (n)</th>
<th>p</th>
</tr>
</thead>
<tbody>
<tr>
<td>Insulin treated gestational diabetes mellitus in previous pregnancy (yes)</td>
<td>2 (0.9%)</td>
<td>1 (0.5%)</td>
<td>0.53</td>
</tr>
<tr>
<td>Sjögren’s syndrome (yes)</td>
<td>5 (2.4%)</td>
<td>2 (1.0%)</td>
<td>0.26</td>
</tr>
<tr>
<td>BDI-II score in early childhood follow-up</td>
<td>6.8 (7.1)</td>
<td>0.0–41.0</td>
<td>6.3 (6.1)</td>
</tr>
</tbody>
</table>

Note: BDI = Beck Depression Inventory; CES-D = Center for Epidemiological Studies Depression Scale; DNAm = DNA methylation
Table S2. Associations between maternal antenatal depression (history of depression diagnosed before pregnancy or Center for Epidemiological Studies Depression Scale score ≥ 16 vs. neither one) and child’s psychiatric problems at 3.7 years.

<table>
<thead>
<tr>
<th>Child’s psychiatric problems:</th>
<th>Boys (n=212)</th>
<th>Girls (n=195)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Mean difference: yes vs. no maternal antenatal depression</td>
<td>95% Confidence Interval</td>
</tr>
<tr>
<td>Total</td>
<td>0.51</td>
<td>(0.21;0.81)</td>
</tr>
<tr>
<td>Internalizing</td>
<td>0.46</td>
<td>(0.16;0.76)</td>
</tr>
</tbody>
</table>

Note: Model adjusted for child’s age at testing.