Relaxation time measurements of 31P metabolites in the human calf muscle at 7 Tesla

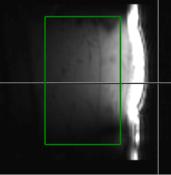
W. Bogner¹, M. Chmelik², A. I. Schmid², E. Moser³, S. Trattnig¹, and S. Gruber¹

¹Radiology, MR Center of Excellence, Medical University Vienna, Vienna, Austria, ²Karl-Landsteiner Institute for Endocrinology and Metabolism, Vienna, Austria, ³MR Center of Excellence, Medical University Vienna, Vienna, Austria

Introduction:

Phosphorus (31 P) MR spectroscopy is a useful tool for non-invasive investigations of human muscle metabolism under various physiological and pathological conditions. In order to optimize measurement parameters (TR, TE) of spectroscopy sequences and to achieve optimal signal-to-noise ratios (SNR) per time, T_1 and T_2 relaxation times must be known accurately. In addition, relaxation times are important for absolute quantification of metabolites, as subsequent corrections for T_1 and T_2 decay are necessary. Relaxation times may vary for different metabolites and with the magnetic field strength (B_0). With the advent of 7 Tesla systems the need for accurate relaxation times of 31 P metabolites will evolve.

Fig. 1: illustrates the localization of the dual-tuned surface coil (${}^{1}H/{}^{\beta 1}P$) and the shimming box adjacent to the calf muscle on a sagittal T_{1} -weighted image.



Methods and Materials:

Data of 4 male healthy volunteers (age 28 ± 7 years) were acquired on a 7T system (Siemens, Erlangen, Germany) using a double-tuned surface coil (${}^{1}\text{H}/{}^{31}\text{P}$) with a diameter of 10 cm.

The right calf of the volunteer was positioned on the surface coil with the medial head of the right gastrocnemius muscle over the center of the coil (Fig.1). T_1 relaxation times were measured with non-localized inversion recovery using ten inversion times (TI) (TR 30s, TE* 0.3ms, TI range 0.02-15 s, spectral width 5000Hz, 1024 points, 5 averages, 3 dummy scans). TR was defined as the time between excitation and next inversion pulse. An adiabatic inversion pulse (sin/cos, 3 ms duration) and a rectangular excitation pulse (340 μ s duration) were adjusted to cover the full bandwidth of the spectrum. Data were acquired interleaved (every tenth acquisition had the same TI) in order to account for possible subject movement.

 T_2 relaxation times were determined via interleaved non-localized spin-echo sequence with ten different echo times (TE) (TR 10s, TE range 8.3-350 ms, spectral width 5000Hz, 1024 points, 10 averages, 3 dummy scans). In order to avoid J-modulation of J-coupled ATP signals due to variable TE (leading to underestimation of T2 times) we applied frequency selective refocusing as proposed by Straubinger et al. [1]. Again rectangular excitation and a Mao refocusing pulse (4 ms duration) with strong crusher gradients (1 ms, 25mT/m) were used allowing reasonably short TE (\ge 8.3 ms). Both methods are similar to those successfully applied previously for measurements of ^{31}P metabolites in the brain at 7T. [2]

Post acquisition processing included zero-filling the FIDs to 8192 points, baseline correction to remove broad resonances from immobile phosphate (only IR experiment), constant phasing for all spectra within a measurement, and applying a 25 Hz exponential line-broadening. The peak height was used for quantification in the T_1 and T_2 experiments. The average SNR and linewidth were determined. Single exponential functions with three parameters were used for T_1 and two parameter fitting was applied for T_2 calculations. In both fitting routines Gaussian weighting ($w = 1/\sigma^2$) for amplitude was applied to account for differences in spectral quality.

Results:

Typical spectra of the IR experiment with variable TI and of the spin-echo experiment with variable TE are shown in Fig.2. Table 2 lists mean and SD of *in vivo* T_1 and T_2 relaxation times of all investigated ^{31}P metabolites. The typical linewidth for PCr was about 13 Hz without line-broadening. Average Pearson's correlation coefficients for all T_1 fits are $r^2 = 0.9996 \pm 0.000$ for PCr and range between 0.96 and 0.9994 for the other metabolites. For T_2 fits of PCr $r^2 = 0.994 \pm 0.001$ and ranging from 0.87 to 0.997 for the rest.

	Pi	PCr	γ-ATP	α-ATP	β-АТР	PDE
T_1	6154±465	4065±85	3394±148	1756±52	1935±244	5432±682
T_2	16±2	220±3	26±2	n/a	n/a	293±23

Table 1: lists both T_1 and T_2 relaxation times (ms) of ^{31}P metabolites at 7T as determined by an inversion recovery and frequency selective spin-echo experiment, respectively. The mean and standard deviation over all subjects are displayed.

Discussion and Conclusion:

Our results found for T_1 times at 7T are similar to those reported previously at 3T and below [3]. However, a decrease in T_2 values can be observed. This trend is consistent with relaxation time measurement of the human brain at 7T. [2] Our results indicate that no SNR per time loss due to longer T_1 can be expected at 7T, while excellent spectral quality can be achieved. This will facilitate *in vivo* measurements in the field of ^{31}P spectroscopy of the muscle. However, T_2 times are decreasing, which has to be taken into account for localized spectroscopy. The method is considerably robust to B_1 inhomogeneities and easily applicable to other parts of the body.

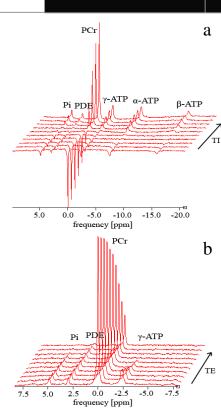


Fig. 2: shows example spectra of (a) T_1 measurement with variable TI (ten TIs; 0.02-15 s) by inversion-recovery method and (b) T_2 measurement with variable TE (ten TEs; 8.3-350 ms) by frequency-selective spin-echo experiment; 20 Hz exponential filtering was applied for display purpose.

References:

- [1] Straubinger K, et al. JMRI 2007; 12:121-129
- [2] Lei H, et al. MRM 2003; 49:199-205
- [3] Meyerspeer M, et al. MRM 2003; 49:620-625