INTRODUCTION

Cycling endurance performance is mainly determined by three factors: maximal oxygen uptake (VO2max), fractional utilization of VO2max and efficiency. Accordingly, the scientific community continuously search for training regimes that best target and improve these factors, particularly in well-trained athletes. It is a long-standing recognition that such training should include high-intensity interval training (HIT). However, the exact composition and nature of HIT remains disputed and evolving. It seems important to maximize the time spent above 90% of VO2max, especially when the aim is to increase VO2max. This is most effectively achieved by HIT comprising of shorter work intervals, as evident from a study by Rønnestad and colleagues, wherein time spent above 90% of VO2max was greater in 30-seconds short intervals (SI) than in 2.8-4.5 minutes long intervals (LI), with the two protocols having similar work-to-recovery ratios (2:1). Indeed, 10 weeks of SI led to superior improvements in VO2max compared to LI in well-trained cyclists and also led to superior changes in power output at 4 mmol·L−1 blood lactate [BLA−] and 40-minutes time-trial performance.
variables, including cardiovascular adaptations and hormonal responses, and muscular adaptations.

Acutely, SI may trigger greater release of anabolic hormones into the blood than LI, perhaps related to its higher work intensity. While this remains unstudied, high-intensity exercise (HIE) in general induces transient increases in circulating levels of growth hormone (GH) and testosterone, which may act to increase plasma volume and erythropoiesis, through which beneficial adaptations in VO2max correlate positively with VO2max. Furthermore, circulating levels of GH, testosterone, and insulin-like growth factor 1 (IGF1) correlate positively with VO2max. Additionally, cycling at higher intensities also induces catabolic responses, measured as increased circulating levels of cortisol. This may exert negative effects on cellular plasticity, impairing adaptations. However, elevated levels of cortisol may also act as important signaling cues for recycling of proteins and cellular structures that are damaged during exercise, resulting in a pool of free amino acids, which in turn may facilitate protein synthesis in the anabolic phase. Hormonal responses to HIE intervals in elite cyclists remains largely elusive, and needs further investigation.

In skeletal muscle, several training-induced changes in cellular functions stand out as plausible explanations behind the superior effects of SI on performance. These include improved metabolic functions possibly due to mitochondrial biogenesis and vascularization, improved ion handling, and increased cross-sectional area of the quadriceps muscles. These adaptations are likely to improve the fractional utilization of VO2max and to improve anaerobic energy metabolism and delay fatigue. Mitochondrial function and biogenesis are primarily under control of the transcriptional coactivator peroxisome proliferator-activated receptor gamma coactivator-1α (PGC-1α), whose regulation is intensity- and muscle activation-dependent, both at the level of transcription and activity. Although PGC-1α responses to training have been a long-standing focus in exercise physiological research, there are aspects of PGC-1α biology that remain a conundrum. For example, cycling at intensities around 100% work intensity. While this remains unstudied, high-intensity training in well-trained subjects. Finally, HIE may acutely increase protein synthesis in muscle fibers, potentially orchestrated through regulation of signaling factors such as PGC-1α, IGF1, and myostatin. Overall, few studies have investigated the effects of HIE on muscle biogenesis, likely due to skepticism connected to muscle biopsy sampling. The introduction of the less invasive micro biopsy procedure into exercise sciences may thus facilitate invasive measurements in elite cyclists.

The aims of the study were to compare the acute effects of time- and effort-matched SI (30-seconds) and LI (5-minutes) on hormone concentrations in blood and mRNA abundances in m. vastus lateralis in elite cyclists, using a randomized crossover design. We also aimed to verify that the applied SI protocol is associated with higher mean power output and longer time above 90% of VO2max compared to LI, as previously shown by our group, and to investigate if this is accompanied by a higher degree of muscle activation. We hypothesized that SI would lead to more pronounced changes in anabolic hormone concentrations in blood and more pronounced changes in muscle mRNA abundances for genes involved in mitochondrial function, angiogenesis, ion-transport, and protein synthesis.

2 | METHODS

2.1 | Subjects and design

Eight male competitive, elite cyclists volunteered, and all completed the study. Subjects’ characteristics are shown in Table 1. Based on VO2max and Wmax, the cyclists were regarded as elite cyclists on performance level 4-5. The study was approved by the local ethical committee at Inland Norway University of Applied Sciences and was performed in accordance with the Declaration of Helsinki, except for pre-registration in a public database. Before participation, all cyclists signed an informed consent form. Participants visited

<table>
<thead>
<tr>
<th>TABLE 1</th>
<th>Physiological parameters from screening</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age (years)</td>
<td>25.3 ± 6.1</td>
</tr>
<tr>
<td>Height (cm)</td>
<td>181.1 ± 4.5</td>
</tr>
<tr>
<td>Body mass (kg)</td>
<td>74.8 ± 3.8</td>
</tr>
<tr>
<td>VO2max (mL·kg⁻¹·min⁻¹)</td>
<td>73.9 ± 7.0</td>
</tr>
<tr>
<td>Wmax (W·kg⁻¹)</td>
<td>6.2 ± 0.5</td>
</tr>
</tbody>
</table>

Note: Values are mean ± SD.

Abbreviations: SD, standard deviation; VO2max, maximal oxygen consumption; Wmax, maximal aerobic power produced the last minute during incremental test.
the laboratory on three occasions. On their first visit, they performed a test battery consisting of a standardized blood lactate profile test, an incremental test to exhaustion to determine \( \text{VO}_2\max \), as well as two sets of SI, as described below. On their second and third visit, they performed the two experimental protocols, either SI or LI, allocated to each of the two days in a randomized manner, with 4-7 days between experimental days.

### 2.2 Testing procedures

All test procedures and exercise sessions were performed on the same electromagnetically braked cycle ergometer (Lode Excalibur Sport, Lode BV), which was adjusted according to each cyclist's preference and used for both tests. For each participant, all tests and exercises were performed at the same time of day (±1 hour). The cyclists were instructed to refrain from all types of intense exercise, caffeine, and alcohol 24 hours prior to testing. Further, they were instructed to consume the same type of meal no later than one hour before each test. All tests were conducted in similar environmental conditions (16-18°C and 20%-35% relative humidity) with a fan ensuring circulating air around the cyclist.

### 2.3 Blood lactate profile test, \( \text{VO}_2\max \) and \( \text{W}_\text{max} \)

On the first test day, participants performed a blood lactate profile and a \( \text{VO}_2\max \) test, as previously described. Briefly, the blood lactate profile test started with 5 minutes cycling at 125 W. Thereafter, power output was increased by 50 W every 5 minutes. Blood was sampled from a fingertip at the end of each 5-minutes bout and was analyzed for whole-blood lactate \([\text{BLa}^-]\) using a lactate analyzer (Lactate Pro LT-1710, Arcray Inc). The test was terminated when \([\text{BLa}^-]\) was \( \geq 4 \text{ mmol·L}^{-1} \). HR was recorded using a Polar S610i HR monitor (Polar). \( \text{VO}_2 \), respiratory exchange ratio (RER), and HR were measured during the last 3 minutes of each bout. \( \text{VO}_2 \) was measured (30-seconds sampling time) using a computerized metabolic system with mixing chamber (Oxycon Pro, Erich Jaeger). Gas analyzers were calibrated prior to every test according to manufacturer's description, using certified calibration gases. Calibration of the flow turbine (Triple V, Erich Jaeger) was performed prior to all tests, using a 3-L, 5530 series, calibration syringe (Hans Rudolph) before every test. After termination of blood lactate profile tests, cyclists were given 15 minutes of recovery cycling before completing an incremental cycling test for determination of \( \text{VO}_2\max \). The test was initiated with 1 minute of cycling at a power output corresponding to 3 W·kg\(^{-1}\) (rounded down to nearest 50 W). Thereafter, power output was increased by 25 W every minute until exhaustion. \( \text{VO}_2\max \) was calculated as the average of the two highest consecutive 30-seconds \( \text{VO}_2 \) measurements. To evaluate if \( \text{VO}_2\max \) was achieved, the following criteria were set: HR \( \geq 95\% \) of the subjects reported maximal HR, RER \( \geq 1.05, \) and \([\text{BLa}^-]\) \( \geq 8.0 \text{ mmol·L}^{-1} \). \( \text{W}_\text{max} \) was calculated as the mean power output during the last minute of the incremental \( \text{VO}_2\max \) test.

### 2.4 Experimental protocols and tissue sampling

On experimental days, participants rested for 30 minutes in a supine position before a blood sample was collected from the antecubital vein. Thereafter, a muscle sample was collected from m. Vastus Lateralis (right leg, Pre) using the micro biopsy technique (Bard Magnum, Bard Nordic, Helsingør, Denmark), as previously described using 14-gauge needles (Medax medical devices) under local anesthesia (~2 mL Lidokain, Mylan). The first biopsy was sampled at one third of the distance from the patella to anterior superior iliac spine with subsequent biopsies sampled approximately 2 cm proximal to the previous sample. Experimental protocols were then initiated, starting with a warm-up procedure consisting of 20-minutes at 175 W, followed by 50 W increases in power output every 3 minutes until >4 mmol [BLa\(^-\)], and concluded by two to three submaximal sprints lasting 20-30 seconds. Then, experimental protocols were performed, either as SI, consisting of 3 sets of 13 \( \times \) 30-seconds work intervals separated by 15-seconds active recovery periods, or as LI, consisting of 4 \( \times \) 5-minutes work intervals separated by 2.5-minutes active recovery periods. Power output during active recovery periods between sets was equivalent to 50% of power output during work intervals in both sessions. [BLa\(^-\)] and rate of perceived exertion (RPE) were recorded at the end of every interval. Total time of work intervals amounted to 19.5 and 20 minutes in SI and LI, respectively. Participants were instructed to perform intervals at the highest possible average power output. A supervisor gave strong verbal encouragement during both sessions. Time spent above 90% of \( \text{VO}_2\max \) and RPE\(_{\text{Peak}} \) during exercises were defined as accumulation of \( \text{VO}_2 \) and HR values at or above 90% of \( \text{VO}_2\max \) and HR\(_{\text{Peak}} \). After finalization of experimental protocols, sampling of blood and muscle biopsies was repeated, with blood being sampled immediately and 30 minutes after termination of the exercise, and muscle biopsies being sampled 3 hours after finalization of the exercise (3 hours post). Blood samples were collected in serum-separating tubes and kept at room temperature for 30 minutes before centrifugation (1500 g for 10 minutes), after which serum was aliquoted into 1.5 mL vials and stored at -80°C until further analyses. Muscle biopsies were after
collection immediately frozen in −80°C cold isopentane and stored for further analysis. Biopsies were only sampled prior to and 3 hours post-exercise, since earlier studies of target proteins, as described later, have shown significant increases in mRNA in this time frame to high-intensity exercise.22,23

2.5 | EMG procedures

To evaluate muscle activity during experimental protocols, EMG measurements were performed using a wireless EMG-module Telemetry DTS wireless system (Noraxon Inc). Surface electrodes (dual surface electrodes, product 272, inter-electrode distance 20 mm from center to center) were attached as recommended by Konrad 2006,31 providing data on left leg m. Vastus Lateralis and m. Vastus Medialis activities. EMG recordings were sampled at 1500 Hz and were high-pass filtered using a cutoff frequency of 10 Hz and low-pass filtered using a cutoff frequency 500 Hz, before they were smoothed over 100 milliseconds (root mean square algorithm). EMG rms was calculated as the average of the smoothed EMG data over approximately 20 seconds (each measuring period constituting of cycles starting and ending at the same crank cycle position). EMG rms were then expressed relative to the average signal on a 275 W power output, obtained during standardized warm-up where participants were instructed to maintain the same pedaling frequency. EMG measurements are only presented from 6 participants due to bad connection at the end of HIE intervals in two participants.

2.6 | Blood and muscle analyses

2.6.1 | Hormonal analyses in blood

Serum concentrations of total testosterone, cortisol, GH, sex hormone-binding globulin (SHBG), and IGFI were measured using an Immulite 1000 analyzer, using kits from the Immulite Immunoassay System Menu (Siemens Medical Solutions Diagnostics). Based on these measurements, we also calculated individual testosterone-to-SHBG ratios, which was used as an indicator of free testosterone in subsequent analyses.

2.6.2 | Gene expression in muscle

To determine expression of target genes in response to the two exercise protocols, real-time RT-PCR was performed as described elsewhere.32 Analyses included genes involved in mitochondrial biogenesis (PGC-1α splice 1, PDK4, and TFAM), angiogenesis (VEGFA and Thrombospondin 1), ion handling (CIC1, MCT1, MCT4, Na+-K+ α1, Na+-K+ α2 and Na+-K+ β1, NHE1), and protein synthesis (IGF1, PGC-1α4, and myostatin), along with 12 potential reference genes (β-actin/ACTB, β2-microglobulin/B2m, charged multivesicular body protein 2A/CHMP2A, follistatin/FST, glyceraldehyde-3-phosphate dehydrogenase/GAPDH, RNA polymerase II subunit A/POLR2A, peptidylprolyl isomerase A/PPIA, Ras-related protein Rab-7a/RAB7A, receptor accessory protein 5/REEP5, ribosomal protein L32/RPL32, TATA-box-binding protein/TBP and Ubiquitin C/UBC). Gene-specific primers were designed using Primer-BLAST and Primer3Plus Sequences as described previously30 (Table 2).

Total RNA was extracted using a combination of phase separation and silica-column clean-up. Muscle tissue (~30 mg) was homogenized in 200 μL of TRIzol® Reagent (Invitrogen, Life technologies AS), using 0.5 mm RNase-free Zirconium Oxide beads and a bead homogenizer (Bullet Blender, Next Advanced), according to manufacturer’s instructions, as previously described.32 Following homogenization, TRIzol® Reagent was added to a total volume of 1 mL and the homogenate was vortexed and incubated at room temperature for 5 minutes, after which 200 μL of chloroform was added, followed by 3 minutes incubation and subsequent phase separation by centrifugation (12 000 g, 10 minutes, 4°C). Four-hundred μL of the aqueous phase mixed with an equal volume of 100% ethanol and incubated 10 minutes at room temperature on a silica spin-column (Zymo-Spin™ IIC, Zymo Research). Following brief centrifugation, the flow-through was discarded and the column was washed by centrifugation once with RWT buffer and twice with RPE-buffer (Qiagen Nordic). RNA was eluted from the column in TE buffer heated to 60°C by centrifugation. RNA purity and quantity were assessed by evaluation of absorbance at 230, 260, and 280 nm using a micro-volume spectrophotometer (NanoDrop 2000, Thermo Scientific).

Samples were reverse transcribed in duplicates (500 ng total RNA) using SuperScript® IV Reverse Transcriptase (Invitrogen, Life technologies AS), using anchored Oligo-dT and random hexamer primers (Thermo Scientific, Life technologies AS), according to manufacturer’s instructions. Real-time RT-PCR was performed on 2 μL cDNA (1:50 dilution) in a 10 μL reaction volume, using 2X SYBR® Select Master Mix (Applied Biosystems, Life technologies AS) and specific primers added at a 0.5 pmol/L final concentration, using a fast-cycling real-time detection system using Applied Biosystems™ QuantStudio 5 Real-Time PCR System (Thermo Fisher Scientific). Cycling consisted of 40 cycles; three seconds at 95°C followed by 30 seconds 60°C. Melt-curve analysis was performed for all reactions to verify single product amplification. Real-time RT-PCR parameters are presented in Table 2.
Quantification cycles (Cq) were determined using the second derivate method from raw fluorescence data, exported from the Applied Biosystems software, and analyzed using the qpcR-library. Gene expression data analysis was done using log-transformed values. In order to control for RNA quantity in cDNA synthesis and subsequent dilution, suitable reference genes were determined from systematic evaluation of 12 transcripts (sequences available on request) with modification for the present repeated measures study design. B2m, TBP, and RPL32 were evaluated as suitable reference genes, as their expression did not change with sampling time points or exercise condition. Normalization of target genes was thus performed using the geometric average of these three internal reference genes, as described elsewhere.

### TABLE 2 Real-time RT-PCR primers utilized for analyses of mRNA expression, including average primer efficiencies and Cq values

<table>
<thead>
<tr>
<th>Gene</th>
<th>Primers for qRT-PCR</th>
<th>Forward primer</th>
<th>Reverse primer</th>
<th>Efficiency Mean ± SD</th>
<th>Cq Mean ± SD</th>
</tr>
</thead>
<tbody>
<tr>
<td>ATP1A1</td>
<td>ATCCCTGAGTACACCAGGCTTGG</td>
<td>TTCTCCTGGACATGCGTTTG</td>
<td>1.62 ± 0.01</td>
<td>32.6 ± 0.8</td>
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<td>ATP1A2</td>
<td>TTCTGGGCTCTGGCAACTCT</td>
<td>GTGGGCTCAGAGGAGGTTTG</td>
<td>2.16 ± 0.01</td>
<td>23.0 ± 0.6</td>
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<td>ATP1B1</td>
<td>ATCTCTCTGTTCTGGGT</td>
<td>ATCTCTCTGTTCTGGGT</td>
<td>2.09 ± 0.01</td>
<td>23.6 ± 0.4</td>
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<tr>
<td>β2-m</td>
<td>TGACTTCTGACAGGCCAAGA</td>
<td>CGGCATCTTAACCTCCATGA</td>
<td>1.98 ± 0.01</td>
<td>23.2 ± 0.3</td>
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<tr>
<td>CLCN1</td>
<td>TCCACGGCTTTGTTTCC</td>
<td>AATCCCGATGAGCAGAACAG</td>
<td>1.82 ± 0.01</td>
<td>29.7 ± 1.2</td>
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<tr>
<td>IGF1</td>
<td>ATGATTGAGCACTCCCTCAA</td>
<td>GTACTCTCTTCTCGGTCTGG</td>
<td>1.86 ± 0.01</td>
<td>28.9 ± 0.6</td>
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<td>MSTR</td>
<td>AGGAAAGAGATGGCCTGAATCC</td>
<td>CCCCCTGATCTTTTGTGTCG</td>
<td>1.91 ± 0.01</td>
<td>32.4 ± 0.9</td>
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<td>PDK4</td>
<td>CGAGCCACCAATAATGATATCAC</td>
<td>TCTAAGTGGGGCCGGATT</td>
<td>2.06 ± 0.01</td>
<td>25.2 ± 2.0</td>
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<tr>
<td>PGC1A1</td>
<td>TTTGAGGAATGACCGATGCACTGG</td>
<td>ACCAGAAGAGTCTCGGTGTCG</td>
<td>1.94 ± 0.01</td>
<td>26.2 ± 0.6</td>
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<tr>
<td>PGC1A4</td>
<td>TGCTCAGATATCTCTCAGTGACC</td>
<td>TCGAGTTCAGAGATGTCACAC</td>
<td>2.06 ± 0.01</td>
<td>27.5 ± 1.3</td>
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</tr>
<tr>
<td>RPL32</td>
<td>AAGTTCCTGTTACACCAAG</td>
<td>CGGCACAGTAAGATTTGGTG</td>
<td>1.97 ± 0.01</td>
<td>22.3 ± 0.1</td>
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<tr>
<td>SLC9A1</td>
<td>TCCACGGGTGCTGCTGTTTG</td>
<td>CTCTCTGTTACAGGCCAGAG</td>
<td>1.87 ± 0.01</td>
<td>31.0 ± 0.6</td>
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<td>SLC16A1</td>
<td>ACCAGTTGGAAATGGCTGTC</td>
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<td>31.5 ± 1.0</td>
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<td>SLC16A3</td>
<td>TTCGCTGTCTCGGTATCAC</td>
<td>TCCAAACTCCTGTATGAGGTC</td>
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<td>TBP</td>
<td>AACAGGTTCAAGATGAGCACTGG</td>
<td>ACGTCGTCTCTGTAATTC</td>
<td>1.87 ± 0.01</td>
<td>30.8 ± 0.4</td>
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<td>TFAM</td>
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<td>AATCCAGGAAATGTCCCTACAC</td>
<td>2.06 ± 0.01</td>
<td>27.0 ± 0.3</td>
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<td>THB1</td>
<td>AACAAACAGGATGCTCAAGGCAAGCC</td>
<td>ACTTGGGCTTCTCGGTG</td>
<td>1.93 ± 0.01</td>
<td>29.5 ± 2.0</td>
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<tr>
<td>VEGFA</td>
<td>CTTGCAAAAAACACAGACTGG</td>
<td>CTGCTGCTGTCACTAG</td>
<td>1.99 ± 0.01</td>
<td>26.2 ± 0.9</td>
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</table>

Abbreviations: ATP1A1, Na+-K+ α1; ATP1A2, Na+-K+ α2; ATP1B1, Na+-K+ β1; CLC-1, Chloride voltage-gated channel 1; IGF1, insulin-like growth factor 1; PDK4, pyruvate dehydrogenase kinase 4; PGC-1A1, peroxisome proliferator-activated receptor gamma coactivator-1α splice 1; PGC-1A4, peroxisome proliferator-activated receptor gamma coactivator-1α splice 4; RPL32, ribosomal protein L32; SD, standard deviation; SLC16A1, monocarboxylate transporter 1; SLC16A3, monocarboxylate transporter 4; SLC9A1, sodium-hydrogen exchanger 1; TBP, TATA-box binding protein; TFAM, mitochondrial transcription factor A; THB1, throbospondin; VEGFA, vascular endothelial growth factor A; β2-m, β2 micro-globulin.

### 2.7 Statistics

Student’s paired t test was used to perform pairwise comparisons of effects of SI and LI on physiological measurements (power output, time spent above 90% of VO\textsubscript{2max} and HR\textsubscript{peak}, [BLA\textsuperscript{−}], and RPE. A marginal model was used for normalized mRNA levels (measured as Log2 fold change from pre- to 3 hours post-exercise) and blood hormone levels, wherein effects of time (pre, post, 3 hours post) and exercise condition (LI, SI) and their interaction (time × condition) were assessed using SPSS software version 23. Time and condition were specified as fixed effects. Repeated measures were specified by subject. To compare changes between conditions, a marginal model with baseline values as a covariate was used. A significant main effect or interaction was further evaluated by a multiple-comparison approach with Sidak adjustment. A significance level of 0.05 was applied. Descriptive data are presented as mean ± standard deviation. Gene expression data are presented as Log2 fold change from pre-exercise with a 95% confidence interval.

### 3 RESULTS

#### 3.1 Physiological measurements

SI resulted in higher mean power output than LI (14% ± 3%, \(P < .05\), Table 3) and was associated with more time spent above 90% of VO\textsubscript{2max} (54% ± 76%, Figure 1A) and more
time spent above 90% of HR peak (153% ± 148%, P < .05, Figure 1B). In SI and LI, mean power output amounted to 90% ± 2% and 80% ± 2% of W max, respectively (P < .05). SI and LI resulted in similar changes in [BLa−] (Table 3), RPE (Table 3), and muscle activity (Figure 2). Muscle activity was not different between conditions and did not change over the course of the two experimental protocols (Figure 2), but pedaling frequency was higher in SI (109 ± 2 rounds per minute) compared to LI (102 ± 3 rounds per minute, P < .05).

### 3.2 Blood hormone responses

Short intervals and LI led to increased blood concentrations of cortisol, testosterone, and GH (all P < .05, Figure 3A-C), measured immediately after the exercise (post), while only SI led to increased testosterone-to-SHBG ratios (P < .05, Figure 3D), and only LI led to increased concentrations of IGF1 and SHBG (both P < .05, Figure 3E,F). Of these variables, SI led to more pronounced increases in testosterone concentrations and testosterone-to-SHBG ratios (P < .05,
Figure 3B,D). At 30 minutes post-exercise, cortisol and GH concentrations remained elevated compared to pre in both intervention groups (both \( P < .05 \), Figure 3A,C), while testosterone and testosterone-to-SHBG ratios were elevated in SI only (both \( P < .05 \), Figure 3B,D). At this time point, neither of the training protocols affected IGF1 and SHBG concentrations (compared to pre, Figure 3E,F). In LI, but not in SI, cortisol concentrations decreased from immediately after the exercise to 30-minutes post-exercise, resulting in a differential cortisol response between training protocols in this period (\( P < .05 \), Figure 3A).

### 3.3 | Gene expression in m. Vastus lateralis

Short intervals and LI led to increased mRNA levels of selected markers of mitochondrial biogenesis and function (PDK4, PGC-1α splice 1, and TFAM) and angiogenesis (thrombospondin and VEGFA), measured 3 hours after finalization of exercise (\( P < .05 \), Figure 4A,B). Overall, no difference was observed between experimental conditions for these transcripts, though a near-significant lower increase in PDK4 mRNA was evident after SI compared to after LI (\( P = .054 \)). SI and LI also led to altered mRNA levels of markers of ion handling and muscle growth. Whereas Na\(^+\)-K\(^+\)β1 and PGC-1α splice 4 increased and myostatin decreased in both conditions (\( P < .05 \), Figure 4C,D), NHE1 decreased after SI only (\( P < .05 \), Figure 4D). For NHE1 only, the response was different between SI and LI (\( P < .05 \)). Neither SI nor LI led to changes in mRNA levels of ClC1, Na\(^+\)-K\(^+\)α1/α2 or IGF1 (Figure 4C,D).

### 4 | DISCUSSION

The present study compared systemic and muscular responses to time- and effort-matched SI and LI in elite cyclists. SI was associated with higher power output and longer working time above 90% of VO\(_{2}\text{max}\) and 90% of HR\(_{\text{peak}}\) than LI, without increasing perceived exertion or [BLa\(^-\)], adding to and supporting knowledge from previous research.\(^{4,9,36}\) In line with this, SI and LI were associated with differential
responses of selected endocrine variables, with SI leading to more pronounced increases in testosterone and testosterone-to-SHBG ratios in blood immediately after the exercise and leading to prolonged cortisol responses. Surprisingly, the two intervals led to similar degrees of muscle activation, measured as EMG rms, and were associated with similar mRNA responses in m. Vastus lateralis, with the exceptions of NHE1 mRNA levels. Overall, SI led to augmented physiological and endocrine responses in elite cyclists compared to LI, suggesting that it may convey beneficial effects even in highly trained individuals.

The superior physiological responses to SI, including higher power output and longer time spent above 90% of VO\textsubscript{2max}, has previously been associated with superior improvements in performance and performance indices in well-trained\textsuperscript{9} and elite cyclists.\textsuperscript{36} This essentially means that SI elicits more pronounced effects on determinants of performance such as VO\textsubscript{2max} and fractional utilization of VO\textsubscript{2max}. While the effects of SI on VO\textsubscript{2max} largely resides on systemic cardiovascular adaptations,\textsuperscript{12} its effects on fractional utilization of VO\textsubscript{2max} likely involves muscle adaptations.\textsuperscript{37} As for the latter, muscle plasticity can be induced and facilitated by both systemic signaling events and by muscle-specific signaling events caused by the mechanical and metabolic stress of the exercise.\textsuperscript{38}

In the present study, we assessed endocrine variables as targets of systemic signaling responses. While both training modalities led to substantial changes in hormone concentrations in blood, SI led to more pronounced responses. This was evident as larger increases in testosterone and testosterone-to-SHBG ratios, suggesting the presence of higher levels of free testosterone immediately after the exercise, and as cortisol responses with prolonged duration. Overall, this supports the notion that these variables respond to

**FIGURE 4** Log2 fold changes in mRNA levels of target genes in m. vastus lateralis in response to short intervals (SI; ●) and long intervals (LI; ○), measured from pre to 3 h post-exercise. (A) Genes involved in mitochondrial biogenesis and function, (B) genes involved in angiogenesis, (C) genes involved in regulation of protein synthesis, (D) genes involved in ion handling. Data are mean with individual values. *indicates significantly \( P < .05 \) different from pre-exercise, †indicates tendency to different from LI \( P < .1 \), ‡indicates significant different from LI \( P < .05 \), n = 8. PDK4; pyruvate dehydrogenase kinase 4, PGC-1α splice 4; peroxisome proliferator-activated receptor gamma coactivator-1α (splice 4), TFAM; mitochondrial transcriptional factor A, VEGFA; vascular endothelial growth factor A, ClC1; chloride voltage-gated channel 1, Na\textsuperscript{+}-K\textsuperscript{+}α1/α2/β1; sodium/potassium-transporting ATPase subunit α1/α2/β1, NHE1; sodium-hydrogen exchanger 1, IGF1; insulin-like growth factor 1
training in an intensity-dependent manner,\textsuperscript{10} which may act to facilitate training adaptations in muscle,\textsuperscript{16,39} as well as in systemic functions.\textsuperscript{1,11,15} As for cortisol, the prolonged response to SI can be interpreted as exerting a negative effect on muscle cellular plasticity.\textsuperscript{15} However, as long-term SI induces superior effects on performance,\textsuperscript{9,36} the prolonged cortisol response may facilitate recycling of proteins and cellular structures that are damaged during exercise, resulting in a pool of free amino acids and other micronutrients, that in turn facilitate protein synthesis and cellular plasticity in the anabolic phase.\textsuperscript{16} To date, the importance of such acute hormonal changes for long-term adaptations remains inconclusive,\textsuperscript{10,15,16} and further research is warranted, including long-term interventions of similar designs to the present study, with more frequent collection of blood samples.

Evidently, SI was associated with higher mechanical and metabolic stress in muscle tissue than LI, as deduced from its higher power output (14\% higher than LI) and its prolonged time above 90\% of \textit{VO}_{2\text{max}} (54\%). It was thus surprising that SI was not associated with increased EMG activity, as expected from previous studies.\textsuperscript{17,40} This discrepancy may be due to numerous factors, including the higher pedaling frequency in SI compared to LI, the short breaks (15 seconds) between short work interval (30 seconds), the relative small differences in power output between SI and LI (90\% vs 80\% of \textit{W}_{\text{max}}), and the small sample size in EMG measurements (\textit{n} = 6). In SI, the increased time above 90\% of \textit{VO}_{2\text{max}} was likely due to the combination of increased intensity during work intervals and the sustained elevation of \textit{VO}_{2} during 15-seconds active pauses.\textsuperscript{41}

In general, SI and LI resulted in similar changes in mRNA levels of genes involved in muscle plasticity and functions in m. Vastus lateralis in elite cyclists. For example, SI and LI resulted in similar changes in expression of genes involved in mitochondrial biogenesis (PGC1\textalpha splice 1 and TFAM), angiogenesis (thrombospondin and VEGFA), regulation of protein synthesis (myostatin and PGC1\textalpha splice 4), and ion handling (Na\textsuperscript{+}-K\textsuperscript{+}β1). These similarities may seem counterintuitive, as many of these genes have previously been ascribed intensity-dependent roles in response to acute exercise.\textsuperscript{17,18,22,23} However, a few characteristics of the present data may shed light on our finding. First, although SI was performed at higher power outputs, the difference between SI and LI was rather small compared to other studies. For example, in the studies by Edgett et al\textsuperscript{17} and Hoier et al,\textsuperscript{23} which disclosed intensity-dependent changes in VEGFA and PGC-1\textalpha mRNA expression, the difference in power output between conditions was 27 percentage points and 60 percentage points, respectively, compared to the mere 10 percentage point difference in our study. Second, the high fitness level of the present participants may have affected our measured responses. Indeed, exercise-induced expression of genes involved in mitochondrial biogenesis and angiogenesis seems to be reduced with increasing level of training status,\textsuperscript{23,42} though this negative relationship is not evident in all studies.\textsuperscript{43} Third, in the present study, SI and LI were associated with similar degrees of muscle activation, measured as EMG activity. While this similarity may be an artifact of the low statistical power of the study, it cannot be ruled out that it had a biological origin that could explain the lack of differences in gene expression patterns between SI and LI.

Of the 15 genes investigated in the present study, only two genes showed or nearly showed differential expression responses to SI and LI: NHE1 and PDK4. For NHE1, SI resulted in decreased expression compared to LI. In a previous review, HIT has been reported to increase NHE1 protein abundances,\textsuperscript{20} and hence, one could expect HIE acutely to increase NHE1 mRNA. In muscle fibers, NHE1 facilitates transport of H\textsuperscript{+} ions from the cytosol to the extracellular fluid and may thus be important for regulating pH, acting as a potential determinant of HIE performance.\textsuperscript{20} The timing of muscle sampling in the present study (3 hours after exercise) might have affected the disclosed changes in NHE1, as HIE-induced changes in mRNA tend to peak 24-48 hours after exercise whereas protein content transiently seem to decrease.\textsuperscript{44} The decreased expression of NHE1 in the current study and the unchanged protein abundance in response to HIT in a previous study,\textsuperscript{25} however, leaves the importance of NHE1 unequivocal. As for PDK4, LI led to a near-significant increase in expression compared to SI, with the lack of significance potentially being related to the low statistical resolution of the study. PDK4 activity acts to decrease oxidation of carbohydrates by inactivating the pyruvate dehydrogenase complex and thus shunts metabolism toward beta-oxidation of fatty acids, playing an important role for metabolic functions during both exercise and recovery.\textsuperscript{45} As both NHE1 and PDK4 were measured on the level of mRNA (and not protein), one should be cautious to interpret the meaning of these findings. Still, the observed differences in PDK4 and NHE1 responses to SI and LI in muscle tissue of elite cyclists hint toward differential adaptations to the two exercise modalities, though the similarities in mRNA responses were clearly greater than the differences in the data set as a whole. There is need for more research to elucidate the acute and accumulative effects of different HIE protocols in highly trained athletes. Such studies are facilitated by the availability of the microbiopsy procedure, which enables biopsy sampling without any appreciable adverse effects and allows sampling of more frequent biopsies, paving the way for data with higher biological resolution.

Taken together, SI elicits higher power output, longer time spent above 90\% of \textit{VO}_{2\text{max}} and \textit{HR}_{peak} compared to LI and a greater endocrine responses despite similar degrees of
muscle activation and perceived exertion, hinting at a beneficial effect of SI over LI in elite cyclists.

4.1 Perspective

Short intervals allowed elite cyclists to ride at higher power outputs and sustain longer periods at intensities above 90% of VO$_{2\text{max}}$ and HR$_{\text{peak}}$ compared to LI. This was accompanied by a greater hormonal response, which might lead to superior training adaptations, as previously reported. However, SI does not seem to induce greater muscle activation and does not lead to clear differences in mRNA responses. On a practical note, the participants experienced SI and LI as equally exhausting in the current study and SI might therefore be an efficient exercise strategy to augment training stimulus without increasing the subjective experience of exertion. Finally, few studies have investigated muscular adaptations in elite cyclists, possibly due to skepticism connected to muscle biopsy sampling. The less invasive microbiopsy procedure used in the present study should open the avenue for more projects in the future, allowing elucidation of both acute and accumulative effects of different HIE protocols in a greater cohort of elite athletes.

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CONFLICT OF INTEREST

None.

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