Mitochondrial dysfunction in oocytes of obese mothers: transmission to offspring and reversal by pharmacological endoplasmic reticulum stress inhibitors

Linda L. Wu1, Darryl L. Russell1, Siew L. Wong1, Miaoxin Chen1, Te-Sha Tsai2, Justin C. St John2, Robert J. Norman1, Mark A. Febbraio3, John Carroll4 and Rebecca L. Robker1,*

ABSTRACT

Over-nutrition in females causes altered fetal growth during pregnancy and permanently programs the metabolism of offspring; however, the temporal and mechanistic origins of these changes, and whether they are reversible, are unknown. We now show that, in obese female mice, cumulus-oocyte complexes exhibit endoplasmic reticulum (ER) stress, high levels of intracellular lipid, spindle abnormalities and reduced PTX3 extracellular matrix protein production. Ovulated oocytes from obese mice contain normal levels of mitochondrial (mt) DNA but have reduced mitochondrial membrane potential and high levels of autophagy compared with oocytes from lean mice. After in vitro fertilization, the oocytes of obese female mice demonstrate reduced developmental potential and form blastocysts with reduced levels of mtDNA. Blastocysts transferred to normal weight surrogates that were then analyzed at E14.5 showed that oocytes from obese mice gave rise to fetuses that were heavier than controls and had reduced liver and kidney mtDNA content per cell, indicating that maternal obesity before conception had altered the transmission of mitochondria to offspring. Treatment of the obese females with the ER stress inhibitor salubrinal or the chaperone inducer BGP-15 before ovulation increased the amount of the mitochondrial replication factors TFAM and DRP1, and mtDNA content in oocytes. Salubrinal and BGP-15 also completely restored oocyte quality, embryo development and the mtDNA content of fetal tissue to levels equivalent to those derived from lean mice. These results demonstrate that obesity before conception imparts a legacy of mitochondrial loss in offspring that is caused by ER stress and is reversible during the final stages of oocyte development and maturation.

KEY WORDS: BGP-15, ER stress, Mitochondria, mtDNA, Obesity, Ovary

INTRODUCTION

Over-nutrition in females, including humans, re-programs offspring metabolism, causing altered fetal and postnatal growth trajectories (Srinivasan et al., 2006; Samuelsson et al., 2008; Shankar et al., 2008; Rattanatray et al., 2010; Ruager-Martin et al., 2010; Yan et al., 2011). Studies in rodent obesity models have demonstrated that maternal over-nutrition contributes at very early stages to offspring metabolic programming through altering the periconception oocyte and development of the pre-implantation embryo (Minge et al., 2008; Igosheva et al., 2010; Jungheim et al., 2010; Wu et al., 2010; Shankar et al., 2011; Luzzo et al., 2012). Impaired fertility also commonly occurs with obesity; for instance, overweight women often require assisted reproductive technologies, such as in vitro fertilization (IVF), and their success rates are lower, owing to poor oocyte developmental potential (Cardozo et al., 2011). However, the fundamental mechanisms in the oocyte and pre-implantation embryo that are changed by maternal over-nutrition, determining fertility potential and establishing the metabolic phenotype of the offspring, are unknown.

Our previous studies have demonstrated that mouse cumulus oocyte complexes (COCs) exhibit lipotoxicity responses in association with obesity or following treatment with high levels of lipids in vitro (Wu et al., 2010, 2012). Lipotoxicity is a cellular response to a high lipid extracellular environment, including high levels of triglyceride, cholesterol and/or free fatty acids, which increase intracellular lipid accumulation and damage organelles, particularly endoplasmic reticulum (ER) and mitochondria (Schaffer, 2003; Borradaile et al., 2006). Impaired ER function, or ER stress, disrupts protein secretion pathways and triggers the unfolded protein response (UPR) (Kauffman, 1999; Ozcan and Tabas, 2012) – adaptive mechanisms to restore protein folding, particularly in secretory cells. In parallel, Ca2+ released from the ER disrupts mitochondrial membrane potential and increases production of reactive oxygen species (ROS), triggering oxidative stress (Malhotra and Kaufman, 2007; Vannuvel et al., 2013). These stressors initiate compensatory survival responses, such as the induction of protein-folding chaperones and autophagy to remove aggregated proteins and damaged organelles; however, if homeostasis is not achieved, cells ultimately undergo apoptosis (Kim et al., 2008; Shore et al., 2011). In mice that have been fed high fat diets, oocytes accumulate lipid, exhibit markers of ER stress and increased ROS, and have altered mitochondrial ultrastructure and membrane potential (Igosheva et al., 2010; Wu et al., 2010; Luzzo et al., 2012). We hypothesize that these disruptions to oocyte organelles are linked and that ER stress underpins the impact of obesity on oocyte developmental potential and offspring metabolism.

Mitochondria are essential for the generation of ATP during oocyte maturation and blastocyst formation (Van Blerkom et al., 1995; Dunollard et al., 2007). Studies using mice lacking TFAM, a nuclear-encoded mitochondrial (mt)DNA replication factor, demonstrate that oocytes must contain threshold numbers of mitochondria, with 40,000 to 50,000 copies of mtDNA, in order for an embryo to give rise to a viable fetus (Wai et al., 2010). Furthermore, because oocyte-derived
RESULTS

Blobby mice exhibit obesity, hyperinsulinemia and dyslipidemia on a chow diet

Female Alms1 mutant mice anecdotally exhibit infertility following the onset of obesity (Arsov et al., 2006) (Australian Phenome Bank, personal communication); however, the underlying reason for this infertility is unknown. We used the Blobby (bbb/bbb) mouse strain to characterize the metabolic defects in females and to determine whether there are defects in ovulation and/or oocyte quality that contribute to their obesity-induced sub-fertility. Female Blobby mice developed significantly increased body weights relative to wild-type and heterozygous littersmates from 5 weeks of age (Blobby, 18.4±0.3 g; wild type, 17.1±0.2 g; heterozygous, 16.7±0.2 g; *P<0.0002, one-way ANOVA at week 5). This excessive weight gain increased progressively with age (Fig. 1A), such that at 14 weeks of age, Blobby mice weighed 36.0±0.5 g, whereas the average weight of wild-type littersmates was 23.6±0.6 g and that of heterozygotes was 22.7±0.5 g (Fig. 1A; *P<0.0001, one-way ANOVA at week 14). Thus, at 14 weeks of age, Blobby mice weighed on average 12.5 g, or 53%, more than wild-type littermates (Fig. 1B). This increased body weight was associated with a 230% increase in abdominal adipose tissue mass (Fig. 1C) and a 53% increase in liver mass (Fig. 1D). The Blobby mice also had significantly higher levels (9.7-fold) of circulating insulin than wild-type littersmates (Fig. 1E), indicating insulin resistance, but circulating glucose was not different (Fig. 1F). Cholesterol,
triglycerides and free fatty acids were also significantly higher (60-74% increased) in Blobby females compared with that of wild-type littermates (Fig. 1G-I). These data demonstrate that Blobby female mice develop hyperinsulinemia and hyperlipidemia by 14 weeks of age, whereas hyperglycemia is not evident.

**Ovulatory dysfunction in obese mice is reversed by ER stress inhibitors**

When treated with ovulatory gonadotropins, the ovaries of Blobby mice often exhibited non-ovulated follicles, which were rarely observed in non-obese wild-type and heterozygous littermates (Fig. 2A; supplementary material Fig. S1). The number of ovulated COCs found in the oviduct was significantly reduced in Blobby mice compared with non-obese littermates (Fig. 2B). At 6 weeks of age, Blobby mice were on average just 1.5 g heavier than wild-type and heterozygous littermates (see Fig. 1A), and ovulation following treatment with gonadotropins was not impaired (Fig. 2B, right panel), demonstrating that impaired oocyte release in Blobby mice is due to obesity rather than the *Alms1* mutation. Treatment of mice with either salubrinal (1 mg/kg) or BGP-15 (100 mg/kg) once daily for 4 days increased the ovulation rate with a significant improvement in response to BGP-15, particularly in obese Blobby mice, where the ovulation rate was more than doubled from an average of 7.5 to 18.8 oocytes per mouse (Fig. 2B). The ability of BGP-15 to increase the ovulation rate in lean mice was verified in additional 8-week-old C57 mice (supplementary material Fig. S2). Treatment of mice (lean or obese) with salubrinal or BGP-15 had no effect on body weight (data not shown).

**Oocyte complexes in obese mice exhibit gene expression and protein changes associated with ER stress**

To determine whether ER stress occurs in COCs of obese Blobby mice on a standard diet, similar to that of COCs of mice fed a high fat diet (Wu et al., 2010), the mRNA expression of ER stress markers (*Aft4*, *Atf6* and the spliced *Xbp1* transcript (*Xbp1s*)) and chaperones (*Hspa5*, *Hspa1a* and *Hspa1b*) was measured in ovulated COCs and granulosa-lutein cells of gonadotropin-treated 14-week-old Blobby mice and compared with those of wild-type and heterozygous littermates. Ovulated COCs from Blobby mice had significantly increased expression of *Atf4*, *Hspa1a* and *Hspa1b* compared with wild-type littermates (Fig. 3), and tended to have higher expression levels of *Atf6* (not shown) and *Xbp1s*, reflective of...
activation of the UPR. COCs from obese mice that had been treated with BGP-15 had significantly decreased expression of Atf4 but increased expression of Xbp1s, Hspa1a and Hspa1b (Fig. 3). Similar effects were observed in granulosa-lutein cells that were isolated at the same timepoint as the COCs. Cells from obese Blobby mice had significantly increased expression of Hspa1a and Hspa1b (Fig. 3), and tended to have higher expression of Atf4, Xbp1s and Atf6 (not shown). Similarly, treatment with BGP-15 decreased Atf4 expression in granulosa-lutein cells and, interestingly, also reduced the expression of Xbp1s, Hspa1a and Hspa1b. The induction of ER stress marker genes in the Blobby mice occurred in association with obesity, and they were not different in the COCs or granulosa-lutein cells of young lean mice (supplementary material Fig. S3).

Increased accumulation of lipid droplets and impaired protein production and secretion are additional key characteristics of lipotoxic induction of the UPR and ER stress. We thus measured these parameters in ovulated COCs of obese Blobby mice and lean littermates, and determined whether the defects were reversible with the ER stress inhibitor salubrinal in vivo. Oocytes of obese Blobby mice had visibly more lipid (green fluorescence) than oocytes from lean littermates, and treatment with salubrinal for 4 days before ovulation did not significantly affect lipid levels within the oocytes (Fig. 4A,B). Extracellular matrix protein pentraxin-3 (PTX3), which is crucial for fertilization (Varani et al., 2004), was measured by using immunocytochemistry and showed an abundance of secreted PTX3 (red fluorescence) in the extracellular matrix of COCs from obese mice, the red punctuate fluorescence in the pericortical region was visibly reduced compared to that of oocytes from non-obese littermates. Oocytes from Blobby mice that had been treated with salubrinal for 4 days before ovulation did not have reduced punctuate fluorescence in the pericortical region. Analysis of the ratio of red to green fluorescence intensity, in order to generate an index of mitochondrial activity, provided further evidence that the significantly decreased mitochondrial activity in

**Oocytes in obese mice exhibit reduced mitochondrial membrane potential and autophagy**

We next determined whether the oocyte mitochondrial membrane potential (ΔΨm) was reduced in ovulated oocytes from obese Blobby mice by staining with the inner membrane potential dye 5,5′,6,6′-tetrachloro-1,1′,3,3′-tetraethylbenzimidazolylcarbocyanine iodide (JC-1). Consistent with previous reports (Van Blerkom et al., 2002; Wu et al., 2010), oocytes of ovulated COCs exhibited red punctuate fluorescence that was localized to the pericortical region, indicating a high ΔΨm, whereas green fluorescence, indicating a low ΔΨm, localized to the central cytoplasm of oocytes (Fig. 5A). In oocytes from obese mice, the red punctuate fluorescence in the pericortical region was visibly reduced compared to that of oocytes from non-obese littermates. Oocytes from Blobby mice that had been treated with salubrinal for 4 days before ovulation did not have reduced punctuate fluorescence in the pericortical region. Analysis of the ratio of red to green fluorescence intensity, in order to generate an index of mitochondrial activity, provided further evidence that the significantly decreased mitochondrial activity in
Ovulated oocytes from obese mice was reversed by treatment with salubrinal (Fig. 5B). Induction of autophagy was also measured in oocytes by using an activity assay, and this showed that oocytes from obese mice exhibited numerous autophagic vacuoles throughout the oocyte cytoplasm (Fig. 5C). Quantification confirmed that levels were fourfold higher in oocytes from obese mice compared with those of lean littermates (Fig. 5D). Furthermore, the treatment of obese mice with either salubrinal or BGP-15 significantly diminished autophagic activity (Fig. 5C,D).

As another measure of mitochondrial capacity, mtDNA copy number was quantitatively assessed in individual oocytes. Oocytes from obese Blobby mice had a small reduction in mtDNA copy number that was not statistically significant (Fig. 5E), in contrast to previous reports (Igosheva et al., 2010; Luzzo et al., 2012). The treatment of obese mice with either salubrinal or BGP-15 resulted in a dramatic increase in oocyte mtDNA, which was not observed in lean littermates that had been treated with either compound. To further investigate how salubrinal and BGP-15 increase mtDNA in oocytes, we measured the expression of the mtDNA transcription factor TFAM and mitochondrial fission marker DRP1, and found that oocytes from obese Blobby mice that had been treated with either drug exhibited dramatically higher levels of both TFAM and DRP1 than either untreated obese mice or their lean littermates (Fig. 5F). The effects of BGP-15 on oocyte mitochondria were verified in a mouse model of high fat diet-induced obesity where, again, the oocytes of obese mice exhibited reduced mitochondrial activity that was normalized after treatment with BGP-15, which also significantly induced mtDNA copy number (supplementary material Fig. S5).

**Poor oocyte developmental competence and skewed fetal growth in obese mice are alleviated after treatment with an ER stress inhibitor**

Ovulated oocyte complexes that had been collected from oviducts were fertilized in vitro, and oocyte viability and embryo development were compared to those of untreated obese and lean control littermates. At 4 h post fertilization, many oocytes (putative zygotes) from untreated obese mice underwent fragmentation (Fig. 6A, arrows) and were deemed non-viable. The percentage of viable oocytes was significantly lower in obese mice than in lean mice, but treatment of obese mice with salubrinal or BGP-15 reversed this defect, and these treated mice had similar proportions of healthy viable oocytes to those of lean mice (Fig. 6A,B). The morphologically viable oocytes and/or zygotes from obese Blobby mice were further monitored, and they exhibited a significantly lower cleavage rate on day 2 compared to those from lean mice (Fig. 6C), and this was normalized in salubrinal-treated and BGP-15-treated obese mice. The percentage of blastocysts that developed from two-cell embryos of obese Blobby mice was further reduced (Fig. 6D) compared with that of lean mice, and development rates were normalized by using salubrinal or BGP-15. These defects in embryo development are specifically due to maternal obesity because ovulated oocytes from 6-week-old bbb/bbb mice, when assessed in an identical way, showed development...
rates comparable to those of control littermates (Fig. 6C,D, right panels).

mtDNA copy number was reduced in the blastocysts derived from the oocytes of obese Blobby mice compared with blastocysts derived from lean littermates. Blastocyst mtDNA content was normalized after treatment with either salubrinal or BGP-15 for 4 days before ovulation (Fig. 6E). Thus, alterations in the oocytes of obese mice lead to a sustained loss of mitochondria in blastocysts that is potentially attributable to ER stress.

Additional cohorts of blastocysts that were generated by IVF of oocytes from obese Blobby mice or lean wild-type littermates were transferred to the uterus of non-obese recipient mice. There were no differences in the implantation rates between embryos generated from any of the treatment groups (data not shown). Fetuses that developed from the oocytes of obese Blobby mice were significantly heavier than those developed from the oocytes of lean littermates (Fig. 7A). By contrast, fetuses that developed from the oocytes of salubrinal-treated or BGP-15-treated obese mice were no longer significantly heavier than fetuses from wild-type oocytes (Fig. 7A). There was no difference in the placental weights of fetuses from the oocytes of obese mice (or obese mice that had been treated with salubrinal or BGP-15) compared to fetuses derived from wild-type oocytes (data not shown).

mtDNA copy number was measured in dissected fetal tissues and was not found to be different in the placentas of any of the treatment groups (data not shown). However, mtDNA content was significantly reduced in the liver and kidney, and a trend towards a reduction in the hearts of fetuses derived from oocytes of obese females was evident (Fig. 7). Treatment of obese Blobby mice with salubrinal or BGP-15 before IVF resulted in restored mtDNA levels in the tissues of the offspring that had been derived from the oocytes of obese mothers to levels that were not significantly different to those of offspring of non-obese controls. To determine whether mitochondrial DNA sequence, i.e. variant load, was affected in fetal tissues, in addition to copy number, next-generation sequencing was performed on the liver samples from each treatment group. There were 56.75±5.9 rearrangements in the mitochondrial genome of livers from offspring conceived from obese mouse oocytes, which was significantly higher (P<0.01) than the level of 37.50±1.4 mtDNA rearrangements in liver samples from control offspring.
and high levels of spindle abnormalities are likely to be responsible for reduced ovulation and poor fertilization rates in obese animals. Most alarmingly, however, following conception, maternal obesity is also associated with adiposity in offspring (Ruang-Martin et al., 2010), suggesting that metabolic change can be transmitted through the generations in a self-perpetuating cycle that is set by maternal over-nutrition. Our findings confirm that fetal growth is altered in obese mothers and further demonstrate that this developmental trajectory is established during oocyte development and maturation. We show the existence of a mechanism whereby nutrition in mothers, in this case obesity, can alter the embryo and fetal mitochondrial endowment.

These fetal programming outcomes are clearly the result of changes to the oocyte within the follicle or before fertilization in the oviduct, because the study design utilized IVF throughout, with subsequent embryo culture and gestation under identical conditions for obese and control oocytes. Furthermore, the outcomes were reversed using drug treatments applied in the days before conception. Thus, we show that maternal mtDNA transmission is determined by mitochondria in the preconception oocyte, which are extraordinarily sensitive to maternal metabolic status and stress, and that reductions in mtDNA content imparted before implantation are perhaps the root cause of later altered energy expenditure and of predisposition to metabolic disease. This would provide a mechanistic explanation for previous studies that have reported that rats fed obesogenic diets before conception through to lactation have offspring with reduced levels of liver and kidney mtDNA, reduced electron transport chain activity, insulin resistance and altered energy expenditure (Taylor et al., 2005; Bruce et al., 2009; Borengasser et al., 2011; Burgueño et al., 2013).

Salubrinal is a well-characterized and widely used ER stress inhibitor; however, BGP-15 also modulated ER stress pathways, specifically, in obese Blobby mice it decreased COC Atf4 mRNA to the normal levels seen in lean mice and it also increased Xbp1s levels. Treatment with BGP-15 also dramatically increased transcripts of the cytoprotective chaperones Hspa1a and Hspa1b, consistent with BGP-15-induced expression of HSP72 protein in muscle (Chung et al., 2008; Gehrig et al., 2012), which is likely to be responsible for the increase in Xbp1s (Gupta et al., 2010). ER stress inhibitor treatment also improved ER secretory protein production, as evidenced by the expression of PTX3, selected because it is rapidly expressed at high levels in response to the luteinizing hormone surge and is essential for ovulation and fertilization (Varani et al., 2002; Salustri et al., 2004). This reduction in PTX3, and probably other cumulus cell secreted proteins, is likely to be at least partly responsible for the anovulation and decreased in vivo fertilization rates seen in obese mice (Fig. 2; Minge et al., 2008; Wu et al., 2010). However, it is equally possible that leptin (or gonadotropin) receptor desensitization occurs in ovarian cells, as occurs in the hypothalamus in response to obesity (Ozcan et al., 2009), or that proteins which are crucial for cumulus cell-oocyte communication and developmental competence, such as gap junctions (Gi and Albertini, 2013), are disrupted. ER stress inhibitor treatment did not affect oocyte lipid content, confirming that their mechanism of action is likely to be stabilization of ER protein production and mitochondrial membrane potential, rather than the alleviation of high intracellular lipid. Both compounds reduced autophagy responses; however, they also increased both TFAM and DRP1, indicating amplified mtDNA replication and mitochondrial fission as the mechanism of action to improve oocyte developmental potential. In support of this, mtDNA content does not change markedly in embryos from obese mice in the oocyte to embryo transition; increasing from an average of $2.6\times10^{5}$ copies

**DISCUSSION**

Obese women have a well-known risk for anovulation and reduced pregnancy rates (Gesink Law et al., 2007; Rittenberg et al., 2011); our data now shows that concerted ER stress responses in both granulosa and cumulus cells, impaired matrix protein production and high levels of spindle abnormalities are likely to be responsible

---

**Fig. 7.** Altered fetal outcomes of oocytes from obese Blobby mice are alleviated after treatment with salubrinal or BGP-15. Obese mice (bbb/bbb) and lean littermates (+/+) were treated with vehicle (Veh; saline), salubrinal (Sal) or BGP-15 for 4 days, followed by the isolation of oocytes from oviducts and fertilization by using IVF. Blastocysts were collected at day 5 of culture and transferred to non-obese pseudo-pregnant recipient mice with six blastocysts per uterine horn. On embryonic day 14.5, fetuses were collected and the relative liver (B), heart (C) and kidney (D) were dissected and the relative mtDNA copy number normalized to β-actin nuclear DNA was determined. Data are presented as means+s.e.m.; lean+Veh, n=18 fetuses from six surrogates; Blobby+Veh, n=20 fetuses from six surrogates; Blobby+Sal, n=22 fetuses from six surrogates; Blobby+BGP-15, n=15 fetuses from four surrogates. (E) Liver mtDNA samples (n=4 fetuses from each treatment group) were analyzed by using next generation sequencing, and rearrangements were identified. Different letters indicate significant differences calculated by one-way ANOVA, Tukey’s post hoc test, P<0.01.

(FIG. 7E). Offspring from the oocytes of obese mice that had been treated with salubrinal or BGP-15 harbored 46.5±2.6 and 51.2±2.1 (Fig. 7E). Liver (B), heart (C) and kidney (D) were dissected and the relative mtDNA copy number normalized to β-actin nuclear DNA was determined. Data are presented as means+s.e.m.; lean+Veh, n=18 fetuses from six surrogates; Blobby+Veh, n=20 fetuses from six surrogates; Blobby+Sal, n=22 fetuses from six surrogates; Blobby+BGP-15, n=15 fetuses from four surrogates. (E) Liver mtDNA samples (n=4 fetuses from each treatment group) were analyzed by using next generation sequencing, and rearrangements were identified. Different letters indicate significant differences calculated by one-way ANOVA, Tukey’s post hoc test, P<0.01.
to just 4.2×10⁵ copies (see Fig. 5E versus Fig. 6E). By contrast, embryos from lean mice increase mtDNA from 2.9×10⁵ copies to 12.9×10⁵ copies, as is known to occur in preparation for implantation (Pikó and Taylor, 1987; Ebert et al., 1988; Thundathil et al., 2005; Spikings et al., 2007; Aiken et al., 2008; Wai et al., 2010). Importantly, these low mtDNA embryos give rise to fetal tissues that have correspondingly reduced mtDNA content and increased mtDNA sequence variants, reflective of an altered metabolic capacity (Park et al., 2001; Meierhofer et al., 2004; Yuzefovych et al., 2013), which is consistent with their significantly increased fetal weight. That placental tissue from fetuses derived from oocytes of obese mice did not have reduced mtDNA content (or altered tissue weight), suggesting that the reduction in mtDNA in blastocysts mostly impacts cells within the inner cell mass, which establish the set point of tissue-specific mtDNA content as fetal tissues differentiate (Facucho-Oliveira et al., 2007; St John, 2012).

BGP-15 is an orally active compound that is currently in human clinical trials for type II diabetes (Literáti-Nagy et al., 2009, 2010). In a rat model of type II diabetes, BGP-15 increases mitochondrial area in muscle and improves insulin sensitivity (Henstridge et al., 2014), and in a model of aceterminophen-induced liver toxicity, BGP-15 induces phosphorylated eIF2α and restores mitochondrial depolarization (Nagy et al., 2010). The observation that BGP-15 had no effect on mitochondrial replication in oocyte complexes from lean mice was not unexpected because this class of compounds had no effect on mitochondrial replication in oocyte complexes (Nagy et al., 2010). The observation that BGP-15 was able to improve embryo and fetal development.

**Isolation of ovaries and cumulus-oocyte complexes**

Ovaries were dissected and fixed in 4% paraformaldehyde (w/v) in PBS (80 mM Na2HPO4, 20 mM NaH2PO4, and 100 mM NaCl (pH 7.5)) for 24 h and processed into paraffin blocks that were then sectioned (5 µm) and stained with Hematoxylin and Eosin. Images were captured at high resolution using NanoZoomer Digital Pathology technology (Hamamatsu Photonics K.K.). Ovulated cumulus-oocyte complexes (COCs) were isolated from the oviducts of mice at 13 or 16 h after hCG injection as indicated, placed in HEPES-buffered α-MEM (Invitrogen) supplemented with 3 mg/ml bovine serum albumin (fatty acid free; Sigma-Aldrich) and counted under a dissection microscope. Granulosa-lutein cells were obtained by the dissection of ovulated follicles from the ovary, these cells were then snap-frozen.

**RNA isolation and real-time reverse transcription (RT)-PCR**

Total RNA was isolated from COCs or granulosa-lutein cells and reversed transcribed, as described previously (Wu et al., 2012). Real-time PCR of cDNA was performed in triplicate using SYBR Green PCR Master Mix (Applied Biosystems) and a Rotor-Gene 6000 (Corbett) real-time rotary analyzer. Ribosomal protein L19 was used as a validated internal control for every sample. Xbp1s primers were: Xbp1s reverse, 5′-AGGCCCTGGTGTATA-3′ and Xbp1s forward, 5′-GGTCTGTAGTCCCGAACGG-3′ (Ozcan et al., 2009), and other primers were Quantitect Primer assays (Qiagen). All Primers were shown to have comparable amplification efficiency against the internal control. Real-time PCR data was analyzed using the 2−ΔΔCT method and expressed as the fold change relative to a calibrator CDNA sample included in each run.

**Lipid droplet staining and immunocytochemistry**

COCs were fixed for 1 h in 4% paraformaldehyde in PBS with 1 mg/ml polyvinylpyrrolidone (PVP; Sigma), then washed thoroughly in PBS with 1 mg/ml PVP, COCs were then incubated in blocking buffer containing 10% normal goat serum (Vector Laboratories) in PBS for 1 h at room temperature, followed by incubation with a rabbit polyclonal antibody against PTX3 (H-300, sc-32866, Santa Cruz Biotechnology), diluted 1:100 in blocking buffer, overnight at 4°C. After washing in PBS with PVP, COCs were incubated with biotinylated goat-anti rabbit IgG antibody (AP132B, Vector Laboratories) in blocking buffer, overnight at 4°C, followed by incubation with a rabbit polyclonal antibody against PTX3 (H-300, sc-32866, Santa Cruz Biotechnology), diluted 1:100 in blocking buffer, overnight at 4°C. After washing in PBS with PVP, COCs were incubated with biotinylated goat-anti rabbit IgG antibody (AP132B, Millipore) 1:1000 in PBS with PVP for 1 h at room temperature. Finally, COCs were washed in PBS with PVP and incubated with 1 mg/ml streptavidin-Alexa Fluor 594 (S32356, Molecular Probes) in PBS with PVP, and then washed thoroughly in PBS with PVP and transferred to 1 µg/ml of the neutral lipid stain BODIPY 493/503 (D-3922, Invitrogen) in PBS with PVP for 1 h in the dark at room temperature before washing thoroughly in PBS with PVP. For spindle staining, oocytes were fixed in 4% paraformaldehyde with 2% Triton X-100 and 1 mg/ml PVP in PBS for 30 min at room temperature, then washed thoroughly in PBS with PVP. Oocytes were then incubated with anti-o-tubulin monoclonal antibody (A1126, Life Technologies) (1:200) for 1 h, followed by donkey anti-mouse IgG Alexa Fluor 488 (A-21202, Millipore) (1:1000) and Hoechst 33342 (Life Technologies; 1 µg/ml) for 30 min, with each step followed by three washes in PBS with PVP. For TFAM and DRP1 detection, fixed oocytes were immunostained with a 1:100 dilution of mouse anti-DRP1 (611112, BD Biosciences), or mouse anti-TFAM (catalog number B01P; Abnova) overnight at 4°C. After washing in PBS with PVP, oocytes were

**METABOLITE AND ENDOCRINE MEASUREMENTS**

Blood samples were collected from mice immediately before humane killing by cervical dislocation. Samples were allowed to clot at room temperature and centrifuged at 4000 r.p.m. (1800 g) for 10 min, followed by collection of serum. Mice were not fasted to avoid the detrimental physiological impact of short-term starvation on ovulation and oocyte quality. Parametrial adipose tissue and liver were dissected and weighed.

Serum insulin levels were measured by using the sensitive rat insulin RIA kit (Millipore) with a sensitivity of 0.03 ng/ml and an intra-assay coefficient of 7.31%. Serum glucose and lipids were determined by using a Roche Cobas Integra 400 plus chemistry analyzer (Roche). Cholesterol levels were measured using the Cholesterol (CHOL2) assay kit (Roche), and the mean coefficient of variation was less than 2.7%. Triglycerides were measured using a triglycerides (TRIGL) assay kit (Roche), and the mean coefficient of variation was less than 2.6%. Each of these assays was calibrated with the Calibrator for Automated Systems (Roche) and the quality controls were PreciControl ClinChem Multi 1 and PreciControl ClinChem Multi 2 (Roche). Total serum non-esterified fatty acids (NEFAs) were measured using the NEFA-C assay kit (Wako Pure Chemical Industries) and quality controls Seronorm Human and Seronorm Lipid (Sero, Norway). The mean coefficient of variation was less than 4.6%. All assays have been validated for use in the mouse.

**RESEARCH ARTICLE**

incubated with 1:1000 donkey-anti mouse IgG Alexa Fluor 488-conjugated antibody in PBS with PVP with 0.5 µg/ml Hoechst 33342 for 1 h at room temperature in the dark, followed by thorough washing in PBS with PVP. Stained COCs or oocytes were visualized, and images were captured by using a Leica TCS SP5 spectral scanning confocal microscope system (Heerbrugg, Switzerland) using identical magnification and gain settings throughout experiments. Fluorescence intensity was determined using AnalysisPro software (Olympus), whereby a circle was placed over the oocyte (or COC) image, and the sum total of fluorescence within the area was determined. Oocyte spindles were scored as described previously (Choi et al., 2007), where spindle and chromosomal configurations were deemed good (score 1, 2) or abnormal (score 3, 4) based on spindle organization and the degree of chromosomal displacement from the plane of the metaphase plate.

**Analysis of oocyte mitochondrial membrane potential (ΔΨm) and autophagy**

Oocytes were denuded as described above, and ΔΨm was measured as described previously (Wu et al., 2012). Autophagic vacuoles in live denuded oocytes were visualized using the Cyto-ID Autophagy Detection Kit (Enzo Life Sciences) according to the manufacturer’s instructions. Briefly, after washing once with 1× assay buffer, oocytes were incubated with dual-detection solution at 37°C in the dark. Then oocytes were washed once with 1× assay buffer and imaged immediately in green and blue fluorescence channels using a Leica SP5 spectral scanning confocal microscope at identical magnification and gain settings throughout experiments. Using AnalysisPro software (Olympus), a square was placed to cover the oocyte image, and green fluorescence intensity was determined as the sum total of fluorescence in the boxed area.

**Quantification of mtDNA copy number and sequence variants**

The mtDNA copy number in individual oocytes or blastocysts was quantified absolutely, as described previously (Kameyama et al., 2010). Briefly, oocytes (denuded as above) or day 5 blastocysts were washed with PBS with PVP (1 mg/ml PVP in PBS), collected individually into 1.5 ml siliconized low retention microcentrifuge tubes (Fisher Scientific) with 5 µl of PBS with PVP and stored at −80°C. Genomic DNA was isolated by using the QIAamp DNA micro kit (Qiagen) according to the manufacturer’s protocol with carrier RNA (1 µg; Qiagen) added to each sample. Genomic DNA was eluted twice with 50 µl of water and diluted ten times for quantitative PCR. To prepare the quantification standards, a 1186 bp fragment of the 12S ribosomal (r)RNA region of mtDNA was amplified from mouse liver by PCR using the primer pair 5′-ACACCCTGGCTTAGCCA-3′ and 5′-TTGGCCACATAGGCAGTT-3′ with the LongRange PCR kit (Qiagen), and then purified by using the QIAquick PCR purification kit (Qiagen) and cloned using the Qiagen PCR cloning kit (Qiagen). Plasmid DNA was purified from bacteria using Plasmid Maxi kit (Qiagen), and the concentration was determined by using a Nanodrop ND1000 Spectrophotometer (Biolab). Plasmid copy number was calculated as: mass of plasmid (g)/mass of plasmid size (bp)×(1.096×10²¹ g/bp); mass of plasmid required to generate 1×10⁷ copy number standard stock=1×10⁷×mass of single plasmid. A standard curve was generated by using seven tenfold serial dilutions (10⁻⁵ to 10⁷ copies), and standard curve correlation coefficients were consistently greater than 0.98. Real-time quantitative PCR using the primer pair 5′-CGTTAGGTCAAGGTG-3′ and 5′-CCAGACACACTTTCCAGTATG-3′ was performed in triplicate using SYBR green PCR master mix (Applied Biosystems) and aRotor-Gene 6000 (Corbett) real-time rotary analyzer. The Ct value for β-actin was subtracted from that for 12S rRNA to give the ΔCt value. mtDNA copy number per nuclear genome (two actin gene copies) was calculated as 2×2ΔCt.

The mtDNA sequence was examined in fetal liver samples by using next generation sequencing, which is detailed in the supplementary methods. Briefly, two overlapping fragments, each spanning 50% of the mitochondrial genome, were produced by using long PCR to generate templates. Purified pairs of amplicons from long PCR from the same sample were combined at equal concentrations. Libraries were generated using the Ion Fragment Library Kit and Ion Xpress Template Kit (Life Technologies) and loaded onto 316 chips for sequencing on the Ion Torrent Personal Genomes Machine (PGM). Variant selection was performed using the CLC Genomics Workbench (v7.0.3), and sequences were mapped to a mouse reference genome (AP013031).

**In vitro fertilization, embryo development and transfer**

Sperm were collected from the caudal epididymis and vas deferens of 8-week-old wild-type male mice and capacitated in fertilization medium (Vitro Cleave; Cook Australia, Brisbane, Australia) for 1 h at 37°C under an atmosphere of 5% CO₂ and 95% air. After sperm capacitation, COCs were isolated from oviducts of mice at 16 h after hCG treatment as above and washed twice in fertilization medium. COCs and 10 µl of sperm (35,000 sperm/ml) were then co-incubated in 90 µl of fertilization medium for 4 h at 37°C under an atmosphere of 5% CO₂ and 95% air. At 4 h after fertilization, the morphology of oocytes (putative zygotes) was assessed visually, with those oocytes showing dark and fragmented cytoplasm indicative of apoptosis (Fig. 6A, black arrows) deemed non-viable, and all viable oocytes were transferred to fresh medium. At 24 h after *in vitro* fertilization (day 2), embryo cleavage and morphology were assessed, and two-cell embryos were classified as ‘on time’ and transferred to a fresh 20 µl drop of medium (Vitro Cleave). Embryo morphology was assessed on day 5 (96-100 h after fertilization), with blastocysts and hatching blastocysts classified as ‘on time’ and the percentage of two-cell embryos that achieved on time development was calculated.

Unhatched blastocysts on day 4 following *in vitro* fertilization and embryo culture conditions as above were transferred into pseudo-pregnant CBA×C57BL/6 F1 female mice at 3.5 days past coitum. Six blastocysts were transferred into each uterine horn for each recipient mouse, and the two horns were given different source embryos. Recipients were humanely killed on E14.5, and fetuses were collected and fixed in 4% paraformaldehyde in PBS. The following day, crown-rump length, fetal weight and placental weight were measured. Fetal liver, heart, kidney and placenta were dissected and retained for DNA extraction as described above.

**Statistical analysis**

All measures are reported as mean±s.e.m. Statistical significance was determined as indicated, by using Student’s *t*-test or one-way ANOVA with Bonferroni post hoc tests, as appropriate, using GraphPad Prism version 5.01 for Windows (GraphPad Software). A *P*-value of less than 0.05 was considered statistically significant.
Acknowledgements
We gratefully acknowledge N-Gene Research Laboratories for supplying BGP-15.

Competing interests
M.A.F. is Chief Scientific Officer of N-Gene Research Laboratories Ltd. J.C.S.J. is funded by OvaScience Inc. L.L.W., D.R., L.N., R.J.N., J.C. and R.L.R. have no competing or financial interests to declare.

Author contributions

Funding
This work was supported by grants from the National Health and Medical Research Council of Australia (NHMRC) [APP1061819 to R.L.R. and J.C.; APP1041471 to J.C.S.J.] The Operational Infrastructure Support Program of the Government of Victoria; and the Women’s and Children’s Hospital Foundation (to L.L.W.). M.A.F. is a Senior Principal Research Fellow of the NHMRC. R.L.R. is a Career Development Fellow of the NHMRC.

Supplementary material
Supplementary material available online at http://dev.biologists.org/lookup/suppl/doi:10.1242/dev.114850/-/DC1

References


Supplemental Figure 1: Lean (+/+ or +/bbb) and obese Blobby (bbb/bbb) mice at 14 weeks of age were treated with gonadotropins as in Methods. Ovaries were collected at 16h post-hCG, fixed, sectioned and H&E-stained as in Methods. Arrows indicate unruptured follicles which are apparent in ovaries from obese mice.
**Supplemental Figure 2:** Female C57 mice (8 weeks of age) were treated with BGP-15 (or were untreated (control) for 4 days concurrent with eCG and hCG as in Methods. N=3 mice per group. A. Number of ovulated oocytes was counted 16h post-hCG. B. Ovulated oocytes were subjected to IVF as in Methods and on-time development assessed at Day 2 (2-cell embryo stage) and Day 5 (blastocyst stage). BGP-15 treatment significantly increased ovulation rate (* p=0.015) but did not affect embryo development.
Supplemental Figure 3: Ovulated COCs were collected from oviducts of +/+ or bbb/bbb mice at 6-8 weeks of age following treatment with gonadotropins as in Methods. Expression of ER stress/ UPR marker genes and heat shock chaperone genes (A: Atf4, B: Xbp1s, C: Hspa1a, D: Hspa1b, E: Atf6, and F: Hsp5a), were determined by RT-PCR as Methods. N=7-8 mice per genotype. There were no significant differences detected between groups.
Supplemental Figure 4: Ovulated cumulus-oocyte complexes COCs obtained from oviducts 13h after ovulatory gonadotropin treatment were stained with neutral lipid dye BODIPY 493/503 (green fluorescence) and for cumulus extracellular matrix protein PTX3 by immunocytochemistry (red fluorescence) as in Methods. Lettered panels are higher magnification of respective boxed areas. Images are representative of 10-15 COCs from 2-3 mice per group. COCs from obese mice have increased lipid content but reduced matrix protein PTX3 that is normalized by salubrinal treatment.
**Supplemental Figure 5:** Female C57 mice were fed a control diet (CD) or high fat diet (HFD; Chen et al. Diabetes 2014 63:3189) from 6 to 14 weeks of age. BGP-15 was administered for 4 days concurrent with eCG/hCG as in Methods. A. Ovulated oocytes were collected, hyaluronidase-treated and stained with MitoTracker Green FM (Molecular Probes) at 100nM in αMEM supplemented with 1% fetal calf serum for 15 min in the dark followed by MitoTracker Orange CM-H2TMRos (Molecular Probes) at 500nM for 30 min in the dark. Oocytes were then washed once in PBS/PVP followed by confocal microscopy imaging. B. Total fluorescence was determined for each stain and expressed as a ratio. N=5-12 oocytes per group. Different letters significantly different by ANOVA; p<0.01. C. Oocytes were snap frozen, DNA isolated and mtDNA copy number determined as in Methods. N= 4-10 per group; p<0.0001.
SUPPLEMENTAL METHODS

Mice and genotyping

The C57BL/6JsfAnu-Alms1bbb/Apb mouse strain (named ‘Blobby’) was sourced from the Australian Phenome Bank (APB ID 31; MGI:3611799). The ‘Blobby’ mutation (bbb/bbb) is an ENU-induced T to A mutation at position 6507 (exon 10) on the Alms 1 gene that results in a truncated Alms1 protein (Li et al., 2007). Blobby mice are a phenocopy of the Alms1 knockout mouse (Collin et al., 2005) and the “Fat Aussie” (foz/foz) strain which has a spontaneous 11-bp deletion in exon 8 of the Alms 1 gene causing a frame-shift, premature termination and elimination of the C-terminal two thirds of the Alms1 protein (Arsov et al., 2006). Each of the three existing Alms1 mutant mouse lines exhibits hyperphagia and profound obesity even when maintained on a standard mouse chow diet (Collin et al., 2005; Arsov et al., 2006; Li et al., 2007).

Experimental mice were generated by heterozygous mating pairs and were genotyped using tail DNA and mutation-specific PCR primers (forward: 5’-AAAGCCCCACATGTAGATCG-3’, reverse: 5’-TGAGGTATATGCTGAACCTCATAT-3’) to screen for the Alms1 (bbb) gene mutation. PCR conditions were 94°C for 2 min, followed by 38 cycles of 94°C 30 seconds, 59°C 1 min, 72°C 2 min, and 72°C 5min. PCR products were digested by PsiI (BioLabs) restriction enzyme and products visualized on 4% agarose gel. Wildtype DNA produced a single 190bp band, heterozygous mice produced 190 and 200 bp bands and homozygous mice produced a single 200bp band. All mice were maintained on a 12-h light, 12-h dark cycle with standard mouse diet (4.8% total fat, digestible energy 14.0 MJ / Kg, Specialty Feeds, Glen Forrest, Australia) and water available ad libitum.
**Next generation sequencing of fetal liver mtDNA**

MtDNA sequence was examined in fetal liver samples by next generation sequencing. Two overlapping fragments, each spanning 50% of the mitochondrial genome, were produced by long PCR to generate templates. Reactions consisted of 50 ng total DNA, 1x High Fidelity PCR buffer, 100 mM MgSO$_4$, 1 mM dNTPs (Bioline, London, UK), 1U of Platinum Taq High Fidelity (Invitrogen, Carlsbad, CA, USA) and 10μM each of the forward and reverse primer (A forward CCGTGCTACCTAAACACCTTATC and A reverse CGTCCGTACCATCATCCAATTA; B forward CCCTTCATCCTTCTCTCCCTAT and B reverse GTGGGATCCCTTGAGTTACTTC ). Reaction conditions were 94°C for 2:00, 94°C for 0:15, 57°C for 0:30, 68°C for 10:00 (34 cycles), 68°C for 10:00, held at 4°C. Products were purified using the QIAquick PCR purification kit (Qiagen). Purified pairs of amplicons from long PCR from the same sample were combined at equal concentrations. Libraries were generated using the Ion Fragment Library Kit and Ion Xpress™ Template kit (Life Technologies). MtDNA was sheared using the Covaris Adaptive Focused Acoustics (AFA™) system. Fragments of ~ 200 bp were selected following electrophoretic separation with the E-gel system (Life Technologies). Product size and quality were assessed using the Agilent High Sensitivity DNA Kit (Agilent, Santa Clara, CA) by the Agilent Bioanalyzer. Each library was barcoded through different ligation adaptors. Libraries were pooled at equal concentrations and loaded onto 316 chips for sequencing on the Ion Torrent Personal Genome Machine (PGM)™.

Variant selection was performed using the CLC Genomics Workbench (v7.0.3). Sequences were mapped to a mouse reference genome (AP013031). Only reads with a Phred quality score of >15 were accepted; reads of <15 bp were excluded and one nucleotide was trimmed from each end. For inclusion, reads had a minimum of 80 % identity to the reference
sequence; a mismatch cost of 2 and an insertion/deletion cost of 3 were set; and duplicate reads were excluded. A minimum mutation threshold of 3 % was set for variant calling.

**Supplemental Table S1**

Click here to Download Table S1