Localised versus unlocalised dynamic 31P MRS acquisition in exercising human muscle at 7T

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Introduction In this work, we compare localised dynamic ^{31}P MRS of a single exercising muscle with pulse-acquire spectra, in a 7T whole body system. Dynamic ^{31}P studies of energy metabolism are often conducted using non-localised acquisitions. Single voxel spectroscopy (SVS) can increase specificity by focussing acquisition to a single organ of interest, albeit at the cost of SNR which may necessitate temporal averaging, eventually decreasing temporal resolution. To overcome these limitations, a short echo SVS with adiabatic refocussing was applied at ultra high field, in aerobically exercising human gastrocnemius muscle. Data are compared to non-localised spectra, acquired in exercise bouts with equal intensity.

Subjects and Methods Healthy subjects (n = 5, aged 30.6±7.9 yrs, BMI = 24.8±3.9, 1 female) performed plantar flexion exercise on an ergometer (as in [1] and an improved version) after written informed consent, in accordance to the local ethics committee. A dual tuned loop coil, d~10 cm (Rapid Biomedical, D) was used in a Siemens 7T whole body MR system. Pulse-acquire spectra were excited with a 250 µs block pulse. Alternatively, an appropriately sized voxel (avg. 37 ml), localised with semi-LASER [2] was placed in the gastrocnemius muscle (Fig. 1). T_E = 23 ms, T_R = 6 s, (cf. PCr T_1 at 7 T [3]). After 3 min of rest, aerobic plantar flexion exercise was performed for 5 min, inducing significant PCr depletion and intracellular pH shift (see results). During subsequent recovery, acquisition was continued for 7 min, storing each data vector (2 k points) separately for post processing in AMARES. PCr amplitudes of recovery were fitted to a 3 parameter exponential function. Three exercise bouts were performed: With, without and again with localisation, separated by a period of inactivity of 15 to 48 min (subjects remaining in the scanner). Pedal force was held constant via the pneumatic pressure of the ergometer.

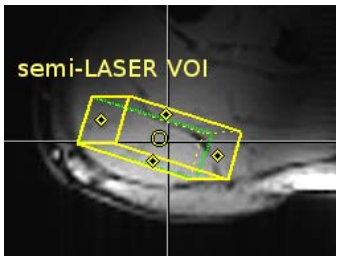
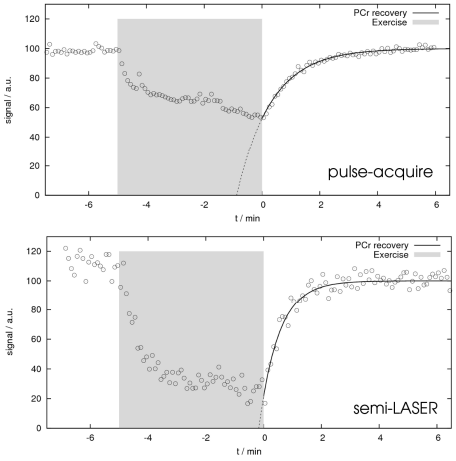


Fig. 1: Position of the VOI in gastroc.

Results Robust quantification of PCr from a single exercising muscle was possible from single acquisitions with a temporal resolution of 6 s (=T_R) to fit PCr recovery time courses (Fig. 2). Four spectra were averaged for pH calculation via Pi. The muscle's resting pH (mean±SD) was 7.05± 0.03, in all experiments . End exercise pH was 6.83±0.17 and 6.85±0.07 in the localised experiments. Only in non-localised experiments a split of the Pi peak with 0.6±0.1 ppm was observed in four (of 5) subjects, resulting in ambiguous end exercise pH quantification of 6.99±0.08 or 6.6±0.13 units. When measured with semi-LASER localisation, PCr depleted by 70±20 % in the first bout and 78±7 % in the second bout, significantly lower (p = 0.02) than the 48±12 % depletion measured without localisation. PCr recovery half times in gastrocnemius calculated from localised spectra were: 33±9.6 s (first bout) and 34±8 s (second bout) while from non-localised spectra we calculated 43±8 s. Highly significant differences in initial d[PCr]/dt were found between non localised and the second (p = 0.0009) and first (p = 0.01) bout of localised acquisitions.



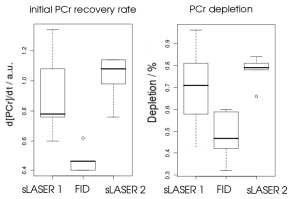


Fig. 2: Typical PCr recovery time course before, during and after aerobic plantar flexion exercise in a healthy subject measured in a pulse-acquire scheme without localisation (top left), and with semiLASER ^{31}P MRS, localised to gastrocnemius muscle (bottom left) in a 7T whole body MR scanner. The top right right part shows initial PCr recovery rates in arbitrary units and depletions measured with and without localisation for all 5 subjects.

Discussion and Conclusion In the past few years, several methods were introduced for dynamic localised ^{31}P MR in human muscle [4, 5]. Our single voxel approach employing adabatic refocussing, as a single shot technique, has relatively high time resolution (6 s, possibly less), and yields SNR which is sufficient to quantify the PCr time course. Also pH quantification is feasible, with lower time resolution. SVS is applicable for absolute quantification with external references [6].

A split Pi peak is often observed in non-localised spectra (here and in literature). In the light of our data which show no (<0.1 ppm) pH split when localised to m. gastroc, Pi peak splitting appears to be attributable to heterogeneous recruitment of different muscles, rather than to a fibre composition effect, at least in gastrocnemius, at the given exercise intensity. Experiments were repeated to provide comparable conditions. The first and last bouts show similar results, in contrast to the intermediate bout with highly significant differences, which was measured without localisation, i.e. the influence of repeated exercise (with a sufficient resting period) can be neglected compared to the effect of localisation on pH, PCr depletion and PCr recovery time constant. The algebraic consequence of varying depletion but constant halftime (assuming roughly monexponential kinetics) is variation in absolute d[PCr]/dt, which should reflect roughly the ATP demand. Interestingly, we observed a trend towards faster PCr recovery in the localised spectra, where PCr depletion is greater. Thus the implied d[PCr]/dt is more than proportionally increased, but apparent physiological implication is that this is achieved by an increase in effective mitochondrial function in 'harder-working' regions. This could be perhaps because they are intrinsically Type I predominant, but more interestingly it might be that they are given (e.g. by selective diversion of oxygenated blood) the oxidative capacity to deal with the harder load they bear. In conclusion, we believe that by its increased specificity, localised dynamic ^{31}P MRS can offer new insights and understanding of energy metabolism in exercising muscle.

References: [1] Meyerspeer, M., et al. *Magn Reson Mater Phy*, 2005. 18(5):257–262. [2] Scheenen, T. W., et al. *Magn Reson Mater Phy*, 2008. 21(1-2):95–101.
[3] Bogner, W., et al. *Magn Reson Med*, 2009. 62(3):574–582. [4] Forbes, S. C., et al. *NMR Biomed*, 2009. [Epub].
[5] Greenman, R. L. et al. In *Proc Intl Soc Mag Reson Med (ISMRM),* 2009 #2473. [6] Kemp, G. J., et al. NMR Biomed , 2007. 20(6):555-565.