Exercise biology

2020 Topics for Bachelor and Masters theses

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BSc projects

NEW: A systematic review of physiological assessments of world class athletes (Supervisor HW)
Several publications include the data of world class athletes such as an lactate exercise testing paper that included the data of Eddy Merckx, one of the greatest cyclists of all times (Mader et al., 1976). Other publications report the data of Paula Radcliffe, Eliud Kipchoge, the shot putter Werner Günthör etc. The aim of this BSc thesis is to systematically search the literature for physiological analyses of world class athletes and to summarise this data.
Reference: Mader, A., Liesen, H., Heck, H., Philippi, H., Rost, R., Schürch, P., and Hollmann, W. (1976). Zur Beurteilung der sportartspezifischen Ausdauerleistungsfähigkeit im Labor. Sportarzt und Sportmedizin 27, 80–88.

NEW: Modelling of AMPK-dependent adaptations in skeletal muscle (Supervisor HW and Hermann Heck)
Exercise causes adaptations in three steps: 1) Exercise associated stimuli such as Ca2+, AMP or mechanical load are sensed by sensor proteins (a subtype of signalling molecules); 2) sensor proteins then activate or deactivate signal transduction proteins; 3) signalling proteins regulate molecular adaptations such as gene expression, protein synthesis (translation) or other cellular functions. In muscle a key sensor protein involved in adaptation to endurance exercise is the AMP-activated kinase (AMPK). AMPK is activated by increased AMP and decreased glycogen and then regulates many functions including mitochondrial biogenesis via PGC-1alpha. Given that the concentrations of AMP and glycogen during exercise can now be calculated, one would just need to know the mathematical relationship between AMP, glycogen and PGC-1alpha or mitochondrial biogenesis to model AMPK-dependent adaptation to endurance exercise. The aim of the thesis is to systematically search the literature for papers that mathematically describe the response of AMPK activity (or proxy measures such as the expression of PGC-1alpha) to the concentrations of AMP and glycogen. The data will then be used to extend Mader's mathematical model (Mader, 2003) that predicts AMPK-dependent adaptations to endurance exercise. We aim to publish this work.
Reference: Mader, A. (2003). Glycolysis and oxidative phosphorylation as a function of cytosolic phosphorylation state and power output of the muscle cell. EurJApplPhysiol 88, 317-338.

Do childhood cancer cells express receptors for hormones, myokines and metabolites that change during exercise? (Supervisor HW)

Exercise has beneficial effects in cancer but how exercise affects the behaviour of a cancer is poorly understood. The general mechanism must be that the exercising organs alter the composition of the blood and that the exercise-conditioned blood then perfuses and influences a tumour. The aim of your project is to complete the following tasks:

1) Produce a list of hormones such as catecholamines and myokines such as Il-6 that change during a bout of exercise.

2) Identify the receptors for these genes through a literature search.

3) Use tools such as Cancer Cell Line Encyclopedia to investigate whether childhood cancer cell lines and/or cancers express these receptors.

4) Use other tools to find out whether childhood cancer cells need these receptors for survival.

Based on this data you can then discuss whether it is likely that childhood cancers respond to exercise-induced hormones and myokines.

What is the role of genetics in iron deficiency and anemia? (Supervisor HW)

Human iron metabolism and haemoglobin concentrations vary greatly in the normal population. Iron and haemoglobin metabolism is influenced by genetics, altitude exposure, nutritional iron intake and endurance training. The aim of your thesis will be to review the role of genetics in the variation of iron and haemoglobin metabolism in the normal population and in athletes (i.e. not diseases of iron metabolism). Based on your research, you should answer the following questions: Should at risk populations (e.g. female elite athletes or individuals that have been previously be identified as iron deficient or anemic) be genetically tested for iron and haemoglobin metabolism alleles? Should at risk individuals supplement with iron without testing? Should with high iron concentrations tested for alleles associated with hemochromatosis? What genetic and other tests should an athlete-focussed iron-haemoglobin lab offer?

Which proteomic biomarkers could be used to explain Unexpected Underperformance Syndrome, Overtraining, and overreaching in elite and/or recreational athlete? (Supervisor MS)

Excessive training and inadequate recovery could cause 'overtraining syndrome' (OTS), which is characterised by underperformance and fatigue. But the pathophysiology of OTS is unclear. In this systematic review, we want to discuss possible proteinogenic biomarkers which are associated with OTS.

Which metabolomic biomarkers could be used to explain Unexpected Underperformance Syndrome, Overtraining, and overreaching in elite and/or recreational athlete? (Supervisor MS)

Excessive training and inadequate recovery could cause 'overtraining syndrome' (OTS), which is characterised by underperformance and fatigue. But the pathophysiology of OTS is unclear. In this systematic review, we want to discuss possible metabolic biomarkers which are associated with OTS.

Which blood born micro RNAs are associated with Unexpected Underperformance Syndrome, Overtraining, and overreaching in elite and/or recreational athlete? (Supervisor MS)

Excessive training and inadequate recovery could cause 'overtraining syndrome' (OTS), which is characterised by underperformance and fatigue. But the pathophysiology of OTS is unclear. Circulating micro RNAs in the blood are new biomarker for diseases. In this systematic review, we want to discuss

MSc projects

NEW: Systematic review of stimuli and exercise modes that increase the expression of glycolytic genes in skeletal muscle (Supervisor HW)

Glycolysis is a metabolic pathway that converts glucose or its storage form glycogen into pyruvate which in turn is used to synthesize lactate or enters mitochondria for oxidative phosphorylation. In addition, glycolysis is a feeder pathway for anabolic reactions such as nucleotide or non-essential amino acid synthesis. Sprinters and middle distance runners aim to increase their glycolytic capacity through specific training and a high expression of glycolytic enzymes could potentially be beneficial in diabetes mellitus patients, as it may increase the capacity to utilise glucose. Whilst the regulation of muscle protein synthesis after resistance exercise and mitochondrial biogenesis after endurance exercise is now partially understood, we know far less about the stimuli and types of exercise that regulate the expression of glycolytic enzymes in skeletal muscle. The aim of the proposed project is therefore to conduct a systematic review to answer the research question „What stimuli or exercise interventions significantly increase the expression or protein abundance of glycolytic enzymes?“ In addition, you will use the MetaMex online database and do further database searches to learn more about the expression of glycolytic enzymes and e.g. muscle fibre type differences. We aim to publish this work.

NEW: A systematic review towards systems understanding of skeletal muscle hypertrophy: a proteomics perspective (Supervisor PB)

Background: Skeletal muscle is a highly plastic tissue, as it is able to change the protein composition (phenotype) depending on different external stimuli. Acute resistance exercise (Tesch et al., 1986) is accompanied with mechanical stress and perturbation of the metabolic homeostasis in skeletal muscle. When the skeletal muscle is repeatedly subjected to external stimuli (e.g. chronic exercise training), the muscle adapt on these exercise stimuli and can causes morphological changes. Gain in skeletal muscle mass (= hypertrophy) and strength are typical phenotypic changes induced by chronic muscle overload, such as resistance training. Resistance training is an effective intervention to maintain a healthy muscle mass and function and it is a cornerstone for the prevention and treatment of muscle wasting or low muscle mass in healthy and diseased populations (Ibañez et al., 2005; Colberg et al., 2010). However, the complex process of skeletal muscle adaptation to chronic overload during skeletal muscle remodeling is only partially understood, as previous research has mainly conducted resistance-training intervention studies with a targeted approach.

Study Goal: In an attempt to address this issue, the goal of this master's project is to perform a systematic review to identify the global response of the proteome during and after skeletal muscle hypertrophy. More precisely, the task will be to review the current knowledge about skeletal muscle

hypertrophy in human and animals with a proteomics-based system approach to gain insight into biological pathways.

Systematic literature review: What molecules significantly stimulate skeletal muscle hypertrophy in myotube cell culture, mice and humans? (Supervisor HW)

Abstract: Testosterone, Igf-1 and β2-agonists are examples for molecules that stimulate skeletal muscle hypertrophy. The aim of this review is to systematically screen the scientific literature (and anti-doping lists) for molecules that stimulate skeletal muscle hypertrophy. We will then discuss the pathways by which these molecules cause hypertrophy. The review will be useful anti-doping information and be a useful source of information for research into skeletal muscle hypertrophy. You will carry out the review together with Marius Meinhold who is a PhD student in the exercise biology group.