

IUGR Alters Postnatal Rat Skeletal Muscle Peroxisome Proliferator-Activated Receptor- γ Coactivator-1 Gene Expression in a Fiber Specific Manner

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ABSTRACT

Uteroplacental insufficiency and subsequent intrauterine growth retardation (IUGR) increase the risk of insulin resistance in humans and rats. Aberrant skeletal muscle lipid metabolism contributes to the pathogenesis of insulin resistance. Peroxisome proliferator-activated receptor- γ co-activator-1 (PGC-1) is a transcriptional co-activator that affects gene expression of key lipid metabolizing enzymes such as carnitine palmitoyl-transferase I (mCPTI). Because gene expression of lipid metabolizing enzymes is altered in IUGR postnatal skeletal muscle, and we hypothesized that PGC-1 expression would be similarly affected. To prove this hypothesis, bilateral uterine artery ligation and sham surgery were used to produce IUGR and control rats respectively. Western Blotting demonstrated that PGC-1 hind limb skeletal muscle protein levels were increased in perinatal and postnatal IUGR rats. Conventional RT-PCR demonstrated that PGC-1 mRNA levels were similarly increased in perinatal hind limb skeletal muscle and juvenile extensor digitorum longus (EDL), but were decreased in juvenile soleus. Because a gender specific trend was noted in PGC-1 mRNA levels, real time RT-PCR was used for further differentiation. Real time RT-PCR

revealed that changes in postnatal skeletal muscle PGC-1 expression were more marked in male IUGR rats *versus* female IUGR rats. Down stream targets of PGC-1 followed a similar pattern of expression. We conclude that PGC-1 expression is altered in rat IUGR skeletal muscle and speculate that it contributes to the pathogenesis of insulin resistance in the IUGR rat. (*Pediatr Res* 53: 994–1000, 2003)

Abbreviations

- CD36**, fatty acid translocase
- CoxIV**, cytochrome *c* oxidase subunit I
- EDL**, extensor digitorum longus
- IUGR**, intrauterine growth retardation
- mCPTI**, muscle isoform of carnitine palmitoyl-transferase I
- mTFA**, mitochondrial transcription factor A
- NRF-1**, nuclear respiratory factor 1
- PGC-1**, peroxisome proliferator-activated receptor- γ coactivator-1
- UCP-2**, uncoupling protein 2

Barker's Fetal Origins of Adult Disease Hypothesis proposes that fetal adaptation to a deprived intrauterine milieu leads to permanent changes in cellular biology and systemic physiology (1). Intrauterine growth retardation (IUGR) predisposes affected newborns toward the development of insulin resistance and dyslipidemia (2). Although both insulin defi-

ciency and resistance contribute to the IUGR diabetic phenotype, asymmetrical IUGR individuals are often characterized by insulin resistance. Uteroplacental insufficiency, a morbidity associated with many common complications of pregnancy induces asymmetrical IUGR (3, 4). In the rat, uteroplacental insufficiency results in juvenile IUGR animals whose glucose homeostasis is abnormal only when physiologically challenged on a pharmacological level (5). By adulthood, these IUGR rats develop overt diabetes that is characterized by insulin resistance and hypertriglyceridemia (5, 19, 20).

An important component contributing to the pathogenesis of skeletal muscle insulin resistance is altered fatty acid homeostasis (6, 7). Hind limb skeletal muscle from 21-d-old

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IUGR rats is characterized by increased skeletal muscle triglycerides and increased mRNA levels of carnitine palmitoyl transferase I (mCPTI), which is an important rate limiting enzyme of fatty acid oxidation β -oxidation (8, 9). Peroxisome proliferator-activated receptor- γ coactivator-1 (PGC-1) is a transcriptional co-activator that induces expression of mCPTI, as well as other mitochondrial proteins such uncoupling protein-2 (UCP-2) (10, 11). PGC-1 polymorphisms have been linked to an increased genotype relative risk of Type II diabetes, and PGC-1 expression is increased in IUGR rat liver (12–14). We therefore hypothesized that PGC-1 gene expression would be similarly increased in postnatal rat skeletal IUGR skeletal muscle, and that the change in PGC-1 gene expression would be associated with increased expression of mCPTI and UCP-2.

To prove this hypothesis, bilateral uterine artery ligation (IUGR) and sham surgery (CON) were performed on day 19 of gestation (term 21.5 d). In this well characterized and widely published model of asymmetrical growth retardation, IUGR pups are 20% to 25% lighter than the sham operated control animals, and birth weights are normally distributed within and among litters (3, 5, 8, 9, 12, 15–19). Litter size does not significantly differ between control and IUGR groups (8). Skeletal muscle protein and mRNA levels of PGC-1 were measured in rats at day 0 (N0) and day 21 (J21) of postnatal life. The J21 rat were studied because they do not exhibit fasting hyperglycemia, hypertriglyceridemia, or hyperinsulinemia, and their peripheral insulin resistance is evident only when challenged with pharmacological levels of glucose (5, 20).

Conventional RT-PCR was used to determine PGC-1 mRNA levels in soleus (type I) and extensor digitorum longus (EDL) (type II) fibers in J21 animals, and a trend was noted differentiating expression between male and female animals IUGR animals. As a result, real time RT-PCR was used to further differentiate gender specific PGC-1 mRNA expression, as well as two of its down stream targets, carnitine palmitoyl transferase I (mCPTI) and uncoupling protein 2 (UCP2). CD36 mRNA levels were measured to determine whether they are potentially related to PGC-1 expression. CD36 is a fatty acid translocase whose mRNA levels have been directly linked to increased skeletal muscle triglycerides, a characteristic of the juvenile IUGR rat (9, 21).

METHODS

Animals. All procedures were approved by the UCLA Chancellor's Animal Research Committee. These surgical methods have been previous described (8, 9, 20, 22). On day 19 of gestation, the maternal rats were anesthetized with intraperitoneal xylazine (8 mg/kg) and ketamine (40 mg/kg), and both uterine arteries were ligated (IUGR) ($n = 8$ litters). Sham surgery was performed upon control animals who underwent identical anesthetic and surgical procedures except for the uterine artery ligation (CON) ($n = 8$ litters). N0 pups were delivered by caesarian section ($n = 4$ litters CON and IUGR respectively).

For conventional and real time RT-PCR N0 studies, hind limb RNA was isolated and quantified from 3 individual animals. Because N0 animals do not provide a great deal of hind limb skeletal muscle, samples from three animals per litter were pooled for protein isolation. The remaining maternal rats were allowed to deliver spontaneously, and litters were randomly culled to 6 to minimize any effects due to litter size (23).

J21 animals were separated from their dams for 4 h (to minimize individual hormonal variations associated with feeding), anesthetized, and killed ($n = 4$ litters Con and IUGR respectively). Whole hind limb skeletal muscle was harvested at J21 for Western Blotting from 3 animals per litter. Similarly, extensor digitorum longus (EDL) and soleus were harvested at J21 for both conventional and real time RT-PCR from three animals per litter.

Western blotting. Protein was isolated by centrifugation after tissue homogenization in Laemmeli lysis buffer. 100 μ g of protein was separated on a SDS-PAGE gel along with molecular weight markers and subsequently transferred to nitrocellulose. The nitrocellulose was incubated in Blotto solution, and then with rabbit PGC-1 primary antibody (1:100) (Chemicon, Temecula CA). The filters were then washed before incubation with secondary anti-rabbit antibody (1:1000 dilution). The filters were washed, and detection was performed using ECL chemiluminescence (Amersham, Piscataway NJ). The products were quantified by densitometry after standardization for loading. Each blot was replicated three times.

Muscle fiber typing. To determine whether differences in J21 PGC-1 protein levels may be due to differences muscle fiber type distribution, myosin heavy chain isoforms were quantified. Hind limb muscles from 21-d-old rats were removed and scissor minced in four volumes of Guba-Straub high salt buffer, pH 6.5. Extracts were centrifuged at 13,000 \times g and the supernatants were recovered for electrophoresis (24). Extracted myosin was diluted 10-fold in 1 mM EDTA and 0.1% 2-mercaptoethanol, stored overnight at 4°C to precipitate myosin filaments, and centrifuged to pellet filaments. These were subsequently dissolved in 0.5M NaCl and 10mM NaH₂PO₄ and diluted in sample buffer. Electrophoresis was carried out according to the protocol described previously (25). Briefly, mini-gels consisting of 8% acrylamide separating gels and 4% stacking gels were run at 70V for 24 h at 4°C. Both separating and stacking gels contained 30% glycerol. Approximately 1 μ g of myosin extract was loaded per sample. Gels were silver stained and quantitated with a scanning densitometer. Each sample was scanned 5 times.

RNA isolation. Total RNA was extracted from skeletal muscle and quantified in triplicate using UV absorbance (26). Gel electrophoresis confirmed the integrity of the samples. RNA was treated to DNase (Ambion Inc, Austin TX).

RT-PCR Quantification Using Internal Control and Direct Incorporation of Radioactivity. To measure mRNA levels of PGC-1, a well-characterized method of RT-PCR was used that incorporates bovine retinal rhodopsin RNA as an internal control for both reverse transcription and amplification (8, 9, 20, 22). cDNA was synthesized using random hexamers and SUPERSCRIPT II RTTM (Life Technologies Inc., Gaithersburg MD).

burgh MD) from 1.0 μg of skeletal muscle RNA added to 0.01 μg of bovine retinal RNA. Reactions were replicated three times. Primer sequences are found in Table 1. With each set of reverse transcription and amplification, serial dilutions were run to demonstrate that both PCR products were being produced in the exponential phase of amplification. Products were separated and radioactivity was quantified by phosphorimaging. The relative abundance of target mRNA levels were quantified relative to that of the control rhodopsin band from the same reaction.

Verification of PGC-1 Expression in the IUGR Rat. Previous investigators have found that PGC-1 controls expression of genes affecting mitochondrial biogenesis and respiration (10). Because the perinatal IUGR rat is characterized by increased skeletal muscle mRNA levels of the mitochondrial gene NADH ubiquinone-oxidoreductase 4L, we cross-referenced our findings by measuring mRNA levels of nuclear mitochondrial transcription factor A (mTFA), nuclear respiratory factor-1 (NRF-1), and cytochrome oxidase subunit IV (Cox IV) in N0 IUGR rats using the technique described above (8).

Real Time RT-PCR. Skeletal muscle mRNA levels of PGC-1, mCPT1, UCP-2, and CD36 were measured at J21 (12) as previously described. cDNA was synthesized from 0.5 μg of DNase treated mRNA as described above. Target (PGC-1, mCPT1, UCP-2, CD36) primers and probes were designed using Primer Express SoftwareTM (Applied Biosystems, Foster CA) (Table 1); target probes were labeled with fluorescent reporter dye FAM. Before the performance of real time PCR, all primer pairs are tested with serial Mg^{+2} and primer concentrations to determine the optimal reaction conditions and to demonstrate the specificity of each primer pair. Reporter dye emission is detected by an automated sequence detector combined with ABI Prism 7700 Sequence Detection System[®] software (Applied Biosystem, Foster CA). An algorithm normalizes the reporter signal (R_n) to a passive reference and multiples the SD of the background R_n in the first cycles by a default factor of 10 to determine threshold C_T . C_T has a linear relation with the logarithm of the initial template copy number (27). Real time PCR quantification is then performed using the Taqman[®] glyceraldehyde-3-phosphate dehydrogenase controls. Before the use of GAPDH as a control, serial dilutions of cDNA are quantified to prove the validity of using GAPDH as an internal control. Relative quantification of PCR products are then based upon value differences between the target and

Table 2. Hind limb skeletal muscle fiber typing in d 21 control and IUGR

	Type 2A	Type 2X	Type 2B	I (slow)
IUGR	18.5 \pm 2.1	28.7 \pm 0.8	36.7 \pm 3.4	16.2 \pm 1.8
Control	17.4 \pm 0.1	27.3 \pm 0.3	39.6 \pm 2.7	15.7 \pm 1.5

Results are expressed as mean percentage \pm SEM.

GAPDH control using the comparative C_T method (28). Cycle parameters were 55°C \times 5 min, 95°C \times 10 min, and then 40 cycles of 95°C \times 15 s \rightarrow 58°C \times 60 s. Each sample was analyzed in triplicate in assays performed on three occasions.

Statistics. All data presented are expressed as mean percent of control \pm SEM. For RT-PCR using the internal control, statistical analyses were performed using the nonparametric Wilcoxon Matched Pair Test. For muscle fiber typing, Western Blotting, and real time RT-PCR, statistical analyses were performed using ANOVA (Fisher's protected least significance difference) and Student's unpaired *t* test.

RESULTS

Skeletal muscle PGC-1 protein levels at N0 and J21. Uteroplacental insufficiency and subsequent IUGR increased N0 hind limb PGC-1 protein levels to 220 \pm 19%* of sham operated control values (Fig. 1A) (**p* < 0.05). Similarly, J21 hind limb PGC-1 protein levels were increased in IUGR skeletal muscle to 165 \pm 17%* of sham operated control values (Fig. 1A) (**p* < 0.05).

Skeletal muscle PGC-1 mRNA levels using traditional RT-PCR. Using a traditional method of RT-PCR in which radioactivity is directly incorporated into the PCR product, we found that uteroplacental insufficiency increased PGC-1 mRNA levels in N0 hind limb skeletal muscle to 169 \pm 12%* of control values (Fig. 1B) (**p* < 0.05). Consistent with the established link between PGC-1 gene expression and mTFA, NRF-1, and CoxIV mRNA levels, as well as the previous report of increased mitochondrial gene expression in N0 skeletal muscle, day 0 mRNA levels of mTFA (177 \pm 12%*), NRF-1 (201 \pm 9%*), and CoxIV (189 \pm 12%*) were also significantly increased in N0 IUGR hind limb muscle (**p* < 0.05).

At day 21 of life, IUGR similarly increased PGC-1 mRNA levels in EDL skeletal muscle to 142 \pm 11%* of control

Table 1. Sequences of PCR primers

Gene	Sense primer	Antisense primer	Probe sequence	GenBank Accession No.
PGC-1	CGCACAACTCAGCAAGTCCTC	CCTTGCTGGCCTCCAAAGTCTC	NA	AB025784
PGC-1	TCTGGAACACTGCAGGCCCTAACCTC	GCAAGAGGGCTTCAGCTTIG	TCCTCCTCATAAAGCCAACCAAGATAACCT	
CD36	GGAAAGTTATTGCGACATGATTAATG	GGAAAGAACCTCAGTGTGAGACTTC	ATGCAGCCTCCTTCCACCTTTGTTGA	AF072411
CoxIV	TGTTGATCGGGGTGACTACC	GAAGCCGATGAAACATGG	NA	
mTFA	CCCTGGAAGCTTCAGATACG	AATTGCAGGCCATGTGGAGG	NA	AF246196
mCPT1	ACCTGGGCTACACGGAGACA	CCTTGGCTACTTGGTACGAATTCT	AACAAACAAGTTGCCGCCCT	NM013200
NRF-1	TTACAGGGCGGTGAAATGAC	GTAAAGGGCATGGTACAG	NA	RNU27700
UCP-2	CTGAAAGCCAACCTCATGACAG	CAATGACGGTGGTGCAGAAG	CGACCTCCCTGCCACTTCACTCTG	NM019354
Rhodopsin	TATTCTCTGCTACGGCAG	ATGGGTGAAGATGTAGAACG	NA	M21606

NA, not available.

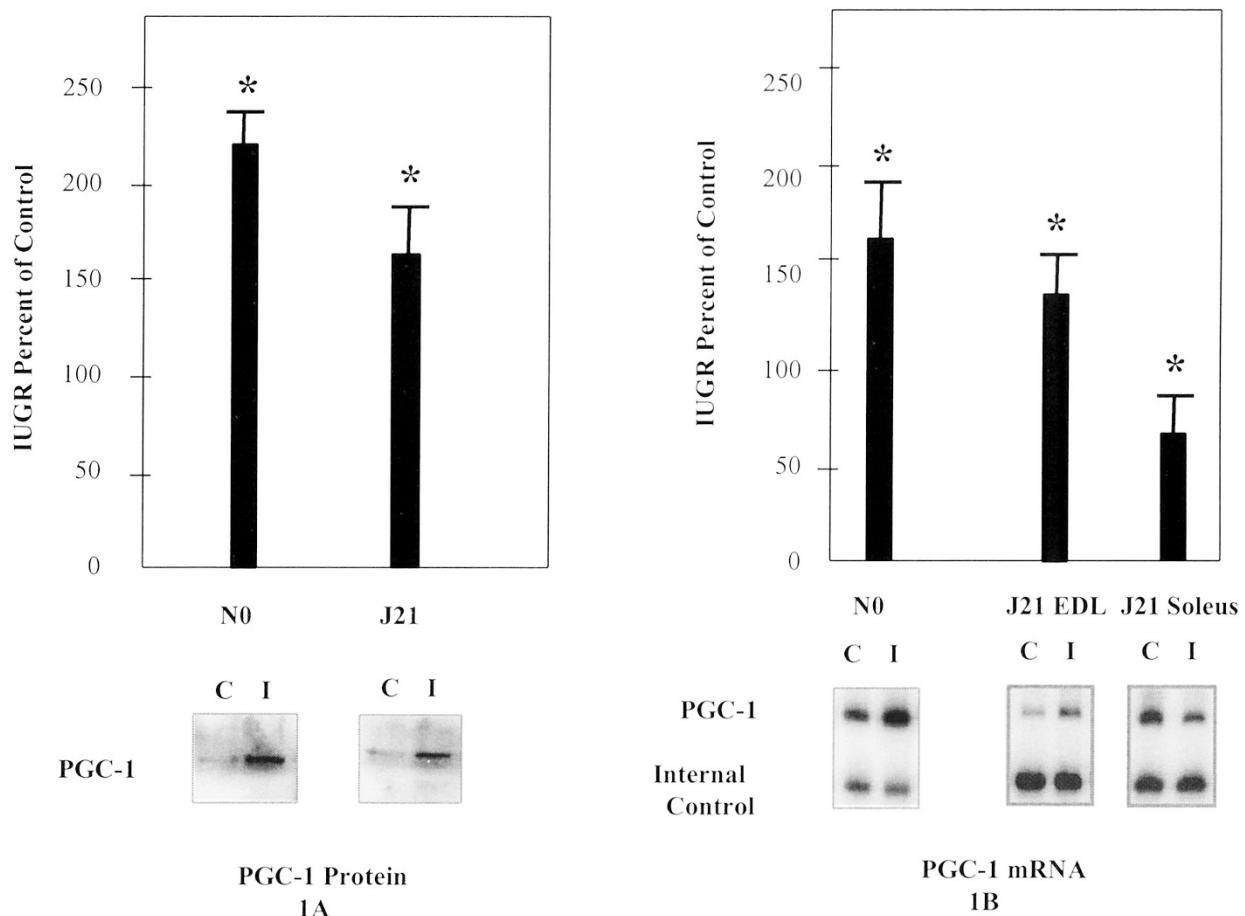


Figure 1. (A) Quantification of sham operated control (C) and IUGR (I) PGC-1 protein levels in N0 and J21 hindlimb muscle with a representative Western blot. Protein levels are expressed as mean IUGR percent of control \pm SD. Protein was quantified using NIH image software. (B) Quantification of sham operated control and IUGR PGC-1 mRNA levels from N0 hindlimb, J21 EDL, and J21 soleus with representative phosphorimages. mRNA levels are expressed IUGR mean percent of control \pm SEM. PCR products were quantified using phosphorimage analysis. * $p < 0.05$.

values; in contrast, PGC-1 mRNA levels were decreased to $67 \pm 10\%$ of control values in IUGR soleus (Fig. 1B) ($*p < 0.05$).

Skeletal muscle fiber typing. To determine whether uteroplacental insufficiency induced IUGR affected skeletal muscle fiber distribution and thereby contributed to the increased J21 PGC-1 hind limb protein levels observed above, whole hind limb skeletal muscle fiber types were determined by proportioning myosin heavy chain isoforms. In J21 control animals, hind limb skeletal muscle was comprised of $17.4 \pm 0.1\%$ Type 2A, $27.3 \pm 0.3\%$ Type 2X, $39.6 \pm 2.7\%$ Type 2B, and $15.7 \pm 1.5\%$ Type I fibers. In the J21 IUGR animals, hind limb skeletal muscle was comprised of $18.5 \pm 2.1\%$ Type 2A, $28.7 \pm 0.8\%$ Type 2X, $36.7 \pm 3.4\%$ Type 2B, and $16.2 \pm 1.8\%$ Type I fibers. No significant difference exists between control and IUGR animals.

Real time RT-PCR. Gender specific analysis of PGC-1 mRNA levels led to the conclusion that the extent IUGR affected PGC-1 mRNA levels differed between the sexes at J21. Real Time RT-PCR was subsequently used to determine PGC-1 mRNA levels in J21 EDL and soleus of both genders because of the technique's precision.

Uteroplacental insufficiency increased PGC-1 mRNA levels to $200 \pm 7\%**$ of control values in J21 male EDL; in contrast,

female PGC-1 EDL mRNA levels were increased to only $123 \pm 5\%*$ of control values (Fig. 2) ($**p < 0.01$) ($*p < 0.05$). In soleus, male IUGR PGC-1 mRNA levels were decreased to $53\% \pm 2\%*$, versus $81 \pm 4\%*$ in IUGR female soleus versus control values (Fig. 2) ($*p < 0.05$).

mRNA values of the proven PGC-1 down stream targets followed a similar pattern. Uteroplacental insufficiency and subsequent IUGR increased male EDL mCPT1 and UCP-2 mRNA levels to $214 \pm 8\%**$ and $282 \pm 11\%**$ of control values respectively, whereas female EDL mCPT1 and UCP-2 mRNA levels were increased to only $115 \pm 6\%$ and $132 \pm 6\%*$ of control values (Fig. 2) ($**p < 0.01$) ($*p < 0.05$). In soleus, male IUGR mCPT1 and UCP-2 mRNA levels decreased to $37 \pm 2\%**$ and $53 \pm 5\%*$ of control values respectively versus a change of $61 \pm 5\%*$ and $62 \pm 4\%*$ in J21 female soleus (Fig. 2) ($**p < 0.01$) ($*p < 0.05$).

Interestingly, CD36 mRNA levels did not follow this pattern. In J21 EDL, uteroplacental insufficiency and subsequent IUGR increased CD36 mRNA levels to $141 \pm 5\%**$ and $246 \pm 13\%**$ in male and female animals respectively (Fig. 2) ($**p < 0.01$). Similarly, soleus CD36 mRNA levels were increased to $114 \pm 6\%$ and $174 \pm 7\%*$ in IUGR male and female animals respectively (Fig. 2) ($*p < 0.05$).

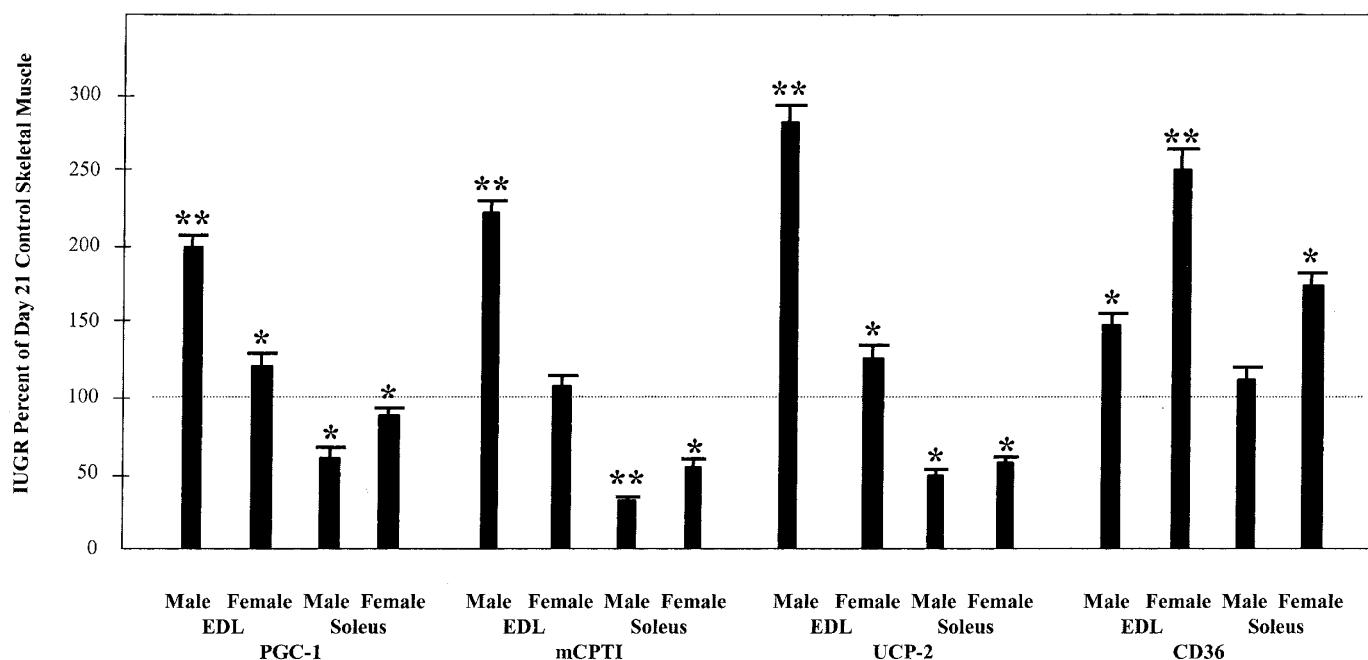


Figure 2. Quantification of PGC-1, mCPTI, UCP2, and CD36 using real time RT-PCR in J21 EDL and soleus. Results are expressed as mean percentages \pm SEM relative to sham-operated controls. Relative quantification of PCR products are based on value differences between the target and GAPDH control, using the comparative C_T method. ** $p < 0.01$, * $p < 0.05$.

DISCUSSION

Uteroplacental insufficiency in the human and the rat causes fetal hypoglycemia, hypoxia, and acidosis (29, 30). The effects of this insult seemingly resolve days after birth in the human and 48 to 72 h after surgery in the rat, yet IUGR individuals are prone to develop insulin resistance and dyslipidemia as they reach maturity (1, 5, 19, 20). In the rat, these pathophysiologies are associated with altered skeletal muscle expression and function of key fatty acid oxidizing enzymes, as well as increased skeletal muscle triglycerides (9). Kelly *et al.* have proven that PGC-1 significantly contributes to the control of nuclear genes encoding mitochondrial fatty acids oxidation enzymes, and that expression of PGC-1 correlates directly with mRNA levels of these genes (11, 31). The finding of altered PGC-1 expression suggests a mechanism through which uteroplacental insufficiency affects mRNA levels of several skeletal muscle fatty acid oxidizing enzymes in the postnatal IUGR animal. This finding is novel because the association between an upstream transcriptional co-activator and subsequently affected gene expression has not been previously made in IUGR skeletal muscle.

PGC-1 stimulates skeletal muscle mitochondrial respiration and biogenesis through the induction of UCP-2 and NRF-1 expression respectively, as well as subsequent mTFA expression (10). The increased expression of NRF-1, mTFA, and COXIV in N0 skeletal muscle corroborate these findings, as well as the previous report of increased skeletal muscle mitochondrial gene expression in the N0 IUGR rat (8). In the adult rat, exercise stimulates PGC-1 expression, and Tunstall *et al.* found that exercise induced expression of PGC-1 was associated with increased expression of mCPTI and the β -oxidation enzyme β -hydroxyacyl-CoA dehydrogenase (32, 33). PGC-1

also restores glucose transporter 4 gene expression in cultured primary myotubes, which is intriguing within the context of the insulin resistance the IUGR rat develops and the decrease in PGC-1 soleus (Type I) muscle fiber expression observed in the present study (34). Primary myotubes exhibit a slow fiber phenotype (35).

This study finds no difference in rat hind limb fiber composition between the control and IUGR J21 rat pups. Little is otherwise known about skeletal muscle fiber type composition or differential expression in rat models that develop diabetes secondary to *in utero* deprivation through either uteroplacental insufficiency or maternal starvation. The WBN/Kob rat, which spontaneously develops diabetes, exhibits no significant change in fiber type composition that is not attributable to aging (36). In humans, the literature is ambiguous, though both Larsson *et al.* and Hickey *et al.* found no significant differences in muscle fiber type composition after the authors corrected the data for body mass index (37, 38).

EDL in the suckling rat contains a large proportion of fast fiber types (39). The increased expression of PGC-1 and mCPTI in EDL thereby explains the previously published findings of increased mCPTI expression and β -oxidation in juvenile hind limb, considering the hind limb predominance of fast fiber type found in this study (9). For soleus, the transition from a mixed fiber phenotype to a slow phenotype occurs over a period of 5 or more weeks (40). This delay may explain the increased lipid oxidation observed in IUGR infants and some of the discrepancies in the adult diabetic literature on whether fatty acid oxidation is increased or decreased in the NIDDM population, though the primary reason for the discrepancies is likely the large number of diabetic subtypes (6, 7, 41–43).

The human adult diabetic literature often uses vastus lateralis biopsies to characterize skeletal muscle metabolism in the diabetic population because of accessibility, and finds that enzyme activity for mitochondrial fatty acid oxidizing enzymes is decreased (44, 45). Vastus lateralis contains 30% to 40% type I muscle fibers (45). Considering the decreased soleus PGC-1 and mCPT1 mRNA levels found in this study, it may be that the type I fibers of the diabetic vastus lateralis express less β -oxidation machinery and thereby oxidize less fatty acid versus nondiabetics, particularly in the adult where the slow fiber phenotype has fully evolved.

This is the first study to observe skeletal muscle gender specific differences in a rat model of IUGR and subsequent insulin resistance, though it is consistent with previous reports of more severely effected hepatic gene expression and function of fatty acid metabolizing genes in male IUGR rats (19, 46). Moreover, i.v. lipid emulsion induces insulin resistance in normal male adult rats to a significantly greater extent than it does in normal female adult rats (47, 48). Humans also metabolize fat in a gender specific manner (48, 49). Sumner *et al.* found that while obese diabetic African-Americans of both genders were resistant to insulin's glucoregulatory effects, only the men were resistant to insulin's antilipolytic effect (50). Because PGC-1 acts a transcriptional co-activator with estrogen and androgen receptors, the effects of PGC-1 gender specific expression, and subsequently the IUGR phenotype, potentially change as the IUGR individual progressively experiences sexual maturation, maturity, and senescence (51).

PGC-1 does not appear to effect CD36 mRNA levels in a manner similar to that of mCPT1 or UCP-2. Uteroplacental insufficiency increases CD36 expression in both EDL and soleus, and the findings are again gender specific, though they are more impressive in the female IUGR rats, which is different from PGC-1 and its down stream targets mCPT1 and UCP2. The female IUGR rat does not exhibit hypertriglyceridemia to the same degree as the male, so it is intriguing that over expression of skeletal muscle CD36 decreases serum triglycerides in transgenic mice. CD36 mRNA expression is associated with increased skeletal muscle acyl-CoA synthase activity and fatty acid tissue storage (21). Increased levels of intramuscular triglycerides characterize both sexes of the IUGR rat, and have been closely linked to insulin resistance in human (9, 52, 53).

Caution is necessary of course when attempting to apply data from a rat model to human pathophysiology. The fetal and juvenile rat is physiologically immature relative to the human, and the insult imposed on the fetal rat in this model of uteroplacental insufficiency is severe and specific. In contrast, the timing and impact of uteroplacental insufficiency experienced by humans range across a continuum.

In summary, uteroplacental insufficiency induces altered expression of PGC-1 and its downstream targets at both N0 and J21 life in hind limb skeletal muscle. RT-PCR demonstrates that the changes in mRNA levels are skeletal muscle group and gender specific. Skeletal muscle CD36 mRNA levels are also altered in the IUGR rat, though in a different pattern than PGC-1. We speculate that these changes in gene expression contribute to the alterations in skeletal muscle fat metabolism

that occur in the IUGR rat and may contribute to the development of insulin resistance.

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