Suppression of plasma free fatty acids upregulates peroxisome proliferator-activated receptor (PPAR) \( \alpha \) and \( \delta \) and PPAR coactivator 1\( \alpha \) in human skeletal muscle, but not lipid regulatory genes

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Abstract

Fatty acids are an important ligand for peroxisome proliferator-activated receptor (PPAR) activation and transcriptional regulation of metabolic genes. To examine whether reduced plasma free fatty acid (FFA) availability affects the mRNA content of proteins involved in fuel metabolism in vivo, the skeletal muscle mRNA content of various transcription factors, transcriptional coactivators and genes encoding for lipid regulatory proteins were examined before and after 3 h of cycle exercise with (NA) and without (CON) pre-exercise ingestion of nicotinic acid (NA). NA resulted in a marked (3- to 6-fold) increase (\( P < 0.05 \)) in PPAR\( \alpha \), PPAR\( \delta \) and PPAR coactivator 1\( \alpha \) (PGC1\( \alpha \)) mRNA, but was without effect on nuclear respiratory factor-1 and Forkhead transcription factor, fatty acid translocase/CD36, carnitine palmitoyl transferase 1, hormone sensitive lipase (HSL) and pyruvate dehydrogenase kinase 4. Exercise in CON was associated with increased (\( P < 0.05 \)) PPAR\( \alpha \), PPAR\( \delta \) and PGC1\( \alpha \) mRNA, which was similar in magnitude to levels observed with NA at rest. Exercise was generally without effect on the mRNA content of lipid regulatory proteins in CON and did not affect the mRNA content of the measured subset of transcription factors, transcriptional co-activators and lipid regulatory proteins during NA. To determine the possible mechanisms by which NA might affect PGC1\( \alpha \) expression, we measured p38 MAP kinase (MAPK) and plasma epinephrine. Phosphorylation of p38 MAPK was increased (\( P < 0.05 \)) by NA treatment at rest, and this correlated (\( r^2 = 0.84, P < 0.01 \)) with increased PGC1\( \alpha \). Despite this close relationship, increasing p38 MAPK in human primary myotubes was without effect on PGC1\( \alpha \) mRNA content. Plasma epinephrine was elevated (\( P < 0.05 \)) by NA at rest (CON: 0.27±0.06, NA: 0.72±0.11 nM) and throughout exercise. Incubating human primary myotubes with epinephrine increased PGC1\( \alpha \) independently of changes in p38 MAPK phosphorylation. Hence, despite the fact that NA ingestion decreased FFA availability, it promoted the induction of PPAR\( \alpha \)/\( \delta \) and PGC1\( \alpha \) gene expression to a similar degree as prolonged exercise. We suggest that the increase in PGC1\( \alpha \) may be due to the elevated plasma epinephrine levels. Despite these changes in transcription factors/co-activators, the mRNA content of lipid regulatory proteins was generally unaffected by plasma FFA availability.

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Introduction

Skeletal muscle is a major site of fatty acid uptake and oxidation at rest and during contraction (for review see van der Vusse & Reneman 1996) and aberrant control of fatty acid metabolism is related to obesity and type 2 diabetes (Kelley et al. 2002). Chronic exercise improves the capacity to utilize fatty acids by a co-ordinated upregulation of proteins involved in the sarcolemmal uptake (fatty acid translocase; FAT/CD36), mitochondrial transport (carnitine palmitoyl transferase 1; CPT1) and \( \beta \)-oxidation (\( \beta \)-hydroxyacyl-coenzyme-A) of fatty acids (Spina et al. 1996, Berthon et al. 1998, Bonen et al. 1999). The upregulation of these proteins is rapid and due, at least partially, to increased gene expression (Hood 2001). In this regard, increased transcription and expression of several metabolic
regulatory genes have been demonstrated immediately after a single prolonged exercise bout (Cortright et al. 1999, Pilegaard et al. 2000, 2002).

Peroxisome proliferator-activated receptors (PPARs) are a family of nuclear hormone receptors that mediate adaptive metabolic responses by ligand-dependent transcriptional activation of target genes (Kliwer et al. 2001). PPARα and δ are considered the most important subtypes in skeletal muscle by virtue of their abundant expression (Braissant et al. 1996). PPARα mediates transcriptional control of nuclear genes encoding for proteins involved in fuel oxidation, including CPT1, pyruvate dehydrogenase kinase 4 (PDK4) and uncoupling protein 3 (UCP3). Consistent with a central role in fatty acid oxidation, PPARα null mice exhibit decreased expression of lipid regulatory genes, decreased β-oxidation and greater lipid accumulation in hepatic and cardiac tissue (Djouadi et al. 1998). Although much less is known regarding PPARδ, recent evidence has demonstrated increased expression of genes involved in lipid catabolism in skeletal muscle cells following acute PPARδ activation (Dressel et al. 2003, Wang et al. 2003). The PPARs are activated by naturally occurring fatty acids and fatty acid metabolites, indicating that they act as fatty acid sensors. Since fatty acids and lipid metabolites (e.g. fatty acyl CoA) are ligands of the PPARs and their availability is increased during prolonged exercise (Watt et al. 2003), the marked increase in fatty acid availability during prolonged exercise may provide a stimulus for increased PPARα/δ activity and subsequent induction of numerous lipid regulatory genes.

Emerging evidence demonstrates the importance of coactivator molecules in the transcriptional activation of nuclear receptor target genes. Fatty acid induction of gene expression through PPARα and δ is enhanced by the PPAR coactivator 1α (PGC1α), which is expressed in oxidative tissues such as skeletal and cardiac muscle (Dressel et al. 2003, for review see Puigserver & Spiegelman 2003). Overexpression of PGC1α and PPARα in 3T3-L1 adipocytes resulted in the induction of PPARα target genes and concomitant increases in palmitate oxidation (Vega et al. 2000). Of note, PGC1α expression is induced during metabolic stresses such as cold exposure (Puigserver et al. 1998), severe caloric restriction (Larrouy et al. 1999) and prolonged exercise (Terada et al. 2002, Pilegaard et al. 2003). In these situations, plasma free fatty acid (FFA) availability is increased dramatically, which provides a clue to a potential mechanism through which PGC1α gene expression is enhanced.

In the present study, we chose to examine the effect of the anti-lipolytic drug nicotinic acid (NA) on the expression of the nuclear transcription factors, PPARα and δ, the transcriptional coactivator, PGC1α and various PPAR target genes encoding for proteins involved in lipid metabolism. We hypothesized that decreased plasma FFA availability would suppress the exercise-induced increase in the lipid regulatory genes, PGC1α, PPARα and PPARδ.

Materials and methods

Experimental subjects

The experimental protocol was approved by the Royal Melbourne Institute of Technology human research ethics committee, and written informed consent was obtained prior to testing. All testing was in accordance with the Declaration of Helsinki. Subjects were recreationally active males (24 ± 3 years; 80 ± 3 kg) who participated in two to four aerobic exercise bouts per week.

Pre-experimental protocol

Subjects performed an incremental exercise bout to volitional exhaustion to determine peak pulmonary oxygen uptake (VO2 peak) which averaged 4·33 ± 0·31 litres/min. Expired contents of oxygen and carbon dioxide and ventilation data were collected and analysed on-line (Quark b2; COSMED, Rome, Italy). At least 2 days later, subjects completed a practice trial, the purpose of which was to familiarize the subjects with the effects of NA and confirm their ability to perform the exercise bout. Subjects ingested 10 mg/kg NA (Aspen Pharmcare, St Leonards, NSW, Australia) and rested for 60 min, after which they cycled for 120 min at 60% VO2 peak. Further NA doses (5 mg/kg) were ingested at 30-min intervals at rest (−30 and 0 min) and throughout exercise. For the day preceding each trial, subjects were provided with a food parcel (14 MJ, 80% carbohydrate) and were required to abstain from exercise, caffeine and alcohol. All trials were performed at an ambient temperature of 19–21 °C.
Experimental protocol

Subjects performed 180 min of cycle exercise at 60% VO_2 peak on two occasions; either with (NA) or without (CON) NA ingestion before and during exercise. The trials were randomly assigned and counter-balanced. Subjects visited the laboratory at 0800 h after an overnight fast. A Teflon catheter was inserted into a forearm vein and was kept patent by saline infusion. A resting blood sample was obtained and the vastus lateralis was prepared for needle biopsy. Three incisions were made through the skin and fascia under local anaesthesia (lidocaine, no epinephrine). During NA, subjects followed the NA ingestion regime as described above. A placebo was not administered in CON subjects because subjects can easily determine the effects of NA ingestion, which include peripheral vasodilation, itchiness and in some instances mild nausea. One blood and one muscle sample were obtained immediately prior to exercise and at 90 and 180 min during exercise. The exercise biopsy samples were obtained while the subjects remained on the cycle ergometer and were rapidly frozen in liquid nitrogen for later analysis. An extra biopsy was not obtained prior to NA ingestion to minimize subject stress, which may have confounded the gene expression measurements. Subjects were not permitted to eat during the trial but were provided with water (1 litre/h) to ensure euhydration.

Blood analysis

Whole blood was mixed in a sodium–heparin collection tube and the plasma was obtained after centrifugation at 5000 g for 2 min. Plasma samples were frozen at −80 °C for later analysis of FFA by an enzymatic colorimetric method (NEFA C; Wako Chemicals, Richmond, VA, USA), insulin (Coat-a-Count; DPC, Los Angeles, CA, USA) and epinephrine (LDN, Nordhorn, Germany) by radioimmunoassay.

Muscle analysis

Muscle tissue was homogenized and extracted for total RNA using the acid guanidium thiocyanate–phenol–chloroform extraction method (Chomczynski & Sacchi 1987) and modified according to methods described elsewhere (Febbraio & Koukoulas 2000). RNA samples were reverse transcribed using a thermal cycler (Perkin Elmer GeneAmp PCR 2400 thermal cycler; Perkin Elmer, Rowville, Victoria, Australia) with Taqman Reverse transcription reagents (Applied Biosystems, Foster City, CA, USA) in 40 μl reaction mixtures containing 1× Taqman RT buffer, 5·5 mM MgCl₂, 500 μM 2′-deoxynucleoside 5′-triphosphate, 2·5 μM random hexamers, 0·4U/μl RNase inhibitor and 1·25 U/μl multiscrIBE reverse transcriptase. Control (reverse transcriptase negative) samples were also made and included in all future PCR analyses to check for genomic DNA contamination.

Real-time PCR analysis

Real-time PCR was employed to quantify the genes of interest. All reactions were performed according to the multiplex comparative critical threshold (C_T) method. This method allows for the detection of the reference gene (ribosomal 18S) and the gene of interest in the same well or tube. Preliminary experiments were first performed to determine the efficiency of amplification of 18S vs the gene of interest.

PCR reactions were performed in 96-well plates on a BioRad i-CYCLER iQ real-time PCR detection system in 25 μl reaction volumes consisting of: BioRad iQ Supermix PCR mix (2×; BioRad, Applied Biosystems, Scoresby, Victoria, Australia), Applied Biosystems pre-developed assay reagent for 18S (Applied Biosystems), the forward and reverse primers and probes of the genes of interest (see Table 1 for sequences) and sterile H₂O. A ΔC_T value was obtained by subtracting 18S C_T values from the C_T value of the gene of interest. For each gene, the ΔC_T value for CON 0 was then subtracted from the ΔC_T values of the other time-points for each subject to derive a ΔΔC_T value. The expression was then evaluated by 2^−ΔΔC_T with all CON 0 values for each subject being 1.

Protein analysis

Muscle was homogenized (Polytron; Brinkman Instruments, New York, NY, USA) in ice-cold buffer containing 50 mM HEPES, 150 mM NaCl, 10 mM NaF, 1 mM Na₃VO₄, 5 mM EDTA, 0·5% Triton X-100, 10% glycerol (v/v), 2 μg/ml leupeptin, 100 μg/ml phenylmethylsulfonyl fluoride
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<th>Gene</th>
<th>Forward primer</th>
<th>Reverse primer</th>
<th>TaqMan probe</th>
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<td>5'-CCTGTCTCCTGGCTGT-3'</td>
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<td>5'-CAAATTTCCGTTGCTGAGGCT-3'</td>
<td>5'-CCCCCAAAAGGCCTGGCAAC-3'</td>
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CPT1, carnitine palmitoyl transferase 1; FAT/CD36, fatty acid translocase; FKHR, forkhead transcription factor; HSL, hormone sensitive lipase; NRF-1, nuclear respiratory factor-1; PGC1α, PPAR coactivator 1α; PPARα, peroxisome proliferator activated receptor α; PPARδ, peroxisome proliferator activated receptor δ; PDK4, pyruvate dehydrogenase kinase 4; UCP3, uncoupling protein 3.
and 2 µg/ml aprotinin. Homogenates were centrifuged and the supernatant was removed and rapidly frozen in liquid nitrogen. Protein concentration of the muscle lysates was subsequently determined (Pierce, Rockford, IL, USA). Muscle lysates were solubilized in Laemmli sample buffer and boiled for 5 min, resolved by SDS-PAGE on 10% polyacrylamide gels, transferred to a nitrocellulose membrane, blocked with 5% bovine serum albumin and immunoblotted with the anti-phospho-p38 MAP kinase (MAPK), anti-phospho-extracellular regulated kinase (ERK), anti-phospho-c-Jun NH2-terminal kinase (JNK) (1:1000; Cell Signaling, Beverley, MA, USA) or anti-PGC1 antibody (Chemicon International, Boronia, Victoria, Australia). After incubation with horseradish peroxidase-conjugated secondary antibody (1:2000; Amersham Biosciences, Castle Hill, NSW, Australia), the immunoreactive proteins were detected with enhanced chemiluminescence (Perkin Elmer) and quantified by densitometry.

Primary cell culture

Muscle tissue from the vastus lateralis was obtained via percutaneous needle biopsy and immediately transferred to ice-cold Ham’s F-10 media (Gibco, Mt Waverley, Victoria, Australia). The tissue was washed three times in ice-cold Ham’s-F10 media to remove any traces of blood, and placed over ice in a sterile Petri dish. The tissue was covered with 3 ml 0.05% Trypsin/EDTA and minced. The homogenate was collected, diluted in 15 ml 0.05% Trypsin/EDTA, agitated for 20 min and the supernatant was collected and stored on ice. This procedure was repeated three times and the supernatant was filtered and then spun for 7 min at 1600 g at room temperature. The cell pellet was re-suspended in growth media (α-minimum essential medium with 10% fetal calf serum, 0.5% antibiotics and 0.5% amphotericin B) and placed in an uncoated 75 cm flask and incubated for 30 min at 37 °C (95% O2/5% CO2) to allow attachment of fibroblasts. The supernatant was collected and placed in another flask pre-coated with extracellular matrix (ECM) and incubated as above for 24 h. Satellite cells appeared after ~7 days and were allowed to reach 60–70% confluence, at which point they were sub-cultured into separate dishes. When the myoblasts reached 70% confluence, the growth medium was replaced with differentiation medium (2% horse serum (HS), 0.5% antibiotics and 0.5% antifungal). Myoblasts were maintained in differentiation media until fully fused myotube cultures were obtained.

Experiments were conducted in overnight serum-starved cells. Myotubes (n=12 plates for each condition) were incubated for 6 h at 37 °C with vehicle (phosphate-buffered saline), 10 µM NA, 500 nM A23187 (calcium ionophore) and 1 µM epinephrine alone or in combination with the specific p38 MAPK inhibitor, SB203580 (10 µM). In one experiment, cells (n=6) were rapidly lysed with the ice-cold buffer used for protein homogenization (see above) and rapidly frozen in liquid nitrogen for later analysis of p38 MAPK phosphorylation. In a second experiment, cells (n=6) were homogenized and extracted for total RNA as described above. RT-PCR was employed to assess PGC1α mRNA content.

Statistical analysis

All values are expressed as means ± s.e.m. (n=7). Statistical analysis was performed by two-way ANOVA with repeated measures followed by a Student–Newman–Kuels post hoc analysis to determine specific differences where appropriate. Correlations were examined using a Pearson correlation analysis. SigmaStat version 2.03 (SPSS Incorporated, Chicago, IL, USA) was used to compute these statistics. Statistical significance was set at P<0.05.

Results

Physiological variables

NA ingestion suppressed (P<0.05) plasma FFA levels at rest (0.41 ± 0.04 to 0.10 ± 0.01 mM) and throughout exercise whereas plasma FFA was increased (P<0.05) from rest at the conclusion of exercise in CON (Table 2). Plasma epinephrine concentration was greater (P<0.05) before and after exercise in NA compared with CON (Table 2). Plasma insulin concentration decreased (P<0.05) from rest by the cessation of exercise in both trials and there were no differences between trials (Table 2).
Skeletal muscle mRNA content

Transcription factors

PPARα (3·8-fold) and PPARδ (3-fold) were elevated \( (P<0·05) \) at rest in NA compared with CON (Fig. 1). PPARα and PPARδ mRNA were increased \( (P<0·05) \) from rest after exercise in CON, but no such changes were observed in NA. There were no differences between trials after exercise. NRF-1 is a key transcriptional activator of nuclear genes that is transcriptionally activated by PGC1α and coactivates with PGC1α to induce mitochondrial biogenesis (Baar et al. 2003). Muscle content of NRF-1 was unaffected by NA ingestion at rest and exercise in both trials (Fig. 2). Although it is well known that the phosphorylation of the FKHR protein is via Akt phosphorylation (Brunet et al. 1999), relatively less is known with respect to the transcriptional regulation of FKHR. Skeletal muscle FKHR mRNA content was not affected by NA ingestion or exercise in NA. FKHR mRNA tended to increase (2-fold, \( P=0·08 \)) following exercise in CON.

Transcriptional coactivators

PGC1α was markedly (\( \sim 6 \) fold) increased \( (P<0·05) \) at rest in NA compared with CON (Fig. 3A). After exercise, muscle PGC1α mRNA content was increased \( (P<0·05) \) in CON, whereas no such change was observed in NA. There was no difference in PGC1α mRNA content after exercise.

Lipid regulatory genes

FAT/CD36, HSL, CPT1 and PDK4 mRNA content were not different between trials at rest, whereas UCP3 was 3-fold greater \( (P<0·05) \) in NA compared with CON (Table 3). Exercise was without effect on CPT1 and HSL mRNA content in both trials, whereas PDK4 was increased \( (P<0·05, \) main effect) after exercise (Table 2). Exercise induced a small (\( \sim 2·5 \) fold) increase \( (P<0·05) \) in FAT/CD36 during NA only. In contrast, UCP3 mRNA was increased \( (P<0·05) \) from rest values after exercise in CON, whereas it was decreased post-exercise in NA. There were no differences between trials for UCP3 after exercise.

Table 2 Plasma FFA, epinephrine and insulin responses before and after 3 h of exercise with (NA) or without (CON) prior NA ingestion. Values (means±S.E.M.) are expressed as fold change from CON at 0 min \((n=7)\)

<table>
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<th>Trial</th>
<th>Pre</th>
<th>Post</th>
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<tr>
<td>FFA (mM)</td>
<td>CON 0·32±0·03</td>
<td>1·42±0·07</td>
</tr>
<tr>
<td>Epinephrine (mM)</td>
<td>CON 0·27±0·05</td>
<td>1·70±0·35</td>
</tr>
<tr>
<td>Insulin (pM)</td>
<td>CON 51·9±4·8</td>
<td>6·9±1·5</td>
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\*\( P<0·05 \) compared with corresponding time-point for CON.

Figure 1 Real-time RT-PCR analysis of (A) PPARα and (B) PPARδ mRNA measured before and after 3 h of moderate exercise with (NA) or without (CON) prior NA administration. Values represent the means±S.E.M. \((n=7)\). \*\( P<0·05 \), different from corresponding value for CON; †\( P<0·05 \), different from 0 min of the same trial.
Protein expression in skeletal muscle

PGC1α protein expression was not affected by NA at rest or after exercise (Fig. 3B). PGC1α protein tended ($P=0.09$, main effect for time) to increase after exercise with increased protein content observed in four of five subjects. Phosphorylation of p38 MAPK was 3-fold higher ($P<0.05$) at rest in NA compared with CON (Fig. 4A). Although exercise did not induce any effects on p38 MAPK phosphorylation in either trial, protein levels remained higher ($P<0.05$) in NA. ERK1/2 phosphorylation was decreased ($P<0.05$) at 180 min, whereas ERK1/2 phosphorylation was unaffected by exercise in NA. JNK phosphorylation was not different between trials at rest and was increased ($P<0.05$) after exercise in both trials (Fig. 4C).

Relationships between PGC1α mRNA, phosphorylated p38 MAPK and plasma epinephrine

PGC1α gene expression is regulated by signals that relay metabolic requirements of the cell, such as examples including p38 MAPK (Knutti et al. 2001) and cAMP (Ichida et al. 2002). The increased PGC1α mRNA content and p38 MAPK phosphorylation correlated significantly at rest ($r^2=0.84$, $P<0.01$), whereas phospho-ERK, phospho-JNK and plasma epinephrine and PGC1α mRNA were not related.

Cell culture experiments

To directly examine the effect of p38 MAPK and epinephrine on PGC1α expression, we incubated human primary myotubes in the presence of A23187, which is a calcium ionophore known to stimulate p38 MAPK phosphorylation (M H S Chan, M J Watt & M A Febbraio, unpublished observations), epinephrine, which is known to elevate cellular cAMP/protein kinase A (PKA) content and NA. Unexpectedly, increasing p38 MAPK phosphorylation (>20-fold) did not affect PGC1α mRNA content following A23187 treatment (Fig. 5). Incubation with NA also increased

![Figure 2](image1.png) Real-time RT-PCR analysis of (A) NRF-1 and (B) FKHR mRNA before and after 3 h of moderate exercise with (NA) or without (CON) prior NA administration. Values represent the means±S.E.M. ($n=7$).

![Figure 3](image2.png) (A) Real-time RT-PCR analysis of PGC1α mRNA and (B) Western blot analysis of PGC1α protein content measured before and after 3 h of moderate exercise with (NA) or without (CON) prior NA administration. Values represent the means±S.E.M. ($n=7$ for mRNA; $n=5$ for protein). *$P<0.05$, different from corresponding value for CON; †$P<0.05$, different from 0 min of the same trial.
p38 MAPK phosphorylation (17-fold) and did not affect PGC1α. In contrast, 6 h of epinephrine treatment increased PGC1α content by 250% (P<0.05) and co-incubation with the specific p38 MAPK inhibitor, SB203580, did not prevent this increase.

Discussion

Fatty acids are endogenous ligands for the PPARs (Forman et al. 1997) and PPARs stimulate gene expression of proteins central to substrate metabolism. Because plasma FFA and intramuscular long chain fatty acyl CoA increase dramatically during prolonged exercise (Watt et al. 2003), we hypothesized that decreasing plasma FFA availability would suppress the exercise-induced activation of metabolic genes. The main finding from the present study was that, despite complete suppression of plasma FFA with NA, PGC1α, PPARα and PPARδ mRNA content were increased at rest; however, these effects were not associated with increased mRNA of proteins central to lipid metabolism. The increased PGC1α mRNA coincided with an increase in plasma epinephrine and cell culture studies revealed that epinephrine elevated PGC1α mRNA. Thus, the measured molecular effects of NA were analogous to those induced with exercise and may be related to increased plasma epinephrine.

PPARα and δ increase gene transcription of numerous proteins involved in fatty acid metabolism including CPT1, FAT/CD36, PDK4 and UCP3 (Gulick et al. 1994, Wu et al. 1999, Huang et al. 2002, Muoio et al. 2002, Dressel et al. 2003). PPARα agonists prevent diabetes in OLETF rats (Koh et al. 2003) whereas PPARδ overexpression increases fatty acid β-oxidation in adipocytes and causes resistance to high fat diet-induced obesity (Wang et al. 2003). In contrast to a previous human study (Tunstall et al. 2002), we report increased PPARα and, for the first time, increased PPARδ mRNA immediately following an acute exercise bout. This is consistent with endurance training studies which have demonstrated increased PPARα mRNA (Russell et al. 2003) and protein content (Horowitz et al. 2000, Russell et al. 2003). The difference between the present study and that of Tunstall et al. (2002) is likely to be due to the duration (60 vs 180 min) of exercise. Thus, PPARα and PPARδ mRNA are rapidly upregulated following a single prolonged exercise bout and may contribute, at least partially, to the tighter metabolic control and improved fatty acid handling observed after short-term endurance exercise training (Phillips et al. 1996, Spina et al. 1996). Reducing plasma FFA availability via NA ingestion also resulted in a rapid and pronounced increase in PPARα and δ. The transcriptional response may be a rapid adaptation designed to increase the potential for increased fat oxidative proteins in the event of reduced fatty acid availability. In this regard, rapid transcriptional responses also occur in response to reduced muscle glycogen availability (Pilegaard et al. 2002), suggesting that the availability of metabolic substrates is important for the transcriptional regulation of several transcription factors and metabolic genes.

Despite the rapid changes in PPARα/δ, the mRNA responses of the measured downstream target genes were limited. Consistent with previous

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<td>UCP3</td>
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*P<0.05 compared with corresponding time-point for CON; †P<0.05 compared with 0 min of the same trial; ‡P<0.05 compared with 0 min (main effect).
studies (Pilegaard et al. 2000, 2002), we report exercise-induced increases in UCP3 and PDK4 mRNA, whereas other proteins involved with fatty acid uptake (FAT/CD36), intramyocellular triacylglycerol hydrolysis (HSL) and mitochondrial fatty acid transport (CPT1) were not altered by exercise, and were generally unaffected by reduced fatty acid availability. These data suggested that changes in the mRNA content of some, but not all, transcription factors and coactivators precede changes in the gene expression of proteins involved in lipid metabolism. Although we observed modest or no increases in the mRNA content of numerous lipid-regulatory genes, we cannot discount the possibility that mRNA changes would occur later in recovery from exercise.

There is currently considerable interest in the role of PGC1α in numerous cellular functions,
including mitochondrial biogenesis and lipid metabolism, and evidence is emerging linking muscle insulin resistance with mitochondrial dysfunction (Petersen et al. 2003). Both acute (Baar et al. 2002, Terada et al. 2002, Pilegaard et al. 2003, Norrbom et al. 2004) and chronic (Goto et al. 2000, Russell et al. 2003, Short et al. 2003, Terada & Tabata 2004) exercise increase PGC1α mRNA. In the present study we observed an ~12-fold increase in PGC1α mRNA immediately following 3 h of cycle exercise in CON and have extended previous studies by demonstrating an ~70% increase (P=0.09, n=5) of PGC1α protein content immediately after acute exercise. On balance, these findings suggest that acute exercise increases PGC1α mRNA and protein content, which is presumably a rapid response to metabolic stress designed to co-ordinate changes in skeletal muscle gene expression.

The regulation of PGC1α is complex and is activated by factors that increase cAMP, and is repressed by estrogen-related receptor (ERR)-α (Ichida et al. 2002), which disassociates from PGC1α when p38 MAPK is activated (Knutti et al. 2001). PGC1α is likely to be regulated by upstream kinases because its protein sequence includes putative phosphorylation targets for PKA, PKC and mitogen-activated protein kinases. NA was unlikely to exert direct effects because the receptor for NA (HM74) is not expressed in skeletal muscle (Tunaru et al. 2003). Instead, the effects are likely to be mediated by secondary changes in the internal metabolic and external hormonal milieu. It is unlikely that the decreased plasma FFA per se affected gene expression, because similar transcriptional responses were observed after exercise when plasma FFA was elevated from rest (0·3–1·4 mM). Plasma epinephrine increased 3-fold with NA at rest (Table 2) and during exercise, and direct examination in skeletal muscle myotubes demonstrated increased PGC1α after epinephrine treatment. Thus, the increased PGC1α observed in vivo is consistent with the stimulatory cAMP/PKA effects.

Another possible mediator was p38 MAPK, which was phosphorylated to a greater extent in NA compared with CON both prior to and following exercise (Fig. 4A). Activation of p38 MAPK increases PGC1α transcription (Knutti et al. 2001) and removes the inhibitory action of p160 myb resulting in increased stability and half-life of PGC1α (Puigserver et al. 2001, Fan et al. 2004). Despite the close temporal association between p38 MAPK phosphorylation and PGC1α mRNA 

in vivo, induction of p38 MAPK phosphorylation 

in vitro did not increase PGC1α mRNA (Fig. 5). The disparity between our in vitro and in vivo data with regard to PGC1α mRNA expression with NA treatment suggests that the major function of p38 MAPKs in skeletal muscle is to enhance PGC1α protein stability, rather than acting as a transcriptional regulator. This finding is consistent with previous work in C2C12 myotubes which demonstrated no increase in PGC1α mRNA despite p38 MAPK activation (Fan et al. 2003). A stimulatory role for the other MAPKs on PGC1α cannot be completely excluded, although ERK1/2 phosphorylation decreased and c-jun N-terminal kinase increased modestly and changes in either of these kinases were not related to the increased PGC1α. Previous studies have suggested that 5-AMP-activated protein kinase (AMPK) and a Ca2+-mediated mechanism (possibly calcineurin) increased PGC1α expression (Terada et al. 2004, Zong et al. 2002). However, AMPK activity was not elevated in human skeletal muscle with NA ingestion at rest (Watt et al. 2004), and it is unlikely that intracellular Ca2+ increases with NA at rest. Thus, our data suggested that the increased PGC1α mRNA content observed with NA is most likely due to a secondary effect of increased epinephrine.

It has been postulated that changes in the PGC1α coactivation of PPAR and NRF-dependent transcription may underlie the aberrant fatty acid metabolism in disease states such as type 2 diabetes (Mootha et al. 2003, Patti et al. 2003). In this study, we have observed that the exercise-induced increase in mRNA content of the PPARs, PGC1α and NRF-1 does not occur following NA ingestion, suggesting that the signalling mechanism/s underlying the NA stimulatory effect and exercise are analogous. Although the mechanism(s) of action of NA remains to be elucidated, and no differences in the gene expression of various lipid regulatory proteins were observed after 1·5 h (data not shown), the rapid and pronounced increase in PGC1α and PPARα/δ may promote NA as a potential therapeutic target for improved fatty acid metabolism. Indeed, NA is administered to treat hypertriglyceridemia and lower cholesterol; however, prolonged treatment (>2 weeks) with NA leads to a modest decrease in insulin sensitivity.
as measured by euglycemic–hyperinsulinenemic clamp (Alvarsson & Grill 1996). Thus, the efficacy of NA as a treatment for metabolic disorders is questionable and requires further investigation.

In summary, the results from this study have demonstrated that the mRNA of proteins central to the control of lipid metabolism were generally unaffected following prolonged exercise when FFA availability was attenuated, suggesting that mechanisms other than FFA are important for their gene expression. Despite total suppression of lipolysis, NA ingestion at rest increased the mRNA content of PGC1α and PPARα/δ, which was associated with elevated plasma epinephrine. The magnitude of these changes was analogous to those induced by prolonged exercise. The absence of further increases in the mRNA content of PPARα/δ and PGC1α following exercise in NA suggests that the signaling mechanism(s) underlying the NA stimulatory effect are homologous to those induced by exercise.

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