The effect of pre-existing maternal obesity on the placental proteome: two-dimensional difference gel electrophoresis coupled with mass spectrometry

Karen Oliva1,2,3, Gillian Barker1,2,3, Clyde Riley2,3, Mark J Bailey1, Michael Permezel2,3, Gregory E Rice1 and Martha Lappas2,3

1UQ Centre for Clinical Research, The University of Queensland, Brisbane, Queensland, Australia
2Department of Obstetrics and Gynaecology and 3Mercy Perinatal Research Centre, Mercy Hospital for Women, University of Melbourne, Level 4/163 Studley Road, Heidelberg, Victoria 3084, Australia

(Correspondence should be addressed to M Lappas at Department of Obstetrics and Gynaecology, Mercy Hospital for Women, University of Melbourne; Email: mlappas@unimelb.edu.au)

Abstract

Our aim was to study the protein expression profiles of placenta obtained from lean and obese pregnant women with normal glucose tolerance at the time of term Caesarean section. We used two-dimensional difference gel electrophoresis (2D-DIGE), utilising narrow-range immobilised pH gradient strips that encompassed the broad pH range of 4–5 and 5–6, followed by MALDI-TOF mass spectrometry of selected protein spots. Western blot and quantitative RT-PCR (qRT-PCR) analyses were performed to validate representative findings from the 2D-DIGE analysis. Eight proteins were altered (six down-regulated and two up-regulated on obese placentas). Annexin A5 (ANXA5), ATP synthase subunit beta, mitochondria (ATPB), brain acid soluble protein 1 (BASP1), ferritin light chain (FTL), heterogeneous nuclear ribonucleoprotein C (HNRPC) and vimentin (VIME) were all lower in obese patients. Alpha-1-antitrypsin (A1AT) and stress-70 protein, mitochondrial (GRP75) were higher in obese patients. Western blot analysis of ANXA5, ATPB, FTL, VIME, A1AT and GRP75 confirmed the findings from the 2D-DIGE analysis. For brain acid soluble protein 1 and HNRPC, qRT-PCR analysis also confirmed the findings from the 2D-DIGE analysis. Immunohistochemical analysis was also used to determine the localisation of the proteins in human placenta. In conclusion, proteomic analysis of placenta reveals differential expression of several proteins in patients with pre-existing obesity. These proteins are implicated in a variety of cellular functions such as regulation of growth, cytoskeletal structure, oxidative stress, inflammation, coagulation and apoptosis. These disturbances may have significant implications for fetal growth and development.

Journal of Molecular Endocrinology (2012) 48, 139–149

Introduction

There is no disputing the extent of the worldwide obesity epidemic (Chu et al. 2008, Colagiuri et al. 2010). The proportion of women who are obese at the beginning of pregnancy has dramatically increased (Heslehurst et al. 2010). Obesity in pregnancy is associated with substantially increased risks for both mother and infant (Heslehurst et al. 2008). Gestational diabetes, pre-eclampsia, Caesarean section, instrumental vaginal delivery, birth trauma and pelvic floor damage are increased in the mother (Sebire et al. 2001, Bhattacharya et al. 2007). Infants born to overweight and obese mothers are often macrosomic (Ehrenberg et al, 2004, Surkan et al. 2004) with increased adiposity (Hull et al. 2008). Perhaps of greatest importance for the health system as a whole is that these infants are at increased risk of later metabolic disease, including obesity, diabetes, cardiovascular disease and certain cancers (Boney et al. 2005, Drake & Reynolds 2010).

The placenta plays a vital role in the regulation of fetal growth and development during pregnancy. Roles include nutrient supply to the fetus, removal from the fetus of metabolic waste and hormone production. Placental phenotypes for intrauterine growth restriction (McCarthy et al. 2007, Struve et al. 2010), pre-eclampsia (Hass et al. 2006, Dexlin-Mellby et al. 2010, Zhang et al. 2011) and diabetes in pregnancy (Radaelli et al. 2003, Zhao et al. 2011) have been described, but these have not specifically been studied in the context of maternal obesity. However, animal models have been crucial in delineating the impact of obesity on placental function. For example, maternal obesity and overnutrition alter fetal growth rate and cotyledonary vascularity and angiogenic factor expression in the ewe placenta (Ma et al. 2010). There is, however, a paucity of data on the effect of maternal
obesity in humans. For this reason, we considered it of interest to determine the effect of pre-existing maternal obesity on the protein expression profiles of human placenta. Thus, the aim of this study was to use two-dimensional difference gel electrophoresis (2D-DIGE) to identify novel proteins associated with pre-existing maternal obesity in human placenta. Validation of the 2D-DIGE data will be done by quantitative RT-PCR (qRT-PCR) and western blotting.

Materials and methods

Tissue collection

Approval for this study was obtained from the Mercy Hospital for Women’s Research (Heidelberg, Australia) and Ethics Committee and informed consent was obtained from all participating subjects. Human placenta was obtained from lean and obese pregnant women with normal glucose tolerance at the time of term Caesarean section before the onset of labour (Table 1). Indications for Caesarean section included repeat Caesarean section or breech presentation. Women with any adverse underlying medical condition (i.e. including asthma, diabetes and pre-eclampsia, polycystic ovary syndrome or thyroid or adrenal abnormalities) were excluded. None of the women conceived by artificial reproductive technology. Lean women were categorised as a body mass index (BMI) of <25 kg/m² and obese patients with a BMI of >30 kg/m². Placenta was collected from patients undergoing Caesarean section only to account for any effects of human labour and delivery on the protein profile. Placenta was obtained within 10 min of delivery and thoroughly washed in ice-cold PBS to remove any blood. Placental lobules (cotyledons) were obtained from various locations of the placenta; the basal plate and chorionic surface were removed from the cotyledon; and villous tissue was obtained from the middle cross-section. Placental tissue was blunt dissected to remove visible connective tissue and calcium deposits. Tissue samples were snap frozen in liquid nitrogen and immediately stored at −80 °C.

Sample preparation and DIGE labelling

Placenta (n=6 lean and n=6 obese) was homogenised into DIGE lysis buffer (30 mM Tris, 7 M urea, 2 M thiourea, 4% 3-(3-cholamidopropyl)dimethylammonio-l-propane sulphonate (CHAPS)). Proteins were extracted during 1 h at 4 °C, and lysates were clarified by centrifugation at 25 000 g at 4 °C for 20 min. The supernatant was precipitated with acetone, and protein extracts were then prepared following the general guidelines recommended for subsequent DIGE labelling. Briefly proteins were precipitated using the 2D clean-up kit (GE Healthcare, Piscataway, NJ, USA) and then buffer was exchanged against DIGE lysis buffer using Vivaspin-2 (3 kDa) concentrators (Sartorius Stedim, Goettingen, Germany) until conductivity could be reduced to below 200 μS/cm and the pH was adjusted to ~8-5.

A lean pooled sample and an obese pooled sample were obtained (containing 50 μg of each sample; 300 μg total in each pool). This was then labelled with 400 pmol of Cy3 (obese samples) or Cy5 (lean samples; CyDye DIGE Fluors; GE Healthcare). Labelling was performed on ice and in the dark for 30 min. The reaction was then quenched by incubating with 1-5 μl of 10 mM lysine on ice and in the dark for 10 min. The Cy3-labelled obese samples were then combined with the Cy5-labelled lean samples and used for 2D gel electrophoresis analysis as detailed below.

OFF-GEL fractionation

To perform peptide fractionation according to their pI, the 3100 OFF-GEL fractionator and the OFF-GEL kit (both from Agilent Technologies, Waldbronn, Germany) were used following the manufacturer’s

<table>
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<th>Clinical characteristic</th>
<th>2D-DIGE study</th>
<th>Validation study</th>
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<td>Maternal age (years)</td>
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<td>32.3±1.6</td>
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<td>20.4±0.8</td>
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<td>Gestational age at birth (weeks)</td>
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<td>Fetal birth weight (g)</td>
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<td>3295±135</td>
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<tr>
<td>Fetal gender</td>
<td>3 Females; 3 males</td>
<td>5 Females; 5 males</td>
</tr>
<tr>
<td>Gravida</td>
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<td>2.8±0.4</td>
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<tr>
<td>Parity</td>
<td>2.3±0.3</td>
<td>2.1±0.3</td>
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</table>

*P < 0.05 vs lean (Student’s t-test).
instructions. The device was set up for the 12 fractions separation by using a 13 cm long immobilised pH gradient (IPG) gel strip with a linear pH gradient ranging from 4 to 7. Six hundred micrograms of DIGE-labelled placenta (pooled placenta samples from six Cy3-labelled obese and six Cy5-labelled lean) were re-suspended with focusing buffer to a final volume of 1.8 ml. One hundred and fifty microlitres of this sample were loaded in each of the 12 wells. The sample was focused using the recommended method for OFF-GEL protein 12 wells fractionation with a maximum current of 50 μA. The focusing was stopped after total voltage reached 20 kVh. After focusing, 50–200 μl of the liquid upper phase sample were recovered for each well and pooled according to their pI. The two fractions used for this study were 4–5 and 5–6.

2D gel electrophoresis and imaging

The two fractions pools were precipitated with acetone, and protein extracts were then prepared following the general guidelines recommended for subsequent DIGE labelling. Briefly proteins were precipitated using the 2D clean-up kit (GE Healthcare) and then buffer was exchanged against DIGE lysis buffer using Vivaspin 2 (3 kDa) concentrators (Sartorius) until conductivity could be reduced to below 200 μS/cm and the pH was adjusted to ~8.5. Proteins were focused on 11 cm, 3-9-5-1 and 4-7-5-9 IPG strips (Bio-Rad). Strips were rehydrated actively at 50 V and then focused overnight. IEF was performed for a total of ~35 000 Vh at 20 °C. IPG strips were then equilibrated in equilibration buffer (50 mM Tris–HCl, 6 M urea, 30% glycerol, 2% SDS) supplemented with 1% dithiothreitol to maintain the fully reduced state of proteins, followed by 2.5% iodoacetamide to prevent re-oxidation of thiol groups during electrophoresis. Proteins were separated on 10-5–14% Criterion Tris–HCl gels (Bio-Rad Laboratories) at 15 mA/gel for 60 min, 30 mA/gel for 2 h and 45 mA/gel for 30 min at room temperature until the bromophenol blue dye-front had run off the bottom of the gels.

CyDye DIGE Fluor-labelled protein gels were scanned at 100 μm using a Typhoon Trio 9100 (GE Healthcare). The emission filters were Green 532 nm (Cy3) and Red 633 nm (Cy5). Gels were automatically aligned and relative protein quantification across lean and obese samples was performed using the Progenesis SameSpots Software 3.3.3.420.25059 (Nonlinear Dynamics, Newcastle upon Tyne, UK). Normalisation was performed using the software algorithm. Student’s t-test was used to calculate significant differences in relative abundances of protein spot features in placenta obtained from lean and obese pregnant women.

The 2D gels were fixed in 50% methanol, 3% phosphoric acid and then stained with Colloidal Coomassie stain and gels spots of interest were excised using a gel pen. Gel spots were then transferred into water for short-term storage at 4 °C. The water was subsequently removed and discarded from each gel plug. Gel pieces were destained by four sequential washes in destaining solution (10 mM ammonium bicarbonate (AmBic), 50% acetonitrile (ACN)), followed by two washes in 100% ACN, and then air dried at room temperature. The gel pieces were rehydrated by adding 10 μl of sequencing grade trypsin (0-02 μg/μl (Promega) in 10 mM AmBic) and left to incubate overnight at 37 °C. Digestion was quenched by addition of 2 μl of 2% formic acid (FA).

To avoid labelling bias arising from the varying fluorescence properties of gels at different wavelengths, samples from the same group were run twice in different gels but with the opposite dye labelling pattern. The Cy channels were individually imaged from each of the two gels using mutually exclusive excitation and emission wavelengths.

MALDI-TOF mass spectrometry and protein identification

Three microlitres of digest supernatant were applied to a Bruker Biosciences Anchorchip MALDI target, prepared with α-cyano-4-hydroxycinnamic acid (CHCA; see the thin layer affinity method for CHCA in the Bruker Anchorchip Manual). After 3 min, this solution was removed and the spots were air dried overnight at room temperature. MALDI-mass spectrometry (MS) was performed on a Bruker Microflex MALDI-TOF mass spectrometer (Bruker Daltonics, Bremen, Germany). Peaklists were generated using Flexanalysis (Bruker Daltonics) and were calibrated by utilising trypsin autolytic peptides. Biotools Software (Bruker Daltonics) and the Mascot search engine were used to interrogate the SwissProt database (release: July 2010, 517802 sequences; 18249287 residues) and proteins were identified by peptide mass fingerprinting. Search parameters were: taxonomy: human; MS tolerance, 100 ppm; missing cleavages, ≤1; enzyme, trypsin; fixed modifications, carbamidomethylation and variable modifications, oxidation (M). Identifications with Mascot expect probability values <0-05 were then manually verified by examination of spectra and/or resubmission of peak lists to Mascot. We took a conservative approach to protein identification and based acceptance on a number of criteria other than these scores. These included theoretical and experimental Mr and pI being in accord, experimental peptide mass accuracy variation across the mass range and repeatability of identification across different gels. If multiple members of a protein family were identified those with the highest ranked hit were selected.
RNA extraction and RT-PCR

Total RNA was extracted from ~100 mg of tissue using Tri reagent according to the manufacturer’s instructions (Sigma–Aldrich). RNA concentrations were quantified using a spectrophotometer (Smart Spec; Bio-Rad). RNA quality was determined via the A260/A280 ratio. One microgram of RNA was converted to cDNA using the SuperScript VILO cDNA synthesis kit (Invitrogen) according to the manufacturer’s instructions. The cDNA was diluted tenfold, and 2 μl of cDNA were used to perform RT-PCR using Sensimix Plus SYBR green (Quintace, Alexandria, NSW, Australia) and 100 nM of QuantiTect Primer Assays (Qiagen). Pre-validated primers for brain acid soluble protein 1 (BASP1; QT01672923) and GAPDH (QT01192646) were purchased from Qiagen. Average gene Ct values were normalised to the average GAPDH values of the same cDNA sample. The specificity of the product was assessed from melting curve analysis. RNA without reverse transcriptase during cDNA synthesis as well as PCR reactions using water instead of template showed no amplification. Gene expression levels were determined using the comparative threshold cycle (Ct) method.

Western blotting

For protein detection by western blot analysis, tissue was homogenised in radioimmuno precipitation assay buffer (1% SDS, 0.25% sodium deoxycholate, 1% Nonidet P-40, 150 mM NaCl, 50 mM Tris–HCl, pH 7.4), supplemented with protease inhibitors (1 mM EDTA, 0.5 mM phenylmethylsulfonyl fluoride, 10 μg/ml aprotinin and 5 μg/ml leupeptin). Cellular debris and lipids were eliminated by centrifugation of the solubilised samples at 25 000 g for 30 min (4°C). Protein concentration was determined by the BCA Protein Assay (Pierce, Rockford, IL, USA).

Assessment of protein expression was analysed by western blotting as previously described (Lappas et al. 2003). Membranes were incubated with mouse monoclonal anti-alpha-1-antitrypsin (A1AT), Clone IC2 (SAB4200198; Sigma) at 0.6 μg/ml; mouse monoclonal anti annexin A5 (ANXA5; WH0000308M1; Sigma) at 1 μg/ml; rabbit polyclonal anti ATP synthase subunit beta, mitochondria (ATPB; HPA001520; Sigma) at 0.2 μg/ml; rabbit polyclonal anti stress-70 protein, mitochondrial (GRP75; HPA000898; Sigma) at 0.1 μg/ml; mouse monoclonal anti vimentin (VIME; clone V9, N1421; Dako) at 2 μg/ml; rabbit polyclonal anti-ferritin light chain (FTL; F8556; Sigma) at 1 μg/ml; rabbit polyclonal anti-ferritin heavy chain (FTH; F8306; Sigma) at 1.8 μg/ml; and mouse monoclonal anti-β-tubulin (T8328; Sigma) at 1.2 μg/ml. The antibodies were diluted in blocking buffer (5% skim milk/tris-buffered saline–Tween (TBS–T; 0.05%)) for 24 h at 4°C. Membranes were stripped and probed with mouse monoclonal anti-β-tubulin (T8328; Sigma) for normalisation of the data. Membranes were viewed and analysed using the Chemi-Doc system (Bio-Rad). Quantitative analysis of the relative density of the bands in western blots was performed using Quantity One 4.2.1 image analysis software (Bio-Rad). Data were corrected for background and then normalised to β-tubulin expression.

Immunohistochemistry

Placenta was placed in embedding cassettes fixed in buffered formaldehyde solution (4%) and embedded in paraffin. Serial sections (4 μm thick) were cut and mounted on sections onto superfrost plus slides. Slides were prepared consecutively for each sample. Each site was immunolabelled with each of the antibodies and one was used as a negative control slide. Sections were deparaffinised followed by an antigen retrieval step (boiled in 10 mM citrate buffer, pH 6.0 for 10 min followed by 20 min incubation). Endogenous peroxidase activity was removed using 3% H2O2 in methanol for 10 min. Sections were transferred to TBS (20 mM Tris pH 7.6, 150 mM NaCl). The sections were incubated in a humidity chamber for 1 h in antibody diluted in 1% BSA in TBS. The primary antibodies are detailed above (see Western blotting section). After incubation the binding sites were labelled with Dako Envision+ polymer linked secondary reagent and visualised using Dako DAB+ (DakoCytomation, Dako, Campbellfield, Vic, Australia). Nuclei were counterstained with Mayer’s haematoxylin and the sections were dehydrated and cover slipped using a resinous mounting agent. Positive controls, which were composite slides with tonsil, breast tumour and ovarian tumour, were included in each run. Negative control slides, where primary antibody was replaced with normal mouse or rabbit IgG serum, were also included.

Statistical analysis

Statistical analyses were performed using a commercially available statistical software package (Statgraphics Plus version 3.1, Statistical Graphics Corp., Rockville, MD, USA). Student’s t-test was used to assess statistical significance of the data. Statistical difference was indicated by a P value of <0.05. Data are expressed as mean ± S.E.M.

Results

Analysis of the patient characteristics

Demographic data of the participants involved in this investigation are summarised in Table 1. All women in
the lean group had a BMI of $< 25 \text{ kg/m}^2$, whereas all women in the obese group had a BMI of $> 30 \text{ kg/m}^2$. There were no significant differences in maternal age, fetal birth weight, gravid, parity and gestational age at delivery between the two sample groups.

Identification of differentially expressed proteins using 2D-DIGE

By using 2D-DIGE, we analysed the placenta proteome from a group of 12 individuals, six lean and six obese. Images for the two pH ranges are presented in Fig. 1. A total of 38 spots were positively identified; corresponding to 27 distinct proteins. Figure 2 shows the position of these spots in the 2D-DIGE gel. Table 2 displays detailed information about the corresponding proteins identified. This table summarises the protein accession number of identified muscle proteins, Mascot scores, the number of matched peptide sequences, the percentage sequence coverage, molecular mass, pI value, accession number, average normalised values and fold change of individual proteins affected by obesity.

ANXA5, ATPB, BASP1, FTL, heterogeneous nuclear ribonucleoprotein C (HNRPC), and VIME were all 1.5-fold higher in lean patients. On the other hand, A1AT and GRP75 were 1.5-fold higher in obese patients.

Validation of proteomic results by qRT-PCR and immunoblot analysis

Western blot and qRT-PCR analyses were used to validate representative findings from the 2D-DIGE analysis. In this study, we used the same six patients whose samples were used in the 2D-DIGE, plus an additional four lean and four obese pregnant women. For normalisation of the data, we used β-tubulin as the 2D-DIGE showed that this was unchanged between the two sample groups. As shown in Figs 3 and 4, the western blot analysis confirmed the 2D-DIGE data. That is, in obese placenta, the protein expression of cleaved A1AT (Fig. 3A) and GRP75 (Fig. 3B) was significantly higher than lean placenta. On the other hand, lower protein expression of ANXA5 (Fig. 4A), ATPB (Fig. 4B), FTL (Fig. 4C) and VIME (Fig. 4E) was observed in placentas obtained from obese women compared to placentas obtained from lean women. Given that ferritin consists of both a heavy and a light chain, we also chose to analyse FTH. As shown in Fig. 4D, FTH protein expression was also significantly lower in placenta obtained from obese women. For BASP1 and HNRPC, we could not find suitable antibodies, thus qRT-PCR was used to confirm the 2D-DIGE data. As shown in Fig. 5, BASP1 mRNA expression was significantly lower in placentas obtained from obese women. For HNRPC was lower in obese placentas, this just failed to reach significance ($P=0.07$).

Localisation of A1AT, FTL and FTH in human placenta

Immunohistochemistry was used to determine the cellular localisation of A1AT, FTL, FTH, ANXA5, ATPB, GRP75 and VIME in human placenta. Placenta exhibited extensive cytoplasmic A1AT staining, which was mainly localised to the syncytiotrophoblast layer and endothelial cells (Fig. 6A). Some A1AT staining was also observed within the villous stoma. FTL (Fig. 6B) and FTH (Fig. 6C) staining was predominantly found.
within the villous stroma, although some staining was also observed in the endothelial cells and the syncytiotrophoblasts. For ANXA5 (Fig. 6D) and ATP5B (Fig. 6E), staining was observed in the syncytiotrophoblast layer. GRP75 was localised to the syncytiotrophoblast layer and the endothelial cells (Fig. 6F), and VIME expression was restricted to the villous stroma of the placenta (Fig. 6G). No staining was present in the negative controls (Fig. 6H).

### Discussion

In this study, we have used 2D-DIGE to determine the effect of pre-existing maternal obesity on the protein profile of human placenta. Using MALDI-TOF MS, we were able to successfully identify 40 protein spots, which corresponded to 29 distinct proteins. Maternal obesity was associated with an up-regulation of three proteins; A1AT, serum albumin (ALBU) and GRP75.

### Table 2 Human placental proteins identified by 2D-DIGE and by MALDI-TOF MS

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<th>Accession no.</th>
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<th>pI value</th>
<th>No. of matched peptides</th>
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other hand, a total of six proteins were found to be down-regulated in the obese placenta. These were ANXA5, ATPB, BASP1, FTL, HNRPC and VIME. Western blot analysis and qRT-PCR analyses of proteins confirmed the 2D-DIGE data. Immunohistochemistry was also used to determine the localisation of protein in human placenta. The roles of these proteins in the regulation of placental function, and how they may influence fetus, are discussed below.

Inflammation

Exposure of the fetus to an intrauterine inflammatory environment may have short and long-term consequences, including developmental programming of obesity (Taylor & Poston 2007). In this study, we found evidence of increased inflammation in the placenta. This is consistent with previous studies demonstrating increased accumulation of a heterogeneous macrophage population and pro-inflammatory mediators in obese placentas (Challier et al. 2008).

A1AT is a 52 kDa protease inhibitor belonging to the serpin superfamily (Gettins 2002). It protects tissues from enzymes of inflammatory cells, especially neutrophil elastase, and as such its circulating levels rise upon acute inflammation. However, inactivation of A1AT is associated with cleavage of A1AT (~4000 kDa lower). In this study, 2D-DIGE revealed a significant increase in cleaved A1AT in obese placenta, which was confirmed by western blotting. In previous studies, term placental syncytiotrophoblast and Hofbauer cells were positively stained for A1AT (Castellucci et al. 1994). Similarly, in this study, A1AT was localised to the syncytiotrophoblasts and the endothelial cells. Pro-inflammatory cytokines TNFα and interleukin 6 induce A1AT in human amnion (Subramaniyam et al. 2009) and A1AT enhances the magnitude of LPS-induced specific cytokine/chemokine production (Subramaniyam et al. 2010) via the transcription factors NF-κB and AP-1 (Dichtl et al. 2000), which may play an important role in amplification of acute-phase inflammatory reactions. ANXA5 has anti-inflammatory, anti-thrombotic and anti-apoptotic properties (Leon et al. 2006, Ewing et al. 2011). It has previously been detected on trophoblasts in the placenta (Shu et al. 2000) and lower ANXA5 expression has been observed in placentas from pregnancies complicated with pre-eclampsia (Shu et al. 2000) and fetal growth restriction (Sifakis et al. 2010). Collectively, increased cleaved A1AT and lower ANXA5 expression in obese placentas is suggestive of increased inflammation in the placenta.

Oxidative stress

Oxidative stress disturbs placental function leading to perturbations in fetal growth and development (Lappas et al. 2011). Animal models have been very useful to demonstrate that increases in reactive oxygen species (ROS), together with increases in reactive nitrogen species, are clearly related to the induction of malformations in the fetus (Lappas et al. 2011). In this study, we found increased expression of proteins that involved in the generation of ROS as well as increased expression of proteins with antioxidant properties.

Ferritin consists of both a light and a heavy chain (FTL and FTH respectively), which share about 50% sequence homology (Theil 1987). In this study, 2D-DIGE revealed a decrease in FTL expression in obese placenta, which was confirmed by immunoblotting. In addition, western blotting also revealed a significant decrease in FTH protein expression. Ferritin is a protein that is involved in the formation of the highly damaging ROS hydroxyl radical (OH·; Bacic et al. 2008). FTL and FTH were mainly found in the villous...
Maternal obesity and the placenta

Maternal obesity down-regulates (A) ANXA5, (B) ATPB, (C) FTL, (D) FTH and (E) VIME protein expression in human placenta. Data represent the mean ± S.E.M. (n = 10 per group). *P < 0.05 vs lean placenta. A western blot image is shown demonstrating the data for eight patients (four lean and four obese) or 14 patients (seven lean and seven obese).

Figure 4

Maternal obesity down-regulates (A) ANXA5, (B) ATPB, (C) FTL, (D) FTH and (E) VIME protein expression in human placenta. Data represent the mean ± S.E.M. (n = 10 per group). *P < 0.05 vs lean placenta. A western blot image is shown demonstrating the data for eight patients (four lean and four obese) or 14 patients (seven lean and seven obese).

Proliferation and differentiation

Changes in placental structure and thus function may adversely affect fetal development. We are not aware of any detailed studies that have examined the effect of maternal obesity on placental structure. However, in this study, we found decreased expression of proteins involved in cell integrity and structure.

BASP1 and VIME are proteins implicated in the maintenance of the cell integrity and the stabilisation of the cytoskeletal interactions (Goldman et al. 1996, Korshunova et al. 2008); as such, they play roles in adhesion, migration, survival and cell signalling. HNRPC is a nuclear pre-mRNA binding protein that has also been implicated in cell proliferation (Kim et al. 2003, Schepens et al. 2007) and DPY30 is a protein involved in differentiation (Jiang et al. 2011). All these human pathologies, including obesity and diabetes (Hojlund et al. 2003, Ritov et al. 2005). The decrease in ATPB expression in obese placentas may lead to mitochondrial dysfunction, leading to an accumulation of lipid metabolites (Vankoningsloo et al. 2006, Mailloux et al. 2007). An accumulation of lipid metabolites could, in turn, partially explain the insulin signalling defects reported in placentas from obese pregnant women (Colomiere et al. 2009). Of note, ATPB is also lower in syncytiotrophoblasts of pre-eclamptic placentas (Hache et al. 2011).

Heat shock proteins act as chaperones, thus having pivotal roles in the cellular stress responses (Prohaszka & Fust 2004). Of note, GRP75 protein, which is primarily localised to the mitochondria, is triggered by oxidative injury (Wadhwa et al. 2002). Increased GRP75 in obese placentas may be part of a stress-adaptive response that may be critical for the protection against oxidative damage, such as that which may be induced by low FTL and FTH or ATPB observed in this study.

Figure 5

Maternal obesity down-regulates BASP1 and HNRPC mRNA expression in human placenta. Data represent the mean ± S.E.M. (n = 10 per group). *P < 0.05 vs lean placenta.
proteins were down-regulated in the obese placenta, which is in keeping with recent studies suggesting that placental proliferation may be reduced in relation to increasing maternal early pregnancy BMI (Higgins et al. 2010).

Study limitations

There are a few limitations to this study. The initial 2D-DIGE data was not stratified according to gender, although equal numbers of males and females were included. However, when the western blotting data was stratified according to gender, there was no difference in expression between males and females (data not shown).

Concluding comments

In this study, we provide evidence demonstrating that maternal obesity at conception affects the protein profile of human placenta, which may have implications for fetal growth and development. Indeed, obesity reduces oxygen supply to unborn baby (El Baky et al. 2010) and neural tube defects and other developmental anomalies are more common in infants born to obese women (Stothard et al. 2009). Further to this, infants born to obese mothers have increased risks of developing the metabolic syndrome later in life (Boney et al. 2005, Taylor & Poston 2007). By further understanding the role of maternal diet and body composition on placental function, we may be able to prevent the intergeneration transmission of disease.

Declaration of interest

The authors declare that there is no conflict of interest that could be perceived as prejudicing the impartiality of the research reported.

Funding

Dr M L was a recipient of a National Health and Medical Research Council (NHMRC) RD Wright Fellowship (grant number 454777). The work described in this manuscript was funded, in part, by a project grant from NHMRC (grant number 454310). Funding for the ChemiDoc system, xMark Microplate Absorbance Spectrophotometer and Leica Qwin Image Analysis System was provided by the Medical Research Foundation for Women and Babies. Proteomic data analysis described in this work was supported by the use of the Australian Proteomics Computational Facility funded by the Australian NHMRC (grant number 381413).

Author contribution statement

M L conceived the idea, designed the study, analysed the data and wrote the manuscript. K O, G B, M J B and C R performed the 2D-DIGE experiments. G E R reviewed the manuscript. M P assisted in patient analysis.

Acknowledgements

The authors gratefully acknowledge the assistance of the Clinical Research Midwives Gabrielle Fleming, Astrid Tiefholz, Lyndall Paolucci, Debra Jinks and Asha Ferguson; and the Obstetrics and Midwifery staff of the Mercy Hospital for Women for their co-operation.

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Received in final form 29 January 2012
Accepted 1 February 2012
Made available online as an Accepted Preprint 1 February 2012