EXERCISE PROTEOMICS

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INTRODUCTION
The molecular mechanisms and the specific proteins involved in human skeletal muscle adaptation to physical exercise are to some extent unknown. Because of the complex interaction among these systems the lack of complete understanding of muscle function is not surprising. The purpose of exercise-induced changes in muscle cell function is to adapt the tissue to a demand of increased physical work capacity. Because of the design and methods used in a majority of studies on muscle adaptation, concerns must be raised, and the question asked whether the paradigm of exercise-induced muscle inflammation in fact is fiction. By using a proteomic approach several hundred, or in some cases thousands, of known and unknown proteins can be differentiated, quantified and identified at one time.

METHODS
Human skeletal muscle biopsies were obtained from the vastus lateralis and biceps brachii muscles before and after three modes of exercise: Eccentric exercise (45 min downhill running, N = 10), twice weekly for 12 weeks of 1) endurance (3 x 30 reps, N = 10) and 2) strength training (5 x 3 reps, N = 10). Muscle tissue samples were homogenized and proteins quantified and analysed by two-dimensional difference gel electrophoresis (DIGE) [1]. Protein detection was performed by mass spectroscopy (MALDI-TOF) and data base search using MASCOT. Physical work capacity in terms of VO2max before the eccentric exercise and muscle strength before and after 12 weeks of endurance or strength training was recorded.

RESULTS
Approximately 2300 protein spots were detected in each muscle sample. Significant changes in protein profile depended on exercise mode: Eccentric exercise changed 32 protein spots (e.g. contractile; Actin, calcium regulation; Calsequestrin-1, metabolic; ATP synthase and stress; Peroxisiredoxin 6), endurance training changed 25 protein spots (e.g. contractile; Actin, metabolic; Fructose-biphosphate aldolase A and stress; Apoptosis Inducing Factor) and strength training changed 16 protein spots (contractile; Actin, metabolic; ATP synthase and stress; HSP 27).

DISCUSSION
By using high sensitive fluorescence dyes and an internal standard, changes in protein expression of < 15 % can be detected in human skeletal muscle by DIGE. Comparisons between exercise modes are complex. Some structural proteins such as actin are changed independent of exercise mode, while others, e.g. desmin only changed after eccentric exercise [2]. In general, oxidative metabolism appears up-regulated while glycolytic metabolism is down-regulated, independent of exercise mode. There were very few signs of an inflammatory response in any of the exercise protocols.

Keywords: Eccentric Exercise, Protein Damage, Muscle Damage

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