TIME COURSE OF METABOLIC RESPONSES AFTER HIGH INTENSITY INTERVAL TRAINING (HIIT): METABOLOMIC STUDY

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Abstract

The High Intensity Interval Training (HIIT) is known for promoting important metabolic responses. The metabolomics has been identified as a highly sensitive method, which allows the identification of large amounts of metabolites that are present in several biological samples. The temporal kinetics of metabolic responses to HIIT is still unclear and there are not comprehensive analysis of these responses after prolonged periods off exercise yet. The aim of this project is to investigate the time course of metabolic responses after an acute session of HIIT through metabolomic analysis. It is expected to identify the greatest moment of expression of the metabolome and the specific moments of the peaks of expression of different metabolites after an acute session of HIIT.

Key words:

Metabolism, nuclear magnetic resonance, HIIT.

Introduction

The high training interval training (HIIT) is characterized by intermittent stimuli of short duration (<5 minutes) and high intensity (near or greater than maximum oxygen consumption VO_{2MAX}), intervalled by rest, either active or passive. There are recent studies showing that the benefits of HIIT can be similar or even higher than that of the continuous aerobic training (TAC) (RAMOS et al., 2015). The changes in the referred functional parameters are also related to the high metabolic responses promoted during and after HIIT. After HIIT is observed intense metabolic activity of amino acid in skeletal muscle and plasma, as well as high levels of glucose and lactate expression (immediately after exercise) in the circulation. In parallel, a substantial increase in tricarboxylic acid, monounsaturated fatty acid and cortisol cycle intermediates is also observed. Such metabolic responses indicate the HIIT potential for the stimulation of hormones such as growth, adrenaline, noradrenaline and adrenocorticotrophic hormones, which are highly related to fat metabolism and mitochondrial biogenesis (PEAKE et al., 2014).

The metabolomics is relatively a new analytical platform within the biochemistry and physiology, which allows a better access to the acquisition of techniques in advanced data processing. Its objective is to identify a large number of analyzes, especially metabolites, in several biological samples such as blood, muscle tissue, saliva, among others (PEAKE, 2014; SHAH, KRAUS, NEWGARD, 2012). Therefore, the investigation of the temporal kinetics of the metabolic responses can contribute to the standardization of data collection in studies related to adaptations promoted by HIIT. The objective of this study will be to investigate the time course of metabolic responses to an acute session of high intensity interval training.

Results and Discussion

Fifteen healthy, recreationally active young men participated in this study. Participants underwent two experimental sessions in a cross-over design: control (CO) and HIIT sessions, in a randomized order with a one-week interval between them. In the HIIT session, 40 min of

exercise in the ergometer cycle were performed at intensities 90% VO_{2MAX} reserve (5 series of 4 min) and active intervals at 50% VO_{2MAX} reserve (5 series of 3 min). In the CO session, participants remained rested for 40 min. Blood samples were collected pre (-0 min) and post 0 min, 15 min, 30 min, 60 min and 180 min throughout both sessions. In serum samples, proton nuclear magnetic resonance Inova Agilent (1H NMR) metabolomics analyzes were performed to quantify the circulating metabolites. To identify the moment of greatest expression of the metabolome (set of metabolites), Principal Component Analysis followed by univariate statistical analyzes.

Figure 1. Experimental design

Conclusions

It is expected to identify the moment of greatest expression of the metabolome, as well as the specific moments of the peaks of expression of different metabolites after an acute session of HIIT. The analysis is being processed.

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