Effects of Normobaric and Hypobaric Hypoxia on Mitochondrial Related Gene Expression

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ININTRODUCTION

• Normobaric and hypobaric hypoxia and are both used in laboratory settings with the assumption that both have similar physiological effects.
• Hypoxic conditions are known to cause decreased muscle mass and decreased mitochondrial function.
• It is not known if mitochondrial gene expression of the skeletal muscle is altered between different modes of hypoxia.
• The purpose of this study was to determine if recovery in normobaric hypoxia and hypobaric hypoxia alter gene expression associated with mitochondrial biogenesis compared to that of normobaric normoxia.

METHODS

• Fifteen recreationally trained participants (8 male, 7 female) each completed three trials of 1-h cycling at 70% of Wmax. Following exercise, participants sat in an environmentally controlled chamber for a 4-h recovery period in NN (975 m), NH (4,420 m), or HH (4,420 m) environmental conditions. Muscle biopsies were taken from the vastus lateralis pre-exercise and after a 4-h environmental exposure period. Samples were analyzed using qRT-PCR to assess gene expression related to mitochondrial development.
• Subjects cycled for 1 h on an electronically braked cycle ergometer (Velotron, Racermate Inc., Seattle, WA) at approximately 70% of work rate associated with VO2peak, followed by 4 h of supine recovery.
• The recovery took place in either an alti du tube to simulate hypobaric hypoxia (HH, 4,420 m; Engineering Innovations, LLC, Littleton, CO), an environmental chamber to simulate normobaric hypoxia (NH, 4,420 m; Tescor, Warminster, PA), or in ambient conditions for normobaric normoxia (NN, 975 m).
• A pulse oximeter (Nonin, Plymouth, MN) was used to assess blood oxygen saturation (SaO2) during the trial.
• Muscle biopsies were taken from the vastus lateralis pre-exercise and 4 h post-exercise.
• Gene expression analysis was performed with qRT-PCR.

RESULTS

Table 1. SaO2 (%) during each hour of recovery in NN, NH, and HH

<table>
<thead>
<tr>
<th>Hour</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
</tr>
</thead>
<tbody>
<tr>
<td>NN</td>
<td>96.4 ± 0.3</td>
<td>96.3 ± 0.4</td>
<td>96.5 ± 0.3</td>
<td>96.1 ± 0.4</td>
</tr>
<tr>
<td>NH</td>
<td>79.8 ± 1.3*</td>
<td>77.3 ± 1.2*</td>
<td>79.9 ± 1.0*</td>
<td>79.8 ± 1.2*</td>
</tr>
<tr>
<td>HH</td>
<td>75.6 ± 1.5*</td>
<td>77.1 ± 1.5*</td>
<td>77.1 ± 1.1*</td>
<td>76.2 ± 1.0**</td>
</tr>
</tbody>
</table>

Data are mean ± SE. * p < 0.05 from NN. † p < 0.05 from NH.

Figure 1. Gene expression after 4 h recovery. p < 0.05 from pre-exercise. † p < 0.05 from other trials. PGC-1α, Peroxisome proliferator-activated receptor gamma coactivator 1 alpha; GABPA, GA-binding protein alpha chain; ERRα, Estrogen related receptor alpha; TFAM, Mitochondrial transcription factor A. Data are mean ± SE.

Table 2. Participant descriptive data

<table>
<thead>
<tr>
<th>Age (y)</th>
<th>Height (cm)</th>
<th>Weight (kg)</th>
<th>Body Fat (%)</th>
<th>VO2 peak (L·min⁻¹)</th>
<th>Power at VO2peak (W)</th>
</tr>
</thead>
<tbody>
<tr>
<td>24 ± 4</td>
<td>178 ±12</td>
<td>72.5 ± 13.8</td>
<td>14.5 ± 6.8</td>
<td>3.60 ± 0.83</td>
<td>274 ± 72</td>
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</table>

CONCLUSIONS

• Despite differences in SaO2 during the 4 h recovery period, only TFAM mRNA was increased in hypoxia.
• PGC-1α, GABPA, ERRα, and TFAM mRNA were not affected by exercise or hypoxia. NRF1 mRNA increased from pre-exercise.
• Further work is needed to determine the impact of long term hypoxia exposure on transcriptional responses related to mitochondrial biogenesis.
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