Glucose deprivation, oxidative stress and peroxisome proliferator-activated receptor-\(\alpha\) (PPARA) cause peroxisome proliferation in preimplantation mouse embryos

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Abstract

Ex vivo two-cell mouse embryos deprived of glucose in vitro can develop to blastocysts by increasing their pyruvate consumption; however, zygotes when glucose-deprived cannot adapt this metabolic profile and degenerate as morulae. Prior to their death, these glucose-deprived morulae exhibit upregulation of the \(\mathrm{H}^+\)-monocarboxylate co-transporter SLC16A7 and catalase, which partly co-localize in peroxisomes. SLC16A7 has been linked to redox shuttling for peroxisomal \(\beta\)-oxidation. Peroxisomal function is unclear during preimplantation development, but as a peroxisomal transporter in embryos, SLC16A7 may be involved and influenced by peroxisome proliferators such as peroxisome proliferator-activated receptor-\(\alpha\) (PPARA). PCR confirmed \(Ppara\) mRNA expression in mouse embryos. Zygotes were cultured with or without glucose and with the PPARA-selective agonist WY14643 and the developing embryos assessed for expression of PPARA and phospho-PPARA in relation to the upregulation of SLC16A7 and catalase driven by glucose deprivation, indicative of peroxisomal proliferation. Reactive oxygen species (ROS) production and relationship to PPARA expression were also analysed. In glucose-deprived zygotes, ROS was elevated within 2 h, as were PPARA expression within 8 h and catalase and SLC16A7 after 12–24 h compared with glucose-supplied embryos. Inhibition of ROS production prevented this induction of PPARA and SLC16A7. Selective PPARA agonism with WY14643 also induced SLC16A7 and catalase expression in the presence of glucose. These data suggest that glucose-deprived cleavage stage embryos, although supplied with sufficient monocarboxylate-derived energy, undergo oxidative stress and exhibit elevated ROS, which in turn upregulates PPARA, catalase and SLC16A7 in a classical peroxisomal proliferation response.


Introduction

Glucose deprivation is a potent cell stressor leading to the activation of cell death pathways. The totipotent cells of cleavage stage preimplantation embryos rely on monocarboxylates, pyruvate and lactate for energy during the first few divisions after fertilization (Brinster 1965, Wilding et al. 2002). Indeed, 5.6 mM glucose can be toxic at this time, and thus media used to culture human embryos in assisted reproductive procedures contain only very low glucose concentrations (for reviews see Biggers 1998, Lane & Gardner 2007). Gradually, co-incident with the initiation of the first differentiation into epithelial trophectoderm, glucose becomes a major ATP source. For preimplantation embryos in vivo, the conversion from monocarboxylate-based to glucose-based generation of ATP is induced by prior exposure to glucose, which is provided in the oviductal milieu (Gardner et al. 1996, Harris et al. 2005), but this supply can be manipulated in vitro. This unusual metabolic profile presents a model for the investigation of cellular stress response induced by glucose deprivation. Subtle changes in embryo culture conditions can increase cell death and may be associated with increased reactive oxygen species (ROS) activity.

Although not used for fuel, glucose is catabolized by early cleavage stage embryos through the hexosamine biosynthetic pathway (Pantaleon et al. 2008) and the pentose phosphate pathway, producing amino sugar nucleotides and nucleic acid precursors that may be required for cell proliferation and NADPH generation. NADPH is predominantly used in triacylglycerol synthesis, of which there is little supporting evidence in these embryos, and in reduction of oxidized
glutathione to support glutathione peroxidase management of hydrogen peroxide (H₂O₂). So we reasoned that if stress was applied by glucose deprivation, pentose phosphate pathway flux would cease and the cells’ ability to generate NADPH so as to reduce ROS would be compromised, thus potentiating further increases in cellular ROS and activation of peroxisome proliferation in order to respond.

Peroxisomes, first noted in rat oocytes in situ (Figueroa et al. 2000) and subsequently in mouse preimplantation embryos (Jansen et al. 2008), both produce and scavenge ROS and house enzymes for fatty acid β-oxidation (Piot et al. 1998) of which there is some evidence in embryos (Kane 1979, Hillman & Flynn 1980, Quinn & Whittingham 1982, Haggarty et al. 2006). Interestingly, SLC16A7 and catalase co-localize to embryonic peroxisomes and are upregulated in embryos deprived of glucose, which later degenerate before blastulation (Jansen et al. 2008). Much of this increased SLC16A7 was found in peroxisomes rather than the plasma membrane, suggesting a role in ROS metabolism. This increased peroxisomal activity suggests that glucose deprivation may result in oxidative stress activating peroxisome proliferation.

Oxidative stress arises from an elevation in ROS including superoxide anions (O₂⁻) or H₂O₂ from various sources. Brief exposure of embryos to H₂O₂ inhibits cell proliferation and causes arrest before blastulation (Cebal et al. 2007). Similar consequences follow from early periods of glucose deprivation in vitro (Sakkas et al. 1989, Brown & Whittingham 1991, Chatot et al. 1994, Martin & Leese 1995). At the heart of peroxisomal proliferation is the activity of the peroxisome proliferator-activated receptors (PPAR). These ligand-activated nuclear receptors or transcription factors affect transcription of a range of peroxisome-related genes. Not surprisingly, PPARs are responsible for regulating catabolism of fats and glucose homeostasis (Lemberger et al. 1996b). There are three subtypes: PPARα, abundant in liver and kidney; PPARγ mostly in adipose and intestinal tissue and both are activated by second messengers from the arachidonic cascade pathways. PPARβ/δ is constitutive to all tissues and by contrast activated preferentially by unsaturated fatty acids (Braissant et al. 1996, Lemberger et al. 1996a, Krey et al. 1997).

This study investigated PPARα in the metabolic stress response of early embryos because of its previously established role in fatty acid oxidation, its upregulation in response to oxidative stress (Schrader & Fahimi 2006) and after fasting (Gremlich et al. 2005) and in later stage ovine embryos after maternal nutrient restriction (Bispham et al. 2005, Budge et al. 2005). The fibrate WY14643, a PPARα agonist that causes peroxisomal proliferation in rodents via activation of PPAR (Nemati et al. 1989, Shearer & Hoekstra 2003), was used to test our hypothesis that complete glucose deprivation induced oxidative stress in the embryo with resultant induction of PPARα, SLC16A7 and catalase.

Results
Induction and phosphorylation of PPARα
Ovulated oocytes and zygotes collected at 18 h post-human chorionic gonadotrophin (hCG) express Ppara mRNA, which persists during culture until the two-cell stage, but could not be detected in ex vivo morulae (72 h post-hCG) or blastocysts (96 h post-hCG) that would develop from these zygotes (Fig. 1A). When embryos were collected and cultured, those supplied with glucose reflected this in vivo pattern of repression in morulae, but a weak signal persisted in glucose-deprived morulae. Studies to locate the protein were more informative. In zygotes, PPARα staining was predominantly distributed diffusely through the cytoplasm and this pattern persisted through development (Fig. 1B–I). Quantitative image analysis showed little change in PPARα over 4 h of culture, but by 8 h there was increased PPARα protein in glucose-deprived embryos, while glucose-supplied embryos showed a slight decrease in PPARα staining that persisted until 54 h post culture to the morula stage (Fig. 1G–J). Also after 8 h of glucose deprivation (Fig. 1G), staining became more granular and this more granular pattern persisted over the next 46 h (Fig. 1G–I).

Phosphorylation of PPARα was monitored with an antiserum against PPARα–phospho-Ser12 (Fig. 1K). Over the 4–24 h period, the most dramatic change was a decrease (48%, P<0.01) in cellular PPARα–phospho-Ser12 staining in embryos supplied with glucose, while there was no significant change in glucose-deprived embryos. Indeed, as total PPARα levels in glucose-supplied embryos remained fairly constant through this period (Fig. 1I), the decrease in PPARα–phospho-Ser12 suggests dephosphorylation of PPARα in embryos growing under these normal conditions. In contrast, in glucose-deprived embryos, total PPARα increased 24% (Fig. 1J), while the level of PPARα–phospho-Ser12 was constant suggesting that in these embryos, although overall PPARα was induced, a smaller proportion was phosphorylated. However, the site of PPARα activity is in the nucleus, so nuclear levels of PPARα–phospho-Ser21 were examined against PPARα at 24 h with dual staining and quantitation (Fig. 1L–N). It was clear that PPARα–phospho-Ser21 concentrated about twofold in the nuclei of glucose-deprived embryos. So assuming both PPARα–phospho-Ser12 and PPARα–phospho-Ser21 behave similarly, this suggests that glucose deprivation produces cell stress leading to increased PPARα expression and greatly increased recruitment of the activated PPARα into the chromatin, possibly with contingent peroxisomal proliferation. Meanwhile, embryos developing with glucose showed reduced phospho-PPARα and reduced PPARα, suggesting a quiescent metabolism (Fig. 1J and K).
To investigate this possibility, the effects of the peroxisome proliferator WY14643 on transcription and translation of a classic peroxisomal marker, catalase, were examined (Fig. 2). In all embryos, cytoplasmic staining was diffuse and granular with these vesicles distributed in the cortical cytoplasm. Catalase immunoreactivity was more intense and granules were more pronounced and numerous in glucose-deprived embryos and embryos treated with the PPARA activator WY14643 in the presence of glucose. Catalase expression was acutely sensitive to glucose deprivation or PPARA activation; as by 4 h of treatment, catalase protein was already elevated by about 20% (Fig. 2A, P < 0.01). Degradation of about 10% of the protein over 12 h was revealed by inhibition of translation with
cycloheximide (CHX; $P<0.001$). Both glucose deprivation and PPARA activation increased the total pool of catalase, by increased transcription and translation ($P<0.01$, Fig. 2A–D), but there was evidence of an inhibition of catalase turnover as even in the presence of $\alpha$-amanitin, expression was increased by 50% after 12 h ($P<0.001$).

**SLC16A7**

As we had already observed that SLC16A7 was located in embryonic peroxisomes, it was similarly examined to determine whether it was under PPAR regulation (Fig. 3). Both plasma membrane and granular cytoplasmic staining were 30% more intense in glucose-deprived embryos ($P<0.001$), but SLC16A7 was not as acutely responsive as catalase (Figs 2 and 3). Studies with the protein synthesis inhibitor CHX revealed no loss of SLC16A7 over 12 h in glucose-supplied embryos (Fig. 3A and B, $P>0.05$), but the 57% ($P<0.001$) increase in expression induced by 12 h of glucose deprivation required both transcription and translation, suggesting transcription was activated by the glucose deprivation. The PPAR activator WY14643 produced similar increases in SLC16A7 transcription and translation to glucose deprivation, indicating that both glucose deprivation and PPARA activation induce SLC16A7 expression via transcription as well as translation.

**Reactive oxygen species**

The peroxisomal proliferation indicated by increased catalase and induction of PPARA induced by glucose deprivation suggested that this nutrient manipulation is a stressor, and it was hypothesized that this might be reflected in increased intracellular ROS. When these were assessed after only 2 h, ROS levels had risen by about 20% ($P<0.05$) in glucose-deprived embryos or embryos stimulated with peroxisome proliferator (Fig. 4). Two hours later, while the ROS peak in the glucose-deprived embryos had abated, it persisted in the peroxisome proliferator-treated embryos, indicating a more persistent induction. To confirm a role for peroxide production in this ROS peak, the experiment was repeated using diphenyleneiodonium (DPI) to inhibit flavoenzymes, particularly NADPH oxidase, and so decelerate the ROS synthesis resulting from glucose deprivation. Again, in the glucose-deprived and PPARA agonist-treated zygotes, ROS levels were about 20% greater than for zygotes developing with glucose (KSOM), but inhibition of flavoenzymes with DPI prevented or reduced this elevated ROS arising from glucose deprivation or PPARA agonism (Fig. 5).

**Effect of DPI on PPARA and SLC16A7 expression**

This suggested that the induction of PPARA might be downstream from the increased ROS. So some embryos from each group were left in culture for 8 or 24 h, before...
they were fixed and subsequently assessed by immunofluorescence for either PPARα (at 8 h, Fig. 6) or SLC16A7 (24 h, Fig. 7). Mean grey levels in zygotes cultured in KSOM (Figs 6A and 7A and white bars in corresponding graphs) were accepted as control levels, and all other mean grey levels were compared with controls. In glucose-deprived zygotes (Fig. 6B and graph), PPARα immunoreactivity was about 15% more intense (P < 0.05), DPI completely blocked this increase (Fig. 6C), but was ineffective on the quantitatively similar WY14643 induction of PPARα (Fig. 6D and E and graph). This pattern was replicated by SLC16A7, except that the glucose deprivation (Fig. 7B and graph) or WY14643 induction (Fig. 7D and graph) was almost 150% in both cases, possibly reflecting the different times of observation, 8 h for PPARα and 24 h for SLC16A7.

Discussion

Although reliant upon monocarboxylates rather than glucose for ATP production, cleavage stage mammalian embryos are exquisitely tuned to glucose supply. Given that glucose deprivation is a potent cell stressor, that glucose can act as a signalling molecule to permit metabolic differentiation (Pantaleon et al. 2008) and that glucose deprivation increases partly peroxisomal SLC16A7 expression (Jansen et al. 2008), we set out to examine the impact of glucose deprivation on early embryonic oxidative stress.

PPARα, SLC16A7 and catalase

PPARα is a nuclear receptor from the steroid receptor superfamily (Issemann & Green 1990) activated by concurrent dimerization with RXR, phosphorylation of specific sites (including Ser12 and Ser21) and the attachment of activating ligands, including unsaturated fatty acids and derivatives of the lipoxygenase route of the arachidonic acid cascade (Diradourian et al. 2005). Activation of PPARα tends to induce further expression of PPARα (Sharifpanah et al. 2008) and subsequent peroxisome proliferation, including the transcription of peroxisomal β-oxidation-encoding genes such as acyl-CoA oxidase, multifunctional protein and thiolase (Bardot et al. 1995).

Never examined in preimplantation embryos, PPARα has been detected in mouse embryonic stem (ES) cells (Sharifpanah et al. 2008) that originate as pluripotent cells of the inner cell mass (ICM) of the day 4 embryo or blastocyst where they are completely isolated from the external/maternal milieu by the epithelial trophectoderm. ICM cells convert all glucose supplied via the trophoderm to lactate (Hewitson & Leese 1993).

Figure 3 Effect of cycloheximide (A) and α-amanitin (C) on SLC16A7 expression in response to the presence or absence of glucose. Embryos were cultured from 18 h post-hCG and SLC16A7 immunoreactive expression was assessed and quantified as described. Results represent the mean ± S.E.M. grey scale intensity per embryo from a minimum of three embryos per treatment, in each of three experiments (A and C); ***P < 0.001 by ANOVA and Bonferroni post-test relative to control treatment within each time point. Representative images of SLC16A7 immunoreactivity following 12 h of culture in response to indicated treatments are also shown. When glucose was supplied (KSOM), SLC16A7 immunoreactivity, which appears localized to cytoplasmic granules as well as on the plasma membrane, is elevated both in response to glucose deprivation and treatment with 10 μM PPARα agonist WY14643. While treatment of embryos with both 2 mg/ml cycloheximide and 1 μg/ml α-amanitin had no apparent effect at 4 h of culture, both treatments completely inhibit this stimulated increase in SLC16A7 expression following 12 h of culture (C and D).
Ppara mRNA is expressed in the zygote and two-cell mouse embryo, but cannot be detected in pooled cDNA from the equivalent of four morulae cultured with glucose. Similarly, the protein disappears from glucose-supplied embryos as they develop through the cleavage stages in vitro. But if embryos are glucose deprived, the mRNA persists in morulae and the protein is upregulated after 8 h deprivation. Moreover, glucose deprivation prevented the dephosphorylation of PPARα–phospho-Ser12 that occurs when glucose is supplied. More importantly, it doubled the concentration of nuclear phospho-PPARα at 24 h, consistent with increased transcriptional activity associated with, among other things, peroxisome proliferation. This pattern was replicated when glucose-supplied embryos were treated with the PPARα agonist WY14643. So one mechanism triggered by glucose deprivation involves nuclear recruitment of phospho-PPARα with consequent peroxisomal proliferation and likely metabolic re-orientation. In different cells and with different stimuli, phosphorylation can activate or deactivate PPARα (Gelman et al. 2005). Supporting these results, there is evidence that glucose deprivation stabilizes PPARα mRNA, reducing its degradation, and increases mRNA levels for PPARGC1A, a major co-activator of PPARα (Bogdanova et al. 2007). Several groups have reported upregulation of PPARα activity in response to fasting (Sterchele et al. 1996, Hashimoto et al. 2000, Escher et al. 2001, Sugden et al. 2001) and in sheep, maternal nutrient restriction between 28 and 80 days gestation induced PPARα expression in offspring (Bispham et al. 2005, Budge et al. 2005). In addition to this induction and activation by glucose deprivation, PPARα activation rapidly increased PPARα levels by parallel self-induction of transcription and also through inhibited polyubiquitination and proteasomal degradation (Hirotani et al. 2001).

Results herein demonstrate that PPARα activation induced SLC16A7 expression even when glucose was supplied, because transcriptional and translational inhibitors had the same degree of inhibition of induction. This suggests that activated PPARα, possibly phospho-PPARα, acts to promote SLC16A7 expression. SLC16A7 has not been identified as a target protein for peroxisome proliferation, but PPARs affect target genes by binding to a specific DR1 motif in a peroxisome proliferator-response element (PPRE) located upstream in the promoter region (Latruffe et al. 2000). A brief assessment of the Slc16a7 gene identified such a DR1 sequence as well as sites for many stress-associated transcription factors such as: GATA; CREB; FKHD; HIF; and NFKB (Table 1), providing further support for the conclusion that the PPARα activation is upstream of SLC16A7 induction. Because of the association of MCT with peroxisomes and peroxisomal metabolism, it is likely that SLC16A7 is induced along with other key peroxisomal proteins during peroxisomal proliferation.

Catalase, on the other hand, appeared to have different regulatory modes from SLC16A7. Both glucose deprivation and PPARα agonism (WY14643) increased catalase expression even after 4 h of culture. These results are supported by evidence of PPARα induction upregulating catalase (Nemali et al. 1989) and the existence of a functional PPRE in the catalase promoter (Girnun et al. 2002). As in mouse zygotes, in both these studies, α-amanitin treatment only marginally reduced the increase in catalase immunoreactivity, suggesting

**Figure 4** ROS production in mouse embryos deprived of glucose. Mouse embryos (CBA/F1) were collected at 18 h post-hCG, cultured for 2 or 4 h in standard KSOM, KSOM-lacking glucose (KSOM-G) or KSOM with 10 μM WY14643 and ROS assayed as described in Materials and Methods. Data represent mean fluorescence of culture groups divided by mean fluorescence of average esterase activity from randomly sampled embryos. Within 2 h of culture, ROS levels in glucose-deprived embryos or WY14643-treated embryos are higher than those in embryos cultured in standard KSOM (*P<0.05). While the ROS levels remain high in the presence of WY14643 at 4 h post-culture (*P<0.05), in glucose-deprived embryos they decline to reach levels not significantly different from glucose-supplied embryos (P>0.05).

**Figure 5** Effect of DPI on embryonic ROS production. CBA/F1 mouse zygotes were collected at 18 h post-hCG, cultured for 2 h in standard KSOM, KSOM-lacking glucose, KSOM-lacking glucose with 0.1 μM DPI, KSOM with 10 μM WY14643 in DMSO, KSOM with 10 μM WY14643 in DMSO and 0.1 μM DPI, KSOM with DMSO 1:10 000. They were then assayed for ROS as described in Materials and Methods. Data represent mean fluorescence of culture groups divided by mean fluorescence of average esterase activity from randomly sampled embryos. The addition of DPI into the media of glucose-deprived embryos reduced ROS levels in these embryos to a level that was not statistically different from that in glucose-supplied embryos. In embryos cultured with WY14643, DPI reduced ROS levels, but they remained significantly higher than those in glucose-supplied embryos. Means with different superscripts are significantly different (P<0.05). Results from embryos cultured in KSOM+DMSO 1:10 000 were not statistically different from KSOM alone (not shown).
Metabolic stress in embryos

Tyrosine kinase and the product of the pathway involving activation of ABL1 non-receptor response to stress is increased in a biphasic pattern via evidence that proteasomal degradation of catalase in different (remained elevated. Means with different superscripts are significantly different from those of glucose-supplied embryos. This was not the case for embryos treated with WY14643 and DPI. When DPI was added to glucose-deprived embryos, SLC16A7 staining was reduced to levels not statistically different from those of glucose-supplied embryos. This was not the case for embryos cultured with WY14643 and DPI, where pan-PPARA staining remained elevated. Means with different superscripts are significantly different (P<0.05).

A more complex regulation of catalase involving transcriptional and post-transcriptional levels. This evidence has been confirmed in many investigations that have identified post-transcriptional controls for catalase activity (Yano et al. 1998, 2004, Yano & Yano 2002, Cao et al. 2003, Vivancos et al. 2004). There is evidence that proteasomal degradation of catalase in response to stress is increased in a biphasic pattern via a pathway involving activation of the ABL1 non-receptor tyrosine kinase and the product of the ABL1-related gene (Arg). It may be that the level of H$_2$O$_2$ generated in the glucose-deprived embryos was insufficient to promote binding of ABL1 and Arg to catalase thus increasing stability (Cao et al. 2003). Additionally, because embryonic genome activation does not occur until the mid-late two-cell stage, it is possible that a greater part of catalase induction relies on pre-formed maternal mRNA delivered in the oocyte and not yet degraded.

Glucose deprivation by preventing pentose phosphate pathway flux and NADPH production induces ROS leading to PPARA induction and peroxisome proliferation. However, PPARA activation similarly leads to ROS and peroxisome proliferation. Investigation herein of the source of ROS in embryos using the NADPH oxidase inhibitor, DPI, revealed attenuation of the ROS peak generated by PPARA agonists, but not completely. In contrast, in mouse ES cells, WY14643-induced activation of PPARA caused ROS elevation that was attenuated with DPI, but not the mitochondrial electron transport inhibitor rotenone (Sharifpanah et al. 2008). However, it is possible that the extended ROS peak produced by the PPARA agonist might arise from the contribution of ROS arising from sources other than those involved in glucose deprivation-induced ROS. It has been demonstrated that hepatocytes in NADPH oxidase-deficient (p47phox-null) mice treated with WY14643 still exhibit acute increased ROS with a rapid increase in oxidative DNA damage and increased cell proliferation, a response that is potentially mediated through nuclear factor kappa B (Woods et al. 2007).

These observations may explain why the DPI protocol was ineffective in reducing ROS levels in agonist-treated embryos to the same extent as those deprived of glucose. Alternatively, the extended ROS peak may arise from β-oxidation of lipids (Piot et al. 1998, Teissier et al. 2004, Poirier et al. 2006). The 10 μM WY14643 used in these experiments is likely to be far in excess of the concentration of activated PPARA induced by glucose deprivation, and it is not unreasonable to assume that exaggerated oxidative stress is occurring in this situation. Studies in rat liver have shown that PPARA induction by

![Figure 6](Image 56x555 to 279x716)

Figure 6 Effect of DPI on embryonic PPARA. Three experimental sets of CBA/F1 mouse embryos cultured for 8 h under varied conditions were fixed and underwent simultaneous immunocytochemistry for PPARA. Immunoreactivity for PPARA in all embryos was diffused throughout the cytoplasm and stained weakly in nuclei, but was noticeably absent from nucleoli. Representative embryos from groups cultured in: KSOM (A, glucose supplied), KSOM-lacking glucose (B, glucose deprived), KSOM-lacking glucose with 0.1 μM DPI (C), KSOM with 10 μM WY14643 in DMSO (D), KSOM with 10 μM WY14643 in DMSO and 0.1 μM DPI (E) are shown. The average grey levels for glucose-deprived embryos or treated with WY14643 were higher than for glucose-supplied embryos. When DPI was added to glucose-deprived embryos, the pan-PPARA staining was reduced to levels not statistically different from that of glucose-supplied embryos. This was not the case for embryos cultured with WY14643 and DPI, where pan-PPARA staining remained elevated. Means with different superscripts are significantly different (P<0.05).

![Figure 7](Image 313x241 to 536x395)

Figure 7 Effect of DPI on embryonic SLC16A7. Three experimental sets of CBA/F1 mouse embryos cultured for 24 h under varied conditions were fixed and underwent simultaneous immunocytochemistry for SLC16A7. In all embryos, SLC16A7 staining was located on the plasma membrane and in the cytoplasm as stippling or tiny granules. Representative embryos from groups cultured in: KSOM (A, glucose supplied), KSOM-lacking glucose (B, glucose deprived), KSOM-lacking glucose with 0.1 μM DPI (C), KSOM with 10 μM WY14643 in DMSO (D), KSOM with 10 μM WY14643 in DMSO and 0.1 μM DPI (E) are shown. When quantified, SLC16A7 staining in glucose-deprived embryos or in glucose-supplied embryos treated with WY14643 was higher than for embryos cultured in KSOM alone. When DPI was added to glucose-deprived embryos, SLC16A7 staining was reduced to levels not statistically different from those of glucose-supplied embryos. This was not the case for embryos treated with WY14643 and DPI whose SLC16A7 staining remained significantly elevated. Means with different superscripts are significantly different (P<0.05).
peroxisome proliferators produces differential regulation of peroxisomal enzymes (Nemali et al. 1989, Yeldandi et al. 2000). WY14643, in particular, induced a 20-fold increase in the genes encoding peroxide-generating enzymes like fatty acyl-CoA oxidase and cytochrome P450 (CYP) 4A isoforms for peroxisomal β-oxidation within 30 min to 1 h, while catalase displayed only a 2-fold increase. This results in overwhelming generation of H₂O₂ within peroxisomes, with possible overflow into the cytoplasm.

While there is very little information on peroxisomal activity in embryos, it is pertinent to note that a knock-out model for the mitochondrial fatty acid oxidation enzyme long-chain acyl-CoA dehydrogenase (LCAD) appears to block mouse embryo development at the morula stage (Berger & Wood 2004). This group demonstrated that Lcad⁻/⁻ embryos cannot complete the development of a blastocoele and formation of a blastocyst, and subsequently degenerate at the morula stage, similarly to embryos deprived of glucose. Supplementation with shorter chain fatty acids that could be readily oxidized did not rescue development, suggesting that longer chain fatty acid oxidation does occur and plays a vital role in mouse development. LCAD and many other mitochondrial β-oxidation enzymes (L-type carnitine palmitoyltransferase I and medium-chain acyl-CoA dehydrogenase) are regulated by PPARA (Ringseis et al. 2007). This brings an interesting insight into our experiments. It seems that while PPARA appears to be activated in the presence of glucose, this in itself is not enough to overcome the block to development. Perhaps this is because mouse embryos at this early stage do not have enough fatty acid stores to derive enough energy via β-oxidation. The addition of exogenous medium and long-chain fatty acid substrates in the absence of glucose may have allowed these embryos to progress. This question needs further study.

The importance of fatty acid oxidation to early development is further illustrated by the benefits to blastulation of supplementation with long-chain fatty acids in rabbit (Kane 1979) and mouse (Quinn & Whittingham 1982); while in mice, palmitic acid oxidation, constant until the eight-cell stage, accelerates as blastulation progresses (Hillman & Flynn 1980), providing a metabolic explanation for this benefit. In humans, palmitic acid uptake increases to the morula stage before declining co-incidentally with increased linoleic acid uptake and blastulation (Haggarty et al. 2006). Supporting evidence for preimplantation peroxisomal function now exists in the present association of SLC16A7 with oxidative stress induced by glucose deprivation or PPARA activation. SLC16A7 might exist in the peroxisomal membrane to facilitate pyruvate import for conversion to lactate via peroxisomal LDH. As hypothesized by McClelland et al. (2003) in relation to rat liver peroxisomes, this would enable recycling of NAD⁺ for continued peroxisomal β-oxidation of long-chain fatty acids and lactate export to the cytoplasm could be facilitated by SLC16A7, either for subsequent mitochondrial metabolism or facilitated excretion to the oviduct. Adding further support to this argument, providing high lactate concentrations in the incubation medium reduced not only pyruvate utilization, but also the NAD⁺/NADH ratio (Lane & Gardner 2000). So it is possible that preimplantation embryos do utilize their peroxisomes for lipid oxidation and that peroxisomal

### Table 1
Putative transcription regulatory sequences in the 2.4 kb region upstream of the mouse Slc16a7 gene.

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The 2.4 kb sequence upstream of the Slc16a7 ATG of the mouse sequence (GenBank: NM_011391) was analysed by MatInspector, a transcription factor database.

¹The positions of the putative binding sites are shown as the distance (bp) from the first nucleotide of the mouse Slc16a7 promoter region (GenBank: NM_011391).

²The (+) and (−) indicate that the putative motifs are located on the plus or minus strands of this upstream 2.4 kb sequences.
proliferation leads to increased ROS production from this source.

The association of PPARA activation and cardiomyogenic inducing transcription factors (Sharifpanah et al. 2008) perhaps reflects metabolic differentiation to lipid oxidation dependent rather than glycolytic, metabolic profile. This is not too different from the requirements of the glucose-deprived cleavage stage embryo that must rely on accelerated uptake of monocarboxylates or perhaps exogenous oocyte-derived lipid. There is evidence in species where oocytes are more lipid loaded than mice, of lipid metabolism being related to developmental potential (Zeron et al. 2001, Boni et al. 2002, Nagano et al. 2006). The analogy between the embryo and ES cells is reinforced by the observation that PPARA activation leads to increased intracellular ROS. In both cases, NADPH oxidase inhibited by DPI contributes to this ROS, but while this is the only ROS source induced in ES cells in embryos, because DPI did not limit ROS concentrations to unstimulated levels, it is likely that other sources also contribute, such as lipid oxidation or mitochondrial respiratory chain. There is a parallelism in the metabolic fate directed by PPARA activation in ES cells and early embryos. ES cells are derived from ICM cells that are known to rely on oxidation of glucose to lactate for energy (Loneragan et al. 2007). The early embryonic cells generate their ATP from of monocarboxylate oxidation. Adult cardiomyocytes oxidize long-chain fatty acids; fetal heart prefers glucose/lactate (van der Vusse 2007). The early embryonic cells generate their ATP from monocarboxylate oxidation. Adult cardiomyocytes oxidize long-chain fatty acids; fetal heart prefers glucose/lactate (van der Vusse 1992). Metabolic differentiation from the progenitor cells thus must produce increased peroxisomal and associated MCT activity. As this study demonstrates, this is exactly the outcome of fibrate activation of PPARA in totipotent embryonic cells. The unusual metabolic profile of the early embryo, relying on mitochondrial ATP generation from the monocarboxylic acids such as pyruvate and lactate, has proved a useful model. The small amounts of glucose normally taken up are thought to be metabolized by the pentose phosphate pathway for the maintenance of reducing power in the cell and in nucleic acid and lipid biosynthesis. In this study, glucose deprivation ablates pentose phosphate pathway activity, of itself limiting NADPH production, but also prevents the dynamic rerouting of metabolic flux to the pentose phosphate pathway, which has been proposed as a conserved post-translational response to oxidative stress (Rals et al. 2007). This suggests that the use of glucose-deficient media in modern-assisted reproductive technologies might require some experimental re-examination.

We have demonstrated that very early embryonic cells experience glucose deprivation as an acute stressor, despite their novel metabolic reliance on monocarboxylates. Within only 2 h of glucose deprivation, ROS was elevated, increasing PPARA levels that preceded peroxisomal proliferation. PPARA activation also leads to peroxisomal proliferation and increased ROS. Interestingly, although not required for energy metabolism, provision of glucose as would be normal in situ does not support induced ROS or peroxisome proliferation, suggesting an important stress monitor role for glucose.

Materials and Methods

Ethics

The Animal Ethics and Experimentation Committees of the University of Queensland and the University of Adelaide approved all experiments on mice. These committees are approved by the National Health and Medical Research Council of Australia.

Media, chemicals and buffers

Handling media

M2 medium (Fulton & Whittingham 1978) modified to contain 0.33 mM sodium pyruvate and 4 g/l of BSA (Sigma–Aldrich, fraction V, A-9647) and lacking glucose.

Culture media

KSOM containing 0.2 mM glucose but no amino acids (Erbach et al. 1994). WY14643 (Sigma–Aldrich), a selective PPARA agonist and peroxisome proliferator, was tested for toxicity on zygotes 18–20 h post-hCG at concentrations of 0.1–10 μM in KSOM. None of these concentrations affected the proportion of embryos developing to the blastocyst stage by 96 h post-hCG, so 10 μM were selected for experiments. CHX (2 mg/l CHX, Sigma–Aldrich (Heo & Han 2006)), and α-amanitin (1 mg/l αAA, Fluka, 06422 from Sigma–Aldrich (Liu et al. 2004)), were used to inhibit translation and transcription respectively. DPI (Sigma–Aldrich), an irreversible inhibitor of flavoenzymes, particularly activated NADPH oxidase, with tenfold lower potency for NADH oxidase (Morré 2002), inhibits the production of peroxide by the blockade of several NADP-dependent enzymes in the pentose phosphate pathway and tricarboxylic acid cycle. DPI was toxicity tested on zygotes 18–20 h post-hCG at concentrations of 0.01–10 μM in KSOM, for 20 and 40 min exposure times and 20 min exposure to 0.1 μM. DPI was used in experiments because it did not affect blastocyst development and was the EC50 for HeLa cell NADPH oxidase (Morré 2002).

Homogenization buffer

Fifty millimoles Tris–HCl; 150 mM NaCl; 10 mM NaF; 1 mM Na3VO4; 1% Triton X-100; 1 complete protease inhibitor tablet per 50 ml buffer (Roche Diagnostics Australia P/L).

Laemmli sample buffer (Laemmli 1970)

Ten percent SDS containing 1% glycerol; 0.125 g/l bromophenol blue; 0.125 g/l xylene cyanol; 100 mM diithiothreitol; 125 mM Tris–HCl, pH 6.8. Towbin transfer buffer (Towbin et al. 1979): 25 mM Tris; 192 mM glycine; 20% methanol, pH 8.3.
Embryo collection and culture

For some experiments (Figs 1–3), female 6–8-week-old Quackenbush mice from a high fecundity colony at the University of Queensland were injected with 10 IU equine chorionic gonadotrophin (eCG, Folligon, Intervet P/L, East Bendigo, VIC, Australia) and 48 h later with 10 IU hCG (Chorulon, Intervet). In experiments involving H2O2 (Figs 4–7), CBA/F1 hybrid mice from a colony at the University of Adelaide were injected with 5 IU eCG (Sigma–Aldrich) and 48 h later with 5 IU hCG (Pregnyl; Organon Inc., Roseland, NJ, USA). Embryos were collected ex vivo at 24, 48, 72 and 96 h post-hCG into glucose-free M2 and cultured in KSOM (Erbach 1988, modified embryo/etch et al 1990) M2, then washed thrice in fresh glucose-free M2. Cumulus cells were removed where necessary using 0.5 g/l hyaluronidase (Sigma–Aldrich) in glucose-free M2, then washed thrice in fresh glucose-free M2.

For experiments in vitro, zygotes (18 h post-hCG) were collected into glucose-free M2 and cultured in KSOM (Erbach et al. 1994) microdroplets under mineral oil at a density of 1 embryo/µl in 4.7% O2, 4.7% CO2, 6.1% H2O and 84.5% N2 at 37°C in a MINC incubator (Cook, Eight Mile Plains, QLD, Australia). KSOM contained 0 mM (KSOM-G, glucose deprived) or 0.2 mM glucose (KSOM, glucose supplied), and in some experiments variations of both KSOM and KSOM-G contained 10 µM WY14643 or 0.1 µM DPI or both. Cultured embryos were sampled at various stages for different experiments as described.

mRNA analysis

Total RNA was extracted from pools of 100 morphologically normal embryos collected after 30 or 54 h culture of zygotes collected at 18 h post-hCG, using phenol/chloroform and the RNeasy Mini Kit (Qiagen). For positive controls, RNA was extracted from mouse kidney or liver and 1 µg used for RT. RNA was reverse transcribed and amplified by PCR (Arcellana-Panilio & Schultz 1993) using specific primers for Ppara: 5’ primer, 5’-tgatgagatgcctcctgct-3’; 3’ primer, 5’-ggtagaagctgaggtagttgtag-3’. Agarose gel (1%) containing 0.5 mg/l ethidium bromide was used to resolve the 412-bp product. All cDNA samples were tested for genomic contamination using parallel PCR for mouse β-actin with primers: 5’ primer 5’-ctgggctgctgcgggtg-3’; 3’ primer, 5’-ttgccctgagcggtagggg-3’, which span the first intron of the mouse β-actin gene producing a 243-bp cDNA fragment and a 330-bp fragment from contaminating genomic DNA (Telford et al. 1990). Using Gel Extraction Kit (Qiagen), PCR products were extracted and ligated into a pGem-T Easy Vector (Promega), then amplified in transformed DH5α Escherichia coli cells and purified using QIAprep Spin Miniprep Kit (Qiagen). EcoRI (Roche Diagnostics GmbH) was used to digest purified plasmid clones, which were then sequenced by the Australian Genome Research Facility (Brisbane, QLD, Australia) to confirm sequence identity.

Antisera

Affinity-purified anti-SLC16A7 IgG was raised in goats against a synthetic peptide mapping to the carboxy terminus of mouse SLC16A7 (14926, Santa Cruz Biotechnology, Santa Cruz, CA, USA). Anti-catalase antiserum was raised in rabbits against whole purified bovine liver catalase (200-4151, Rockland Immunocytotechnologies Inc., Gilbertsville, PA, USA). Affinity-purified anti-PPARA IgG was raised in rabbits against a synthetic peptide corresponding to N-terminal amino acids 1–18 of mouse PPARA (ab8934, Abcam, Cambridge, UK), amino acids 8–19 of serine-12-phosphorylated mouse PPARA (Abcam ab3484) and amino acids 14–25 of serine 21-phosphorylated mouse PPARA (Abcam ab3485). Secondary antibodies used for immunofluorescence or western immunoblotting included: FITC-conjugated rabbit anti-goat IgG (Calbiochem, EMD Chemicals Inc., SanDiego, CA, USA); FITC-conjugated goat anti-rabbit IgG (Calbiochem); Texas Red-conjugated goat anti-rabbit IgG (Calbiochem); HRP-labelled donkey anti-rabbit IgG (Amersham Biosciences); or rabbit anti-goat IgG (Progen Biosciences, Toowong, QLD Australia).

Immunofluorescence

Embryos fixed in 2% paraformaldehyde in PBS (pH 7.4) underwent immunohistochemical processing (Pantaleon et al. 1997). Briefly, overnight incubation in primary antibody (2–10 mg/l) at 4°C was followed by exposure to secondary antisera for 1 h at room temperature. Samples were mounted in glycerol on concave glass slides and observed with a BioRad MRC-1024 confocal laser-scanning microscope mounted on a Zeiss (Oberkochen, Germany) AXiostep using a Zeiss Plan-APOCHROMAT ×60 oil immersion objective. Where necessary for statistical analysis, after fixing, triplicate experimental sets were accumulated and held for 1–3 days at 4°C reducing variability.

Western immunoblotting

Mouse liver was homogenized in ice-cold homogenization buffer and centrifuged at 14,000 g for 15 min at 4°C. Supernatant was removed and mixed with an equal volume of Laemmli sample buffer. Pools of 100 embryos in minimal medium were placed in 5 µl homogenization buffer with equal volume of Laemmli sample buffer. Liver and embryo samples were separated by PAGE and transferred via semi-dry electrottransfer to 0.45 µm Immobilon-P PVDF membrane (Millipore P/L, North Ryde, NSW, Australia) using Towbin transfer buffer. Membranes were incubated at room temperature for 1 h in blocking solution of 7.5% BSA in PBS with 0.1% Tween-20, before incubation with primary antisera (0.1 mg/l) overnight at 4°C. Finally, membranes were exposed for 1 h at room temperature to donkey anti-rabbit secondary antibody conjugated to HRP, and bands revealed with Supersignal West Femto Enhanced Chemiluminescence Detection Kit (Pierce Biotechnology Inc., Rockford, IL, USA) on X-ray film developed in a Kodak M35 X-Omat Processor (Kodak Australasia P/L).

ROS assay

Levels of ROS generation in embryos were assessed fluorometrically using 2’,7’-dichlorodihydrofluorescein diacetate (DCFDA, Sigma–Aldrich) as previously described (Nasr-Esfahani et al. 1990). Esterases within the cells cleave DCFDA to the active form, DCFH, which produces a fluorescent product upon oxidation by superoxide.


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the acetate groups trapping the reduced form of the probe (DCHF) intracellularly, which is readily oxidized to dichlorofluorescein (DCF) by H_2O_2 or OH-, but is relatively insensitive to (Vanden Hoek et al. 1997, Hempel et al. 1999). Zygotes (18–20 h post-hCG) from CBA/F1 hybrid mice collected into M2-lacking glucose were stripped of cumulus before random allocation into: KSOM; KSOM-G; KSOM-G + 0.1 μM DPI; KSOM + 10 μM WY14643 in DMSO (1:10 000); KSOM + 10 μM WY14643 in DMSO + 0.1 μM DPI; KSOM+DMSO (1:10 000). After 20 min, embryos were washed free of DPI (flavoenzyme inhibitor) and returned to the same culture conditions without DPI. (At this time, embryos from each experimental group were randomly sampled and incubated for 30 min in 1 ml media containing 10 μM 6-carboxy-2',7'-dichlorodihydrofluorescein diacetate (DCFDA) that fluoresces upon esterification to measure average total embryonic esterase activity.) After 1.5 or 3.5 h, DCHFDA (10 μM) was applied to each culture for 30 min, and then embryos were washed free of BSA and placed on glass coverslips in 10 μl BSA-free media. Green DCF or CDCF fluorescence from each embryo was quantitated separately using a microfluorometer with filter excitation and emission wavelengths set at 460 and 510 nm respectively. Results were standardized by calculating the fluorescence ratio relative to the total average embryonic esterase activity.

**Statistical analysis**

Immunohistochemical expression levels were estimated from the pixel intensity of images using Image-J Software (National Institutes of Health, Bethesda, MD, USA). Embryos from three separate experiments underwent immunofluorescent staining at the same time, and all were analysed the next day using uniform confocal microscope settings to permit statistical analysis of staining intensity. Average grey level intensity from each embryo in each culture group was quantified with Image J, and mean grey levels per culture group per experiment were calculated. These data and those from measured ROS assays were compared by multi-variance ANOVA using Statgraphics Software. Values are presented are means ± S.E.M. for triplicate experiments.

**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**

This research was supported by grants to P L Kaye and M Pantaleon from the National Health and Medical Research Council of Australia (grant no. 210194) and to M Pantaleon, J G Thompson and P L Kaye from the NICHD (grant no. U01 HD 44664).

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**Acknowledgements**

Sincere thanks to Michelle Lane for technical guidance with ROS experiments.

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Received 6 February 2009
First decision 30 March 2009
Revised manuscript received 3 June 2009
Accepted 16 June 2009