Feasibility and repeatability of the localized ^{31}P MRS Four-Angle Saturation Transfer (FAST) of the human gastrocnemius muscle using surface coil at 7T

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Introduction:

Phosphorus magnetic resonance spectroscopy (^{31}P MRS) provides non-invasive insight into muscle energy metabolism, alterations of which are related to several diseases, e.g., heart failure, stroke and muscle disease [1]. In particular, if combined with a saturation transfer (ST) technique, resting Pi-to-ATP and PCr-to-ATP exchange rates can be estimated *in vivo* [2]. However, even at 7T, the full ST measurement takes ~10 minutes [3]. This is still impractical for the measurement of faster dynamic changes. An alternative method, called Four-Angle Saturation Transfer (FAST), presented by Bottomley et al. [1], can be used to shorten the needed examination time. However, the accuracy of FAST depends strongly on dual-angle-based T_1 measurements and therefore on the accuracy of excitation flip angles. The aim of this study was to test the feasibility and repeatability of the localized FAST method at 7T using a circular surface coils with present B_1 inhomogeneity, to speed-up the measurement of both Pi-to-ATP and PCr-to-ATP reaction rates in the human gastrocnemius muscle.

Materials and Methods:

^{31}P MRS was performed on a 7T Magnetom scanner (Siemens Healthcare, Erlangen, Germany) with a double-tuned (^{31}P/^{1}H), circular surface coil of 10 cm diameter. The originally proposed B_1^+ insensitive, adiabatic BIR4 excitation pulses are very SAR demanding and their off-resonance profile at 7T is insufficient. Therefore, we used a FAST using conventional pulse (i.e., 0.6 ms long sinc pulse). A flip angle distribution map of the used sinc pulse was measured by a recently proposed method [4]. Although it was found inhomogeneous for the whole sensitivity volume, the homogeneity was sufficient in a narrow plane close to the surface coil. Therefore, to ensure accurate flip angle adjustments, we used slice selective excitation, i.e., a depth-resolved surface coil MRS (DRESS) sequence [5], with high localization precision at 7T [6], (Figure 1). Measurements were performed on eight healthy volunteers (6m/2f, age 28.8±2.8 years) lying in supine position, with the right calf muscle placed on top of the coil. Localized FAST measurement were conducted in two experiments, first with a flip angle of 52° and NA=8, and a second with a flip angle of 15° and NA=24. Both experiments were performed w/o γ-ATP saturation (saturation pulse at -2.48 ppm, 2.48 ppm and 12.52 ppm) with the TR=2s, slab thickness=15 mm and four preparation scans. For comparison the reaction rates were measured also using the localized ST method with T_1^{app} measured by conventional Inversion Recovery in the presence of γ-ATP saturation. The measurement time for the localized FAST experiment was 4 minutes in comparison to the 10 minutes of the conventional localized ST experiment. To test its repeatability, the FAST measurement was repeated four times within one session on 6 of the recruited volunteers. The unidirectional exchange rate constants (k) measured by FAST and conventional ST were compared via a Bland&Altman analysis of agreement [7] and the repeatability of localized FAST measurements was evaluated by a coefficient of variation (CV). Repeatability of conventional ST experiment at 7T was assessed earlier [3].

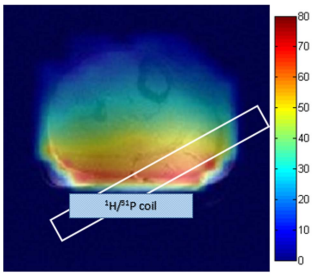

Figure 1 Localizer image of a calf muscle overlaid with the FA map of used excitation pulse with nominal FA = 52° and with depicted slice selection of the DRESS localization sequence

Results:

Results for the DRESS localized conventional ST and FAST measurements of the Pi-to-ATP and PCr-to-ATP forward reaction rate constants in a human gastrocnemius muscle are given in Table 1. The results of the k_{ATP} and k_{CK} measured by the FAST method at 7T (k_{ATP} = 0.11±0.05 s^{-1} and k_{CK} = 0.26±0.05 s^{-1}) are comparable to those measured by the conventional ST (k_{ATP} = 0.14±0.06 s^{-1} and k_{CK} = 0.27±0.02 s^{-1}). Figure 2 depicts the agreement analysis of the two methods. The CVs for measurement of PCr-to-ATP and Pi-to-ATP exchange rate constants by the DRESS localized FAST method at 7T is under 10% and under 20 % (see Table 1), respectively.

	PCr-to-ATP		Pi-to-ATP	
	$T_1^{app}{}_{PCr}$ [s]	k_{CK} [s^{-1}]	$T_1^{app}{}_{Pi}$ [s]	k_{ATP} [s^{-1}]
conv. ST	1.58 ± 0.12	**0.27 ± 0.02**	3.22 ± 0.67	**0.14 ± 0.06**
FAST	1.52 ± 0.09 (4%)	**0.26 ± 0.05 (9%)**	3.05 ± 0.61 (8%)	**0.11 ± 0.05 (19%)**

Table 1 Calculated apparent T_1s and k constants of the PCr-to-ATP and Pi-to-ATP reactions given as mean ± stdev from all 8 volunteers and (CV) from repeatability of the 6 volunteers

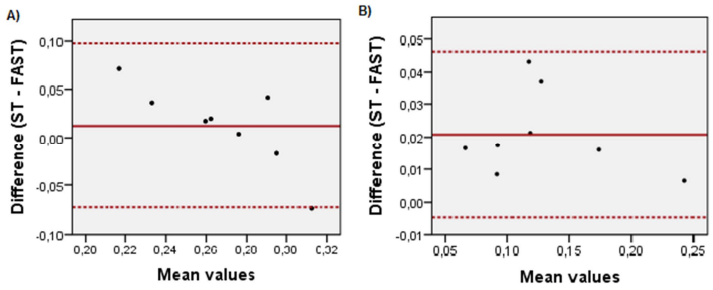

Figure 2 Plots of agreement between measurements of k_{CK} (A) and k_{ATP} (B) by FAST and by conventional ST at 7T

Discussion and conclusion:

We have shown that the measurement of DRESS localized FAST method in the gastrocnemius muscle is feasible at 7T even without the use of adiabatic excitation pulses. The Pi-to-ATP and PCr-to-ATP exchange rates measured in the gastrocnemius medialis muscle by the FAST method were comparable to the results of conventional ST. Measured k values for PCr-to-ATP and Pi-to-ATP reactions are in good agreement with previously published results of localized experiments [1, 8]. The DRESS localized FAST experiment can be at 7T performed within 4 minutes with high repeatability. The time resolved localized FAST method offers new opportunities for studies of human metabolism by ^{31}P MRS, especially when scan time is critical [1].

References:

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