Investigations of metabolic differences due to differences in the muscle fiber distribution by using 31P-MRS at 3.0 T

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Purpose

Muscle performance is significantly determined by its fiber distribution. Hence, for many sport disciplines a congenital optimal fiber distribution in special muscles is a prerequisite to become a high performance athlete. However, due to inactivity or training conversions between different fiber types can also be induced [1]. Biopsy probes harvested from high performance athletes indicate a correlation between training activities and fiber distribution [2]. Due to metabolic differences between different muscle fibers types their distribution affects the corresponding concentration of high energy phosphates. ^{31}P-MRS is a reliable and non-invasive tool to detect metabolic differences between high energy phosphates [3] and can be used to monitor changes during rest and exercise. Under load the ^{31}P-MR spectra can show a split of the inorganic phosphate (Pi) signal due to different pH values which are realized in different compartments [4]. These compartments can be identified as different fiber types, whose pH values drift differently due to differing activities of anaerobic glycolysis. The peak area ratio of the resulting Pi components should reflect the fiber distribution of the muscle. In this study the metabolic ratios of PCr and ATP in the resting state and the ratio of the separated Pi components during exercise were compared for athletes with different sportive activities.

Methods and Materials

Six male volunteers (age: 23 - 31 years) including two basketball players, two sprinters, one biathlon athlete and one control with normal sportive activities were examined during rest and during an exhaustive dynamic load of the M. gastrocnemius. The load was realized by pushing an ergometer pedal within the scanner (Fig. 1). The pedal force was individually adjusted to 30% of the maximum voluntary contraction (MVC). A 3.0 T whole body scanner (Magnetom TIM Trio, Siemens, Erlangen) and a double tuned ^{1}H/^{31}P-Surface coil (Biomedical Rapid GmbH, Würzburg, Germany; diameter: 80mm) were used for the ^{31}P-MRS measurements. The coil was fixed on the leg by elastic Velcro stripes underneath the muscle. A FID-sequence (TR=5s, NEX =1) without gradient mediated volume selection was used to avoid motional artifacts and to achieve a high time resolution. Prior to spectroscopy T_1-weighted MR images were acquired for shimming the volume sensitivity range above the coil. MRS was performed as a series of dynamic single measurements. First, measurements were performed during rest (150s). Triggered by a special acoustic signal the volunteer started to push the pedal in an acoustically mediated tact of 2/s during 300s. The exercise was terminated by a second acoustic signal and data were further acquired during recovery for the following 450s. Postprocessing and quantification of peak areas were performed using the software package MRUI (http://www.mrui.uab.es).

Results

During rest lowest values of the PCr/ATP ratio were observed for the endurance trained athlete and highest ratios for both sprinters as indicated in Tab. 1. Pi/ATP ratios were less uniform, with the highest ratio for the endurance trained athlete and the lowest ratios for one sprinter and the untrained control. Only small differences were observed for the pH value, with marginal higher values for sprinters compared to the others. During exercise PCr was strongly decreased and Pi increased in all volunteers (see Fig. 2). The Pi signal was split into 2 or 3 components with different chemical shifts indicating different pH values. The ratio between the high and low pH component of the split Pi peak showed a more inhomogeneous distribution compared to the PCr/ATP ratios during rest. However, with the exception of subject B, subjects with a high PCr/ATP ratio during rest showed high intensities of the low-pH Pi component during exercise (Tab. 1).

Tab. 1 Metabolic ratios in the M. gastrocnemius of the 6 volunteers in rest and the ratio of the maximal peak areas of the Pi component between high and low pH peak

	A	B	C	D	E	F
sportive activity	basketball	basketball	sprint	sprint	biathlon	untrained
PCr/ATP	3.45	3.36	3.78	3.63	3.10	3.77
Pi/ATP	0.46	0.40	0.38	0.43	0.48	0.35
PCr/Pi	7.53	8.48	9.97	8.53	6.45	10.87
pH	7.04	7.04	7.09	7.06	7.03	7.04
high-pH/low-pH peak area ratio	54/46	33/67	39/61	50/50	69/31	42/58

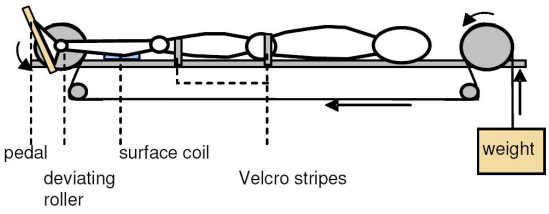

Fig. 1: Schematic presentation of the exercise. To standardize the course of movement and to avoid activations of additional muscles upper and lower leg were fixed by Velcro stripes. The load was achieved by pushing the pedal against an individual adjusted force of 30% MVC.

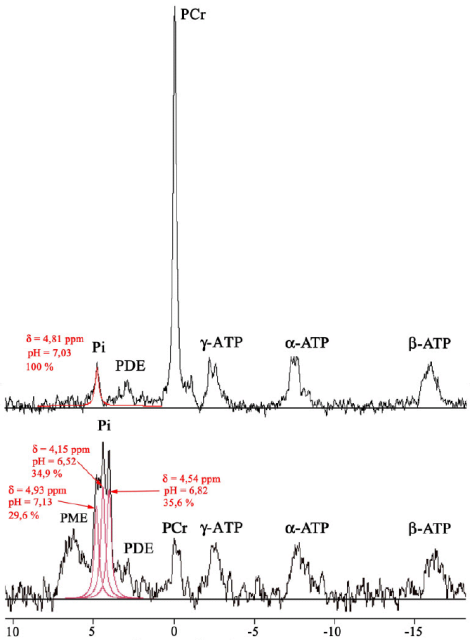

***Fig. 2:** Representative ^{31}P-MR spectra during rest (a) and exercise (b). The fitted line shapes of the Pi components are highlighted by the red color. The 3 components in (b) include a nearly unshifted, a moderately and a strongly shifted component representing the three different fiber types of slow, fast aerobic and fast anaerobic type.*

Conclusions

In vivo ^{31}P-MRS investigations of the muscle fiber distribution have already been published (for instance by Schunk *et al.* [5]), but mostly by using 1.5T scanners. Due to the higher spectral resolution and the higher SNR at 3.0 T the separation of different overlapping pH-components of the Pi signal and the time resolution should improve. In fact, the spectral separation was sufficient to estimate different Pi components in all volunteers. Compared to the relatively small metabolic differences during rest the intensity ratio of the split Pi components showed a stronger dependence on the fiber distribution and thus seems to be more suitable to estimate fiber distributions in muscle. Some uncertainties remain currently due to the necessity to activate all motor units and temporal changes of the Pi intensity caused by Pi trapping in the glycogenolytic pathway [6]. Standardization of the exercise performance and investigations of the reproducibility are necessary to use this method to analyze muscle fiber distributions without biopsy.

References

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