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Citation for published version:

Digital Object Identifier (DOI):
10.1016/j.psyneuen.2017.04.018

Link:
Link to publication record in Edinburgh Research Explorer

Document Version:
Publisher's PDF, also known as Version of record

Published In:
Psychoneuroendocrinology

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Maternal lipids in pregnancy are associated with increased offspring cortisol reactivity in childhood

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ARTICLE INFO

Prenatal programming of hypothalamic-pituitary-adrenal (HPA) axis activity has long term implications for offspring health. Biological mechanisms underlying programming of the offspring HPA axis are poorly understood. We hypothesised that altered maternal metabolism including higher maternal obesity, glucose and lipids are novel programming factors for altered offspring HPA axis activity. Salivary cortisol levels were measured in 54 children aged 3–5 years under experimental conditions (before and after a delay of self-gratification test). Associations of child cortisol responses with maternal obesity in early pregnancy and with fasting glucose, triglycerides, HDL and total cholesterol measured in each pregnancy trimester were tested. Higher levels of maternal triglycerides and total cholesterol throughout pregnancy were associated with increased offspring cortisol reactivity. The associations were independent of maternal obesity and other confounders, suggesting that exposure to maternal lipids could be a biological mechanism of in utero programming of the offspring’s HPA axis.

1. Introduction

Early life programming of the hypothalamic pituitary adrenal (HPA) axis is one of the key mechanisms proposed to link prenatal development with later life disease (Reynolds, 2013). Increased offspring HPA axis activity is associated with an adverse in utero environment and is observed at birth (Gitau et al., 2004), and persists through adulthood (Reynolds et al., 2001; van Montfoort et al., 2005). Altered HPA axis activity is associated with a range of health problems including an increased risk of metabolic disease, psychiatric symptoms, and cognitive decline (Chrousos, 2009; Constantinof et al., 2016). Mechanisms underlying the early life programming of the HPA axis remain poorly understood.

The evidence that physical and psychological adversity in prenatal or early postnatal life associates with altered child’s HPA axis activity has been systematically reviewed (Hunter et al., 2011). Yet few studies have considered biological mechanisms such as whether maternal metabolic status during pregnancy could alter the offspring HPA axis. In one study higher maternal body mass index (BMI) during pregnancy was not associated with salivary cortisol diurnal rhythm or stress reactivity in preschool children (Elhassan et al., 2015), but in another higher maternal central obesity during pregnancy predicted higher fasting plasma cortisol levels in 8.5 years-old children (Phillips et al., 2005). In children exposed to maternal gestational diabetes, there were no salivary cortisol differences following the Trier Social Stress Test for children (TSST-c) at age 13 (Krishnaveni et al., 2015). To our knowledge no studies have considered whether in utero exposure to other maternal metabolites, including lipids, influences the HPA axis responses in younger children.

We hypothesised that increased prenatal exposure to an adverse maternal metabolic milieu would be associated with altered child cortisol reactivity under experimental conditions. To test this hypothesis we studied a cohort of children born to mothers with very severe obesity (SO, BMI ≥ 40 kg/m² at first antenatal visit) and lean controls (BMI ≤ 25 kg/m²) in whom maternal metabolic profiles, including glucose and lipids had been characterized at gestational weeks 17, 28 and 36 (Forbes et al., 2015; Mina et al., 2015). Previously we reported that mothers with SO had higher glucose and lipids levels than the lean (Forbes et al., 2015), thereby providing a sample with variability among the maternal metabolic markers of interest. The case-control design of this larger cohort (SO vs. lean)
also enabled us to examine the consequences of exposure to maternal SO compared with lean on child cortisol reactivity. In the current study, we characterized children’s HPA axis responses by measuring salivary cortisol profiles under experimental conditions before and after a test of delay of self-gratification.

2. Methods

2.1. Participants

Participants were children aged 3–5 years born to SO or lean mothers who were taking part in a follow-up study of the consequences of exposure to obesity in pregnancy in Midlothian, Scotland (Forbes et al., 2015; Mina et al., 2015). Ethical approval (REC: 14/WS/1046, R & D: 2014/0278) and written consent were obtained from all participants. The protocol for the follow-up study has been previously described (Mina et al., 2017). We collected saliva samples for the measurement of cortisol levels from 79 term-born children under ‘experimental’ conditions i.e. before and after a test of self-gratification, the ‘Marshmallow Test’. Eight sample sets were incomplete and 17 could not be linked to maternal data, leaving 54 salivary cortisol profile datasets (31 lean and 23 SO) for analysis.

2.2. Saliva sample collections for cortisol measurement

Mothers were asked not to give their child drinks or food for at least half an hour before the appointment at the Wellcome Trust Clinical Research Facility for Children, the Royal Hospital for Sick Children, Edinburgh. Children’s saliva samples were collected before and after the Marshmallow Test, a test of delayed self-gratification (Mischel et al., 1989), which shows predictive validity on cognitive and behavioral outcomes in child- and adulthood (Mischel et al., 1989; Casey et al., 2011). Briefly, the children were presented with a single marshmallow and instructed that they may eat it immediately, but if they waited for 15 min, they would receive a second marshmallow as a reward. Thus the collection time of the after-test saliva samples ranged between 0 and 15 min depending on the test outcome. Marshmallows do not interfere with salivary cortisol levels (Clements et al., 2007), but the second saliva sample was always collected before any marshmallow reward was given. Children’s saliva samples were collected using SalivaBio Children’s Swab set (Salimetrics, Suffolk, UK) as per the manufacturer’s protocol, extracted from the cotton swab by centrifuging the tube at 3500 rpm (1500 g) for 15 min at 4 °C, and frozen at −80 °C.

2.3. Laboratory analyses

Salivary cortisol levels were measured by Enzyme-Linked Immunoabsorbent Assay (ELISA) using an expanded-range-high-sensitivity salivary cortisol enzyme immunoassay kit (Salimetrics, Pasadena, USA) as per the manufacturer’s protocol. Samples were run such that each 96-well plate contained randomly selected sample sets of children of both lean and SO mothers in duplicates. Plates were read at 450 and 490 nm by the Optimax tunable microplate reader using Softmax Pro 4.8 (Molecular Devices, Sunnyvale, USA).

The sample reading (B) = [reading at 450 nm] − [reading at 490 nm] − [mean reading from non-specific binding wells]. The values (B) were then divided by mean values of standard zero (Bo). The B/Bo sample values were fitted to a standard curve using Log (inhibitor) vs. response-variable slope (four parameters) of dose-response inhibition (Graphpad Prism 6, La Jolla, USA). When salivary cortisol levels were found to be > 3 μg/dl (maximal end-point of the standard curve), they were diluted using the diluent (Salimetrics’) as per the manufacturer’s protocol. When the salivary cortisol levels were < 0.012 μg/dl (minimal end-point of the standard curve), they were assumed to be = 0.012 μg/dl. Intra-assay coefficient of variation (CV) was 3.7% (all samples) and 4.7% (standard only) as compared to the manufacturer’s 4.6%. The inter-assay CV was 4.6% as compared to the manufacturer’s 6.0%.

2.4. Characterizing children’s salivary cortisol profile under experimental conditions

We quantified 3 output variables, including: 1) Δ = cortisol after test − cortisol before the test; 2) Area-under-the-curve- by increase (AUC) = [Δ × Δ time]/2; 3) steepness = Δ cortisol/Δ time, where Δ time represents the duration of the self-gratification delay. AUC indicates changes in salivary cortisol levels over the course of time, whereas steepness implies the individual cortisol reactivity to the experimental conditions.

2.5. Measurement of maternal prenatal metabolic markers

Maternal blood was sampled at 9 AM following an overnight fast three times during pregnancy as previously described (Forbes et al., 2015; Mina et al., 2015). Glucose levels were measured with a hexokinase-based assay and lipid components including triglycerides, HDL and total cholesterol with a colorimetric assay (Forbes et al., 2015).

2.6. Covariates and statistical analysis

We considered a number of potential covariates. The following covariates were excluded as the n < 10 and/or they were not significantly associated with dependent variables: gestational diabetes, maternal symptoms of prenatal and concurrent psychiatric distress, maternal smoking, level of socio-economic deprivation, time of saliva collection, seasonal variability. The final regression model included as covariates: maternal obesity status, child’s age at visit (in months), sex, parity and child birthweight obtained from hospital records.

Statistical analyses were performed using SPSS 23.0 and α = 0.05. The average levels of maternal metabolic measures across pregnancy were calculated. All independent and dependent variables were standardized; children’s cortisol variables were rank-normalised using Blom’s formula. Student’s t-tests (for continuous variables) and chi-square tests (for categorical variables) were used to compare the covariates and dependent variables between SO and lean groups. Student’s t-tests were applied to determine the associations of the covariates with the dependent variables, and to compare the levels of salivary cortisol according to the completion status of the Marshmallow Test. Paired Student’s t-test was used to compare the raw levels of salivary cortisol before and after the Marshmallow Test.

Linear regression analyses were used to determine the associations between the predictors including maternal SO status and the averaged levels of prenatal metabolic measures and the 3 output variables of the child’s cortisol profile. In the regression model of prenatal metabolic milieu, we adjusted for child’s sex, age, maternal SO status, parity and child’s birthweight. False Discovery Rate (FDR) with Benjamini- & Hochberg method was set at 0.1.

3. Results

3.1. Cohort demographic and variable descriptions and background associations

Compared to lean mothers, SO mothers had elevated triglycerides and lower HDL cholesterol levels during pregnancy, though glucose and total cholesterol levels were similar (Table 1). Children born to SO mothers had higher birthweight, and were older when enrolled into the follow-up study (Table 1). Table A1 describes the associations of children’s salivary cortisol profiles with the covariates.

3.2. Maternal prenatal metabolic milieu and child’s salivary cortisol profiles

In all children the average levels of salivary cortisol were higher after the Marshmallow Test than before (Mean difference after-before [SD], 0.03 [0.08] μg/dl, p = 0.003, Fig. 1). Furthermore, the levels of salivary cortisol collected after the test were also higher among the 10 (4 lean, 6 SO)
children who delayed gratification for 15 min as compared to those 
(n = 44, 26 lean, 18 SO) who ate the marshmallow before 15 min (mean 
[SD], complete vs. non-complete = 0.33 [0.12] vs. 0.19 [0.11] μg/dl, p = 0.002, 
Fig. 1). There were no differences in cortisol profile variables or derivatives 
between children of SO and lean mothers in unadjusted analyses 
(Table 1). However, following adjustments for the covariates in the regression 
analysis, maternal SO predicted significantly higher cortisol 
steepness (cortisol reactivity) during the Marshmallow Test (Table 1).

Maternal prenatal triglyceride and total cholesterol levels were signifi-
cantly correlated with higher child cortisol reactivity under experimental 
conditions. In the adjusted regression models (Table 2), higher averaged 
levels of maternal prenatal triglycerides (Δ [p = 0.004, p_{Adj} = 0.006], 
AUCi [p = 0.011, p_{Adj} = 0.013]) and total cholesterol levels (AUCi 
p = 0.02, p_{Adj} = 0.013) remained as significant predictors of increased child 
cortisol reactivity in experimental conditions. Neither maternal glucose or HDL 
levels were associated with child salivary cortisol profiles (Table 2).

### 4. Discussion

Our findings of associations between higher maternal obesity, and also of 
higher maternal lipids independent of obesity, and greater child cortisol 
reactivity under experimental conditions suggest a novel biological mecha-
nism underlying prenatal programming of the offspring HPA axis. 
Further, we have shown, for the first time that the Marshmallow Test a test 
of delay of self-gratification, elicits a cortisol response in 3–5 year old 
children.

The mechanisms underlying the link between associations of higher 
maternal triglycerides and total cholesterol levels with greater child cortisol 
reactivity under experimental conditions are unknown. In mice, pre-
natal exposure to a high fat diet was shown to alter gene expression levels of 
glucocorticoid receptor and its downstream inflammatory markers in the 
amygdala, resulting in heightened stress response (Sasaki et al., 2013), and 
slower recovery post-stress exposure (Grissom et al., 2017) suggesting 
programming of central HPA axis feedback sites. The lack of associations 
with glucose is consistent with the absence of salivary cortisol differences 
following the Trier Social Stress Test (TSST) in children exposed to gesta-
tional diabetes (Krishnaveni et al., 2015), suggesting that the programming of 
the HPA axis is metabolite-specific.

There remains debate about how best to evoke cortisol “stress re-

desponses” in young children under experimental conditions. The TSST is 
widely used in adult studies (Allen et al., 2014) and the modified version for 
children has been validated in children aged ≥7 years (Gunaratne et al., 2009; 
Kudielka et al., 2004). However, many of the challenges trialled in pre-
school children do not consistently elicit increased salivary cortisol (Gunarat 
et al., 2009). The Marshmallow Test was not originally designed as a stress 
test, but the unfamiliar environment, the strange situation (mother out of 
sight) and the frustrating task are likely stressors for young children (Gunarat 
et al., 2009). In this study, we observed increased average cortisol levels 
after the Marshmallow Test as compared to before the test, and in children 
who delayed gratification until 15 min as compared to those who failed the 
test. Further, we found associations of lower birthweight with elevated 
experimental cortisol profiles, suggesting heightened stress reactivity, and 
consistent with other studies showing links between low birthweight and 
increased HPA axis activity in later life (Reynolds et al., 2001; van Montfoort et al., 2005). Therefore, we believe that salivary cortisol levels
measured before and after the Marshmallow Test can be interpreted as a cortisol response to stress under experimental conditions.

The strength of this study include the prospective design with detailed biological measurements from the mother and the child. Although our sample size was small, the participants were representative of the maternal metabolic milieu of the larger cohort (Forbes et al., 2015) as no specific selection criteria were applied. Another strength is the use of a delay of gratification test as a “stress” test of cortisol reactivity. The limitations of the study include that we could not reliably examine moderation effects between maternal obesity and maternal metabolites on child cortisol reactivity due to low statistical power. Neither could we perform curvilinear analyses due to the case-control study design, nor distinguish the effects be- between maternal obesity and maternal metabolites on child cortisol reactivity due to stress markers from child programming.

5. Conclusions

Prenatal exposure to higher maternal lipids is associated with changes in the children’s cortisol reactivity in experimental conditions, independenly of maternal obesity, and other confounders. Alterations in maternal lipids could be a novel mechanism of in utero programming of the offspring HPA axis.

Conflicts of interest

None.

Acknowledgement

This study is funded by Tommy’s the Baby Charity, UK. THM thanks mother-and-baby participants for saliva sample provision, Joan Thomson and the rest of nurse team in the Clinical Research Facility, The Royal Hospital for Sick Children, NHS Lothian for sample processing and storage, Lynne Ramage, Neil Johnston, and Dr. Chris Kenyon for the guidance on ELISA. THM is funded by Principal Development Scholarship, Charles Darwin Scholarship and Global Research Scholarship, University of Edinburgh, Scotland. ML is funded by the Academy of Finland and University of Helsinki Funds. SF was supported by a Diabetes UK Clinical Intermediate Fellowship (BDA: RD04/0002483). AJD was supported by Scottish Senior Clinical Fellowship (SCD/09). We acknowledge the support of the British Heart Foundation and the Medical Research Council Centre Grant MR/N022556/1.

Appendix A

Table A1

Background associations of children’s salivary cortisol profiles with the covariates. The components of salivary cortisol profiles were rank-normalised and converted to z-scores prior to analysis.

<table>
<thead>
<tr>
<th>Sample</th>
<th>Glucose</th>
<th>Triglycerides</th>
<th>HDL</th>
<th>Total Cholesterol</th>
</tr>
</thead>
<tbody>
<tr>
<td>AUCi</td>
<td>-0.12 (0.44, 0.21)</td>
<td>0.42 (0.14, 0.70)</td>
<td>0.06 (0.28, 0.39)</td>
<td>0.33 (-0.04, 0.70)</td>
</tr>
<tr>
<td>Steepness</td>
<td>-0.82 (0.39, 0.22)</td>
<td>0.17 (0.13, 0.47)</td>
<td>-0.27 (-0.58, 0.05)</td>
<td>-0.24 (-0.60, 0.12)</td>
</tr>
</tbody>
</table>

AUCi = Area-under-the-curve by increase, implying changes over time. Δ = delta, the difference in cortisol levels across two time-points, Steepness = gradient of line created by changes in cortisol levels.

Bold text: italic, underlined text: p ≤ 0.1.

Table 2

Children’s cortisol reactivity was associated with higher levels of maternal triglycerides and total cholesterol across pregnancy

<table>
<thead>
<tr>
<th>B (95% CI), unadjusted</th>
<th>Glucose</th>
<th>Triglycerides</th>
<th>HDL</th>
<th>Total Cholesterol</th>
</tr>
</thead>
<tbody>
<tr>
<td>A, μg/dl</td>
<td>-0.06 (-0.37, 0.26)</td>
<td>0.42 (0.15, 0.69)</td>
<td>0.05 (-0.24, 0.33)</td>
<td>0.34 (0.00, 0.68)</td>
</tr>
<tr>
<td>Steepness</td>
<td>-0.02 (-0.33, 0.30)</td>
<td>0.25 (0.03, 0.54)</td>
<td>-0.18 (-0.46, 0.10)</td>
<td>-0.05 (-0.39, 0.30)</td>
</tr>
<tr>
<td>AUCi</td>
<td>-0.10 (0.43, 0.24)</td>
<td>0.39 (0.10, 0.67)</td>
<td>0.10 (-0.20, 0.41)</td>
<td>0.42 (0.07, 0.77)</td>
</tr>
</tbody>
</table>

AUCi = Area-under-the-curve by increase, implying changes over time. Δ = delta, the difference in cortisol levels across two time-points, Steepness = gradient of line created by changes in cortisol levels.

All associations were derived from the z-scores of both independent and dependent variables using multiple linear regressions. The regressions were adjusted for child’s sex and age at visit, maternal SO status, parity, and child’s birthweight.

Bold text: B with p ≤ 0.05, underlined text: p ≤ 0.1.
References


Grissom, N.M., George, R., Reyes, T.M., 2017. The hypothalamic transcriptional response to stress is severely impaired in offspring exposed to adverse nutrition during gestation. Neuroscience 342, 200–211.