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Published in: The Journal of Physiology

DOI: 10.1113/JP280428

Publication date: 2020

Document version Publisher's PDF, also known as Version of record

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Citation for published version (APA):
Contraction influences Per2 gene expression in skeletal muscle through a calcium-dependent pathway

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Edited by: Scott Powers & Troy Hornberger

Linked articles: This article is highlighted in a Perspectives article by Wolff & Esser. To read this article, visit https://doi.org/10.1113/JP280783.

Key points

- Exercising at different times of day elicits different effects on exercise performance and metabolic health. However, the specific signals driving the observed time-of-day specific effects of exercise have not been fully identified.
- Exercise influences the skeletal muscle circadian clock, although the relative contribution of muscle contraction and extracellular signals is unknown.
- Here, we show that contraction acutely increases the expression of the core circadian clock gene Period Circadian Regulator 2 (Per2) and phase-shifts Per2 rhythmicity in muscle cells. This contraction effect on core clock genes is mediated through a calcium-dependent mechanism;
- The results obtained in the present study suggest that a proportion of the ability of exercise to entrain the skeletal muscle clock is driven directly by muscle contraction. Contraction interventions may be used to mimic some time-of-day specific effects of exercise on metabolism and muscle performance.

Abstract  Exercise entrains the central and peripheral circadian clocks, although the mechanism by which exercise modulates expression of skeletal muscle clock genes is unclear. The present study aimed to determine whether skeletal muscle contraction alone could directly influence circadian rhythmicity and uncover the underlying mechanism by which contraction modulates clock gene expression. We investigated the expression of core clock genes in human skeletal muscle after acute exercise, as well as following in vitro contraction in mouse soleus muscle and cultured C2C12 skeletal muscle myotubes. Additionally, we interrogated the molecular pathways by which skeletal muscle contraction could influence clock gene expression. Contraction acutely

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DOI: 10.1113/JP280428

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increased the expression of the core circadian clock gene Period Circadian Regulator 2 (Per2) and phase-shifted Per2 rhythmicity in C2C12 myotubes in vitro. Further investigation revealed that pharmacologically increasing cytosolic calcium concentrations by ionomycin treatment mimicked the effect of contraction on Per2 expression. Similarly, treatment with a calcium channel blocker, nifedipine, blocked the effect of electric pulse stimulation-induced contraction on Per2 expression. Increased calcium influx from contraction lead to binding of the phosphorylated form of cAMP response element-binding protein (CREB) to the Per2 promoter, suggesting a role of CREB in contraction-induced Per2 transcription. Thus, by dissociating the effect of muscle contraction alone from the whole effect of exercise, our investigations indicate that a proportion of the ability of exercise to entrain the skeletal muscle clock is driven directly by contraction.

Introduction

The central regulation of circadian rhythm is controlled by the suprachiasmatic nucleus (SCN), a discrete component of the hypothalamus that is entrained by light and signals for many circadian behaviours, such as eating and sleeping (Hastings et al. 2003). In addition to receiving input from the central clock, peripheral tissues have their own molecular clocks comprising positive and negative regulatory proteins that control transcription of each other. The positive element proteins BMAL1 (Arntl) and CLOCK dimerize and bind to an E-box motif in the promoter regions of NR1D1 to drive its transcription, as well as expression of the Period Circadian Regulator (Per1, 2 and 3) and Cryptochrome (Cry1 and 2) genes. NR1D1 in turn feeds back to bind the DNA response element in the BMAL1 promoter, blocking its subsequent transcription, whereas the CRY and PER proteins translocate to the nucleus to block BMAL1 activity. This entire process forms the molecular clock in which core clock genes and proteins display rhythmic expression in many of the core clock genes. Important to the present study, the mouse C2C12 immortalized myoblast line, differentiated into myotubes, displays robust oscillations in the expression of core clock genes and clock-controlled genes after synchronization with 50% serum shock (Altıntaş et al., 2020).

The molecular clock is calibrated to the diurnal activities of an organism by external entraining signals or zeitgebers. The most well characterized zeitgeber is light, which rapidly phase-shift clock gene transcription in the SCN and more slowly in peripheral tissues (Kiessling et al. 2010). Other zeitgebers that have been hypothesized include food intake and activity. A role for exercise in entraining central and peripheral circadian clocks is becoming increasingly apparent (Gabriel & Zierath, 2019). In rodents, both voluntary access to a running wheel (Maywood et al. 1999) and enforced exercise paradigms (Schroeder et al. 2012) influence clock gene expression in the SCN. Exercise modulates rhythmic physiological processes such as body temperature and levels of circulating melatonin, which potentially contributes to the diurnal variations in performance (Lewis et al. 2018). In the skeletal muscle, exercise induces changes in specific clock genes in rodents (Yamanaka et al. 2008; Wolff & Esser, 2012; Ezagouri et al. 2019) and humans (Zambon et al. 2003; Popov et al. 2019). In humans, some of these differences persist in one-leg exercise paradigms in which one leg was exercised and contralateral leg was used as a resting control (Zambon et al. 2003; Popov et al. 2019), suggesting that this response may be intrinsic to the exercised muscle.

Exercise is associated with multiple physiological events, including changes in blood flow, sympathetic activity, and plasma hormone and substrate levels (Hawley et al. 2014), which are putative modulators of the effect of exercise on central clocks (Tahara et al. 2017). However, the mechanism by which exercise modulates expression of skeletal muscle clock genes is unclear. Therefore, the present study aimed to determine whether skeletal muscle contraction could directly influence circadian rhythmicity.
and uncover the underlying mechanism by which exercise modulates clock gene expression. We investigated changes in clock gene expression in human skeletal muscle in response to acute exercise and compared these responses to in vitro contraction models to remove the signals from conflicting zeitgebers such as light and hormonal and sympathetic changes. We exposed C2C12 myotubes to electric pulse stimulation (EPS), which results in visible contractions in myotubes and evokes many of the physiological changes that occur in skeletal muscle during exercise, including effects on energy metabolism, calcium gradients and the expression of exercise responsive genes (Nikolić et al. 2016; Pattamaprapanont et al. 2016).

Here, we describe that contraction acutely increased Per2 expression in human skeletal muscle directly following exercise and in mouse soleus muscle and C2C12 myotubes contracted in vitro. We suggest that calcium influx from actively contracting muscle cells may be the mechanism by which exercise acutely increases Per2 expression. Finally, we report that contraction of myotubes in vitro acts as a zeitgeber and is able to phase-shift Per2 expression. Collectively, our results provide evidence to suggest that contraction, potentially via a calcium-mediated signalling pathway, directly entrains the intrinsic skeletal muscle clock in response to acute exercise.

Methods

Ethical approval

All animal experiments were approved by the Danish Animal Experiments Expectorate (license number 2015-15-0201-00796) and were carried out in accordance with the guidelines of the University of Copenhagen Department of Experimental Medicine, and also conform with the principles and regulations described in Grundy (2015). Use of 2,2,2-tribromoethanol as an anaesthetic for terminal procedures was approved by the above licence from the Danish Animal Experiments Expectorate.

Human muscle samples

The present study was carried out in accordance with the recommendations of the Ethic Committee from the Capital Region of Denmark with written informed consent from all subjects. All subjects gave written informed consent in accordance with the Declaration of Helsinki, apart from registration in a database. The protocol was approved by the Ethics Committee from the Capital Region of Denmark (reference H-1-2013-064). Sixteen healthy Danish male volunteers, aged between 18 and 27 years old, were recruited to participate in the study. Clinical characteristics have been previously published (16 individuals from cohorts A and B in the untrained state from Ingerslev et al. (2018). The participants performed an intense (80% $\tilde{V}_{O_2,max}$) 15 min exercise bout, in the fasted state, in the morning, for which details of have been reported previously (Pattamaprapanont et al. 2016). Biopsies were obtained from the vastus lateralis muscle immediately prior to and 60 min following exercise using the Bergström needle technique, and they were immediately snap-frozen in liquid nitrogen and stored at $-80^\circ C$ for further analysis. RNA was purified from muscle biopsies using an AllPrep kit (Qiagen, Valencia, CA, USA).

Meta-analysis of clock gene expression from human exercise studies

Studies of aerobic and resistance exercise in healthy, young, non-athletes, non-obese (body mass index $<30$ kg m$^{-2}$) individuals were selected from the MetaMEx database (http://www.metamex.eu). Acute exercise studies with skeletal muscle biopsy collection occurring within 0–3 h after the exercise bout were selected. Meta-analysis was calculated for each clock gene with restricted maximum-likelihood as described previously (Pillon et al. 2020).

Ex vivo muscle contraction

Twelve-week old male C57BL/6NTac (Taconic, Germantown, NY, USA) mice were housed under a 12:12 h light/dark photocycle and maintained on a standard chow diet, with food and water available ad libitum. Mice were anaesthetized with an I.P. injection of a 2.5% solution of equal parts 2,2,2-tribromo ethanol and tertiary amyl alcohol diluted in sterile saline (Sigma, St Louis, MO, USA), at a dose of 16 µL g$^{-1}$ body weight between 15.00 h and 16.00 h (zeitgeber time 9–10) and soleus muscles were isolated from tendon to tendon and tied with silk ties. Muscle isolation was commenced after deep anaesthesia (determined by complete lack of pedal withdrawal reflex) and, directly following muscle isolation, animals were killed by cervical dislocation. Muscles were incubated at 30℃ in oxygenated (95% O$_2$ and 5% CO$_2$) Krebs–Ringer phosphate buffer (117 mM NaCl, 4.7 mM KCl, 2.5 mM CaCl$_2$, 1.2 mM KH$_2$PO$_4$, 1.2 mM MgSO$_4$ and 24.6 mM NaHCO$_3$) supplemented with 0.1% BSA and 5 mM glucose in a muscle strip myograph system (820MS; Danish Myo Technology, Hinnerup, Denmark). Muscles were tied and placed under tension and allowed to rest for 30 min before they were stimulated to contract using 0.2 ms pulses at 12 V and 20 Hz. Trains of 30 pulses were delivered every 10 s for three rounds of 6 min contraction with 6 min of rest. This protocol induces contractions approximating 30–40% of maximal force production, mimicking high-intensity
aerobic intervals and, in a similar protocol, increased the expression of exercise responsive genes (Barrès et al. 2012). Muscle tissue was collected 1 h after the last round of contractions. Muscle was homogenized in 400 µL of RLT buffer (Qiagen) with β-mercaptoethanol using steel beads and subjected to 2 × 30 s at 30 Hz of disruption using the TissueLyser II (Qiagen) and RNA was extracted using the RNeasy mini kit (Qiagen).

Cell culture

C2C12 myotubes (#CRL-1772; American Type Culture Collection, Manassas, VA, USA) were cultured as described previously (Pattamaprapanont et al. 2016) and circadian synchronized using 50% horse serum shock for 2 h on day 5 of differentiation. EPS was applied to the cells in culture to induce contractile activity, 12 h after serum shock (12, 18 and 24 h after serum shock in Fig. 3), using the Ion-optics system C-dish electrode in a six-well format. The EPS protocol consisted of 30 min with 1 Hz frequency, 2 ms in duration and 30 V, which induces expression of exercise responsive genes (Pattamaprapanont et al. 2016). Differentiated myotubes were treated with pharmacological agents, 12 h after serum shock, to interrogate contraction-mediated signalling at the following concentrations: forskolin 1 µM (#F3917; Sigma), ionomycin 1 µM (#I3909; Sigma), AICAR 1 mM (#S8820; Sigma), dissolved in DMSO or DMSO (vehicle), added directly to the media, which induces expression of exercise responsive genes (Pattamaprapanont et al. 2016). For extraction RNA, cells were harvested in RLT buffer with β-mercaptoethanol and RNA was isolated using the RNeasy mini kit (Qiagen). To extract protein, cells were harvested in RIPA buffer containing protease and phosphatase inhibitors.

cDNA synthesis and quantitative PCR

cDNA was synthesized using the Bio–Rad iScript cDNA synthesis kit from 1µg of RNA. A quantitative PCR was performed using conventional Sybr Green chemistry utilizing the primers reported in Table 1. All primers were used at a final concentration of 200 nM. Relative quantification was determined by comparing samples to a standard curve of pooled cDNA or using the ΔΔCT method (in which case efficiency had been previously tested to be 100 ± 10%) for each gene and normalized to the housekeeping genes 18S (for mouse samples) and GAPDH (for human samples). GAPDH was chosen for human samples because its expression is stable following endurance exercise (Mahoney et al. 2004) and between night and day (Wefers et al. 2018) in human skeletal muscle. 18s rRNA was chosen for mouse samples because it remains relatively consistent over the diurnal cycle (Nakao et al. 2017) and is routinely used as a housekeeping gene for circadian mouse experiments in skeletal muscle (Kinouchi et al. 2018; Altıntaş et al. 2020).

Immunoblotting

Cells were harvested in RIPA buffer containing protease (#S8820; SIGMAFAST Protease Inhibitor Cocktail Tablet; Sigma) and phosphatase inhibitors (10 mM NaF, 1 mM Na2VO4). Protein amounts were normalized after determination of protein concentration using BCA protein assay kit (Pierce, Rockford, IL, USA) in a standard laemmli buffer and subjected to SDS-PAGE, transferred to polyvinylidene fluoride membranes, blocked in 2% BSA and blotted for phosphorylated cAMP response element-binding protein (pCREB) (#9198; Ser133) or total CREB (#9197) antibodies (Cell Signaling Technologies, Beverly, MA, USA) at a dilution of 1:1000 and then goat anti-rabbit IgG–HRP conjugate (#1706515; Bio-Rad, Hercules, CA, USA) at a dilution of 1:5000 in 2% BSA. Total CREB was visualized on the same membrane as pCREB after stripping (15 min; Restore Stripping Buffer; Thermo Fisher, Waltham, MA, USA) and re-probing.

Table 1. Primer sequences

<table>
<thead>
<tr>
<th>Gene</th>
<th>Sequence (5′- to 3′)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mouse</td>
<td></td>
</tr>
<tr>
<td>18S</td>
<td>Forward: AGT CCC TGC CTC TTG TAC ACA</td>
</tr>
<tr>
<td></td>
<td>Reverse: GAT CCG AGG GCC TCA CTA AAC</td>
</tr>
<tr>
<td>Arntl</td>
<td>Forward: TAG GAG GTG ACC GAG GGA AG</td>
</tr>
<tr>
<td></td>
<td>Reverse: TCA AAC AAG CTC TCG CCA AT</td>
</tr>
<tr>
<td>Per2</td>
<td>Forward: AAT GGC CAA GAG GAG TCT CA</td>
</tr>
<tr>
<td></td>
<td>Reverse: ATG CTT CCT GCT GTC CTC CA</td>
</tr>
<tr>
<td>Per1</td>
<td>Forward: TGA AGC AAG ACC GGG AGA G</td>
</tr>
<tr>
<td></td>
<td>Reverse: CAC ACA CCG CTG CAC ATC AA</td>
</tr>
<tr>
<td>Nr1d1</td>
<td>Forward: GTC TCT CGG TTG GCA TGT CT</td>
</tr>
<tr>
<td></td>
<td>Reverse: CCA AGT TCG CCG CTC CT</td>
</tr>
<tr>
<td>Cry1</td>
<td>Forward: AGC GCA GGT GTG TAT GAC C</td>
</tr>
<tr>
<td></td>
<td>Reverse: ATA GAC GCA GCG GAT G GT GTC G</td>
</tr>
<tr>
<td>Per2 promoter (CHIP-PCR)</td>
<td>Forward: CCA GAA CAA TGT AGC CAC CA</td>
</tr>
<tr>
<td></td>
<td>Reverse: ACA CTC CCC AAC ACA CAC AA</td>
</tr>
<tr>
<td>CHIP negative control region (upstream of Actb, chromosome 5)</td>
<td>Forward: CTC TCC CAG CCC TGT TTT G</td>
</tr>
<tr>
<td></td>
<td>Reverse: ACC TTA AAT CCC ACC ACT CAG G</td>
</tr>
<tr>
<td>Human</td>
<td></td>
</tr>
<tr>
<td>GAPDH</td>
<td>Forward: GTC AGC CGC ATC TTC TTG TT</td>
</tr>
<tr>
<td></td>
<td>Reverse: TAC GAC CAA ATC CGT TGA CT</td>
</tr>
<tr>
<td>ARNTL</td>
<td>Forward: TGC CTC GTC GCA ATT GG</td>
</tr>
<tr>
<td></td>
<td>Reverse: ACC CTG ATT TCC CGG TTC A</td>
</tr>
<tr>
<td>PER2</td>
<td>Forward: GAC ATG AGA CCA ACG AAA ACT GC</td>
</tr>
<tr>
<td></td>
<td>Reverse: AGG CTA AAG GTA TCT GGA CTC TG</td>
</tr>
<tr>
<td>PER1</td>
<td>Forward: GCC GTG CTG CTC GCT GAT</td>
</tr>
<tr>
<td></td>
<td>Reverse: GGC AGC TGG GTG TGG GCC</td>
</tr>
<tr>
<td>NR1D1</td>
<td>Forward: CTT CAA TGG CAA CCA TGC AT</td>
</tr>
<tr>
<td></td>
<td>Reverse: CCT GAT TTT CCC AGC GAT TT</td>
</tr>
<tr>
<td>CRY1</td>
<td>Forward: GCA TCA AGT GGG GAT TT</td>
</tr>
<tr>
<td></td>
<td>Reverse: TGG GTC TGC TTC TGT TCC AA</td>
</tr>
</tbody>
</table>
Protein loading was determined using Bio-Rad stain-free technology.

Calcium imaging

Differentiated C2C12 myotubes were washed in PBS and incubated in serum-free, indicator-free Dulbecco’s Modified Eagle’s Medium (DMEM) in the presence of 1 mM fluo-4 acetyloxymethyl ester (#F14201; Thermo Fisher) for 30 min. Before fluorescence measurements were commenced, cells were washed with PBS and incubated in indicator-free DMEM for 30 min. Live cell imaging was performed on an LSM 780 Confocal microscope (Carl Zeiss, Oberkochen, Germany). Cells were excited with an argon laser and sequential images were taken during the EPS protocol described above.

Chromatin immunoprecipitation (ChIP)-PCR

Immediately following the 30 min EPS protocol (and/or treatment with vehicle, ionomycin 1 µM, or nifedipine 100 µM), cells were washed with PBS and fixed in PBS with 1% formaldehyde for 10 min at room temperature. ChIP was performed as described previously (Williams et al. 2020). The antibodies used for ChIP were: pCREB Ser 133 (#9198; Cell Signaling Technologies) and Normal Rabbit IgG (#2729; Cell Signaling Technologies). Quantitative PCR was performed on immunoprecipitated DNA using the primers reported in Table 1.

Statistical analysis

Data are presented as the mean ± SD or means displaying all data points. Human vastus lateralis and mouse soleus muscle data were tested for normality and analysed by a paired t test (normally distributed) or a Wilcoxon matched pairs signed rank test (not normally distributed); n indicates the number of individual subjects or animals for these tests. C2C12 experiments were analysed either by the Mann–Whitney test, one or two-way ANOVA, or corresponding non-parametric tests, as appropriate; n indicates the number of replicates. The rhythmicity analysis presented in Fig. 3 was performed by a two-way ANOVA with type-II error assumption as a result of non-equal group sizes at the same time as considering the main effects ‘group’ as different EPS treatment times and ‘time’ as the measurement time (expression ~ group + time). ANOVA assumptions of univariate normality and homogeneity of variance were not met and the data were power transformed using Tukey’s ladder approach. Time points of EPS treatment groups were shifted back to control condition to ensure a proper evaluation of treatment effect. All C2C12 experiments were performed between two to three times on separate days. P < 0.05 was considered statistically significant.

Results

Contraction acutely increases Per2 expression in skeletal muscle

To determine whether exercise can influence the expression of core clock genes in skeletal muscle, we analysed the expression of several clock genes in the vastus lateralis muscle of young men immediately before and 60 min following an intense 15 min exercise bout (80% \( \dot{V}_O_{2\text{max}} \)) on a bicycle ergometer. PER1 and PER2 expression was acutely increased by ~1.5-fold at 60 min following acute exercise, whereas NR1D1 expression was decreased (Fig. 1). Conversely, ARNTL and CRY1 expression was not changed following acute exercise (Fig. 1). Publicly available skeletal muscle transcriptomic data from human exercise studies revealed a similar pattern, where acute aerobic and resistance exercise (0–3 h post-exercise) altered the expression of specific clock genes (Fig. 1F and G). Acute exercise induced the expression of PER2 and CRY1 in skeletal muscle in both aerobic and (to a greater extent) resistance exercise modalities.

To account for the possibility of changes in clock expression as a result of sampling time and to isolate the contribution of muscle contraction per se to this effect, two separate in vitro models of muscle cell contraction were used. In the first model, we performed ex vivo contractions of isolated mouse soleus muscle, comparing the expression of circadian clock genes between the rested and contrac- ted muscle from the same animal 60 min after a 30 min contraction stimulus. Per2 expression was increased by ~1.4 fold 60 min after the ex vivo muscle contraction procedure (Fig. 2A). Additionally, ex vivo contraction increased Arntl expression, whereas Per1, Nr1d1 and Cry1 were unaffected (Fig. 2A). We then performed a time course study to determine the effect of EPS-mediated contraction on gene expression. C2C12 myotubes were harvested 0, 30, 60 and 240 min following a 30 min EPS stimulus. Per2 expression (Fig. 2B), but not the expression of Per1, Bmal1, Nr1d1 or Cry1 (Fig. 2C–F), was increased by ~1.5-fold, 60 min following EPS; however, Per2 expression returned to the unstimulated level 4 h post contraction (Fig. 2B; although, after adjusting for multiple comparison testing, this did not reach significance).

Contraction induces a phase-shift in the rhythmicity of Per2 expression in muscle cells in vitro

Because Per2 expression was induced after exercise in human skeletal muscle as well as after contraction in both in vitro contraction models used, we further investigated
the mechanisms by which Per2 expression was influenced by skeletal muscle contraction. To determine whether the acute contraction-mediated increase in Per2 expression is associated with longer term differences in circadian rhythmicity, we subjected synchronized C2C12 myotubes to a single 30 min bout of EPS 12, 18 or 24 h after circadian synchronization (serum shock). Cells were harvested every 6 h for 24 h after each bout of EPS (Fig. 3A). When cells were exposed to EPS at any time point, this induced a phase-shift in Per2 oscillation to its low expression starting point (Fig. 3B).

Modulating intracellular calcium levels alter Per2 expression

To explore mechanisms by which contraction increases Per2 expression, we treated C2C12 myotubes with several agents that mimic the effects of exercise on signal transduction using concentrations of the compounds that are commonly used with in vitro skeletal muscle cell models (Carter & Solomon, 2018). We tested the effect of forskolin (1 µM), which raises cAMP levels, the Ca²⁺ ionophore, ionomycin (1 µM) and the AMPK agonist AICAR (1 mM) on Per2 expression in C2C12 myotubes after 90 min of treatment. Interestingly, treatment with ionomycin, but not forskolin or AICAR, increased Per2 expression by ∼2.5 fold (Fig. 4A). To confirm that EPS induced changes in intracellular calcium levels in C2C12 myotubes, we performed EPS on C2C12 myotubes pre-treated with the calcium indicator, fluo-4, which fluoresces in the presence of calcium, and we visualized the contracting cells using fluorescence microscopy. Cells that were exposed to EPS displayed visible flashes of fluorescence coincident with the electrical pulses, indicating increased cytoplasmic calcium levels in response to contraction (see Supporting information, Fig. S1).

We next performed an abbreviated experiment in which we treated circadian synchronized C2C12 myotubes...
in the absence or presence of nifedipine (calcium channel blocker) or EPS, 12 h after serum shock, and then monitored Per2 expression at 18 and 24 h after serum shock (Fig. 4B). We used a dosage of nifedipine (100 µM) that has been previously used in C2C12 myotubes to reduce contraction-mediated calcium flux (Porter et al. 2002). Nifedipine had no visible effects on cell viability in differentiated cells; however, we did note that EPS-mediated contraction was compromised in these cells, as indicated by fewer visible contractions, confirming the efficacy of nifedipine with respect to reducing calcium flux (data not shown). We assessed the

![Graphs showing gene expression](image)

Figure 2. The effect of exercise on Per2 expression can be recapitulated in skeletal muscle by in vitro contraction

A. mRNA expression of Per2, Per1, Arntl, Nr1d1 and Cry1 from contracted mouse soleus muscles compared to the housekeeping gene 18S rRNA. One soleus muscle from each mouse was contracted for 30 min and then further incubated for 60 min and then harvested with the rested contralateral muscle. Pairwise comparison from the rested vs. contracted muscle, with relative expression depicting the fold change (FC) compared to the mean of the rested muscle, analysed by individual paired t tests (n = 7). mRNA expression of (B) Per2, (C) Per1, (D) Arntl, (E) Nr1d1 and (F) Cry1 from EPS-treated C2C12 myotubes compared to the housekeeping gene 18S, 12 h after serum-shock after a 30 min contraction protocol, with relative expression compared to non-contracted control cells at each timepoint, analysed by individual Mann–Whitney tests corrected for multiple comparisons (n = 6–12). *P < 0.05. #P = 0.0242. AdjP = not significant. Data are presented as the mean ± SD.
oscillatory behaviour of Per2 by calculating the slope of gene expression from 18 to 24 h. We chose these timepoints because C2C12 myotubes display different slopes of Per2 expression between 18 to 24 h when EPS is performed at 12 h post serum shock (Fig. 3B). EPS caused a significant change in the slope of gene expression in vehicle treated cells compared to the control cells without stimulation (Fig. 4C). Nifedipine treatment reduced Per2 expression and abolished the effect of EPS on Per2 expression. Conversely, Nr1d1 showed a difference in expression with time, but no difference with nifedipine treatment or EPS (Fig. 4D), whereas Arntl expression was not altered by either time or EPS, although it was increased by nifedipine treatment (Fig. 4E).

Contraction induces CREB phosphorylation and binding to the Per2 promoter

To determine the mechanism by which calcium levels influence Per2 expression, we investigated the phosphorylation status of CREB. pCREB binds to cAMP response elements (CREs) in promoters of period gene isoforms in fibroblasts (Pulivarthy et al. 2007), PC12 neuroblasts (Impey et al. 2004) and the SCN (Tischkau et al. 2003). In C2C12 myotubes, EPS acutely increased phosphorylation of CREB, whereas nifedipine treatment prevented this increase (Fig. 5A and B). Ionomycin treatment produced an expected robust increase in CREB phosphorylation. Mirroring these results, EPS and, to a greater extent, ionomycin treatment increased pCREB antibody-mediated pull-down of the Per2 promoter region (Fig. 5C). This was not the case with a negative control region (upstream of the β-Actin promoter) (Fig. 5D). Taken together, these data show that contraction-mediated increases in cytosolic calcium leads to increases in phosphorylated CREB, which binds to CREs on the Per2 promoter. Our results suggest a role of calcium-mediated CREB binding in the positive regulation of Per2 expression.

Discussion

Evidence obtained in studies conducted in mice (Ezagouri et al. 2019; Sato et al. 2019) and humans (Savikj et al. 2019) suggests that exercise performed at different times of day results in diverse metabolic outcomes. However, there is still no consensus on the mechanisms that underlie these differences. Because metabolism is strongly influenced by the intrinsic core clock machinery (Dyar et al. 2014), one possibility is that exercise-induced changes in the skeletal muscle core clock machinery...
may alter the expression of clock-controlled genes and impact metabolic processes. Although several reports suggest exercise-induced alterations in specific skeletal muscle clock genes (Zambon et al. 2003; Yamanaka et al. 2008; Wolff & Esser, 2012), determining the mechanisms driving these changes has been a challenge because exercise influences many physiological processes. We hypothesized that skeletal muscle contraction during exercise was partly responsible for exercise-mediated changes in clock gene expression. To address this question, we utilized an in vitro contraction model to isolate the contribution of contraction from other elements associated with exercise in the working muscle.

We found that PER1 and PER2 were increased and NR1D1 was decreased in human skeletal muscle 1-h post-exercise. Similarly, a meta-analysis of publicly available data revealed that PER2 and CRY1 expression in human skeletal muscle was acutely increased after both aerobic and resistance exercise, with resistance exercise having a larger effect. Interestingly, only Per2 was similarly increased in contracting mouse skeletal muscle and cultured C2C12 myotubes in vitro. Treadmill running acutely increases Per1 and Per2 expression in mouse plantaris muscle 1 h following the exercise bout (Saracino et al. 2019). This increase in Per1, but not Per2 expression, was attributed to exercise-secreted hormones.
such as epinephrine. Because PER2 expression is acutely increased in skeletal muscle after one-legged exercise regimes (Zambon et al. 2003; Popov et al. 2019) and by contraction in vitro, systemic hormonal cues probably do not play a role, suggesting that expression of Per1 and Per2 isoforms are driven by separate exercise stimuli. Similarly, acute resistance exercise, but not in vitro contraction, led to a substantial up-regulation of CRY1 expression in skeletal muscle, suggesting that CRY1 expression is regulated by a separate exercise stimulus, and not muscle contraction per se.

In synchronized C2C12 myotubes that are removed from conflicting zeitgebers, we show that the induction of Per2 by contraction is transient because it disappears after 4 h. However, this transient increase in Per2 expression at 1 h post-EPS is followed by a decrease in Per2 expression to its lowest point 6 h after EPS, resetting its cycle. Interestingly, contraction phase-shifted Per2 rhythmicity in C2C12 myotubes at multiple timepoints of the circadian cycle. A similar ability of exercise to modulate Per2 rhythmicity has been reported in mouse skeletal muscle explants taken from mice with access to voluntary running wheels or forced treadmill running, which display shifted Per2 rhythms for multiple days ex vivo (Wolff & Esser, 2012).

Contraction of C2C12 myotubes cells alters the rhythmicity of Arntl, as evidenced by a small (~1 h) contraction-induced phase-shift (as determined by monitoring of Arntl-luciferase luminescence) (Kemler et al. 2020). Thus, either Arntl and Per2 are regulated differently by contraction or, alternatively, the resetting effect of contraction on Per2 rhythmicity as described in our study may only be at the transcript level and the translated protein may have a different rhythmicity. By contrast to our results, Per2 expression was reduced immediately after 1 h of contraction in C2C12 myotubes performed at 22 and 28 h after synchronization (Kemler et al. 2020). Potentially, this discrepancy is a result of the time after contraction (1 h in the present study; immediately after contraction in Kemler et al. 2020), time after synchronization (12 h in the present study; 22 or 28 h after synchronization in Kemler et al. 2020) or method of synchronization (serum shock in the present study; dexamethasone in Kemler et al. 2020). However, overall, the report by Kemler et al. (2020) supports the hypothesis that skeletal muscle contraction can entrain core clock genes.

The effect of EPS to phase-shift clock gene expression in cultured cells is not entirely surprising because the rhythmicity of cultured cells is synchronized by
multiple signals, including serum shock, dexamethasone, epidermal growth factor and ionomycin (Izumo et al. 2006). However, in an in vivo setting, exercise probably acts as a relatively weak zeitgeber compared to light, and therefore the ability of acute exercise or contraction to influence clock rhythmicity over a long period is probably limited. Supporting this, a recent study performed by our group found few differences in the rhythmicity of core clock genes in mouse skeletal muscle for 24 h following acute treadmill exercise at two different times of day compared to skeletal muscle from non-exercised mice investigated at the same times (Sato et al. 2019). However, immediately following exercise, the expression of several clock genes was transiently increased, and this was dependent on the time of day when the exercise bout was performed. Correspondingly, one limitation of the present study is that the acute transcriptional response to contraction was tested at only one timepoint in human and mouse skeletal muscle. Potentially, contraction-mediated changes in clock gene expression may rely on a certain expression level, which may occur only during a distinct period for each respective gene over the circadian rhythm.

Calcium flux has a well-established role in the entrainment of circadian rhythms in the neurons of the SCN. In particular, Per2 expression is dependent on functional calcium transport in SCN neurons (Lundkvist et al. 2005) and fibroblasts (Noguchi et al. 2012). We provide novel evidence indicating that alterations in cellular calcium flux mediated by contraction may be partly responsible for the entrainment of specific core clock genes in skeletal muscle. Increasing cytosolic calcium with the calcium ionophore ionomycin increased Per2 expression, whereas blocking calcium transport with nifedipine decreased Per2 expression, increased Arntl expression (potentially as a result of the large decrease in Per2 expression) and abolished the effect of EPS on Per2 expression. However, because nifedipine treatment reduced the appearance of visible contractions in EPS-stimulated cells, this may be the result of an effect of nifedipine on contraction per se rather than on calcium flux itself. Because calcium flux is necessary for muscle contraction, it is difficult to isolate the contribution of one from the other.

CREB phosphorylation plays a role in regulating the response of the SCN clock to stimuli such as light (Gau et al. 2002; Wheaton et al. 2018). A CRE has been identified in the Per2 promoter (Impey et al. 2004) and Per isoforms are driven by CREB binding to CREs in promoter regions (Tischkau et al. 2003; Pulivarthy et al. 2007). We provide evidence indicating that, in C2C12 myotubes, CREB phosphorylation at Ser 133 is responsive to increasing cytosolic calcium through EPS stimulation and ionomycin treatment. Furthermore, our ChIP-PCR experiments suggest that phosphorylated CREB binds to the Per2 promoter, and this effect is enhanced after either EPS or ionomycin treatment. Although we find that, in C2C12 cells, CREB is phosphorylated immediately after contraction, in human skeletal muscle, CREB phosphorylation decreases immediately following exercise (compared to the rested leg) (Widegren et al. 1998), with an increase not occurring until 3 h post-exercise (Egan et al. 2010; Stocks et al. 2019). Therefore, the exact time-course for CREB phosphorylation after exercise is unclear, indicating that other factors occurring in the human setting, such as exercise intensity and duration, as well as differences in secreted factors, may be involved in regulating the expression of Per2 after exercise. Although we focused on the Ser 133 phosphorylation site of CREB, because of the availability of a ChIP-verified antibody, it is also possible that other CREB phosphorylation sites may play a role in this process, such as Ser 142, which is involved in the regulation of light-induced phase-shifts in the SCN (Gau et al. 2002).

The physiological role of exercise on clock components in skeletal muscle is unclear. The acute exercise-induced changes in skeletal muscle clock genes probably do not affect long-term circadian rhythmicity in mammals that have a normal sleep/wake cycle aligned with the light. Potentially, longer scheduled exercise routines have a greater effect on the clock and it is possible that, in situations in which there is a divergence between the central and peripheral clock, such as with jet-lag, exercise may have a fine-tuning effect to rapidly align the peripheral clock with the organism’s behaviour. Along these lines, aerobic exercise at different times of the day had some capacity to phase-shift diurnal melatonin secretion (Youngstedt et al. 2019). Potentially, when adapting to a new light-dark schedule, the ability of contraction to entrain the muscle clock may allow the tissue to more quickly adapt to behavioural changes.

In conclusion, the results obtained in the present study add to an increasing body of evidence indicating that exercise alters the transcription of skeletal muscle clock genes. Evidence is also provided indicating that a proportion of this effect is directly a result of muscle contraction per se. Additionally, we show that the ability of contraction to alter Per2 expression is dependent on contraction-mediated changes in cytosolic calcium content. This work advances our understanding of how non-light zeitgebers influence circadian rhythmicity in peripheral tissue, with applications towards delineating the links between lifestyle factors, circadian rhythms and metabolic disease.

References


**Additional information**

**Data availability statement**

The data that support the findings of this study are available from the corresponding author upon reasonable request.

**Competing interests**

The authors declare that they have no competing interests.

**Author contributions**

LS, RCL and RB were responsible for the study conception and design. LS, AA, RCL, AE, PP, JV, NJP and RB were responsible for data acquisition, as well as analysis and interpretation. LS, RCL, JRZ and RB were responsible for drafting and revising the article. All authors approved final version of the manuscript.
submitted for publication and agree to be accountable for all aspects of the work.

**Funding**

The Novo Nordisk Foundation Center for Basic Metabolic Research is an independent research Center at the University of Copenhagen, partially funded by an unrestricted donation from the Novo Nordisk Foundation (NNF18CC0034900). This work was funded by a Novo Nordisk Foundation Challenge Grant (NNF14OC0011493) and partly supported by a research grant from the Danish Diabetes Academy, which is funded by the Novo Nordisk Foundation (NNF17SA0031406).

**Acknowledgements**

We acknowledge the Core Facility for Integrated Microscopy, Faculty of Health and Medical Sciences, University of Copenhagen for assistance with live cell microscopy. The authors would like to thank the staff of the Department of Experimental Medicine, University of Copenhagen for assistance with animal care.

**Keywords**

calcium, clock genes, contraction, period genes, skeletal muscle

**Supporting information**

Additional supporting information may be found online in the Supporting Information section at the end of the article.

**Video S1.** Live cell imaging video of individual C2C12 myotubes treated with the cytosolic calcium fluorophore, fluo-4, undergoing EPS-mediated contraction.

**Statistical Summary Document**