Relaxation Parameter Mapping Adapted for 7T and Validation against Optimized Single Voxel MRS

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INTRODUCTION The previously published T1 relaxation times for brain tissue at 7T vary greatly in results and in methods [1-7] while only two publications [8, 9] assessed in vivo T2 relaxation times in the human brain at 7T. These two articles published T2 values from the visual cortex where it is known that T2 relaxation is different than in other brain regions. The aim of this study was hence the development and validation of reliable, high resolution T1 and T2 mapping sequences applicable to 7T in the presence of related transmit B1 inhomogeneity and the determination of T1 and T2 relaxation times of water in multiple brain regions. For T1 relaxation time mapping, a Look-Locker sequence [10] with an adiabatic inversion prepulse and a modified fitting routine was implemented and validated against spectroscopic data. For T2 relaxation time mapping the vendor pre-implemented mixed imaging sequence [11] was validated with MRS data and proofed to be a reliable T2 mapping sequence for application at ultra-high field systems. For cross validation purpose T1 and T2 relaxation times were also measured in the human brain at 7 Tesla at selected anatomical locations like white matter (wm), grey matter in the perigenual anterior cingulate gyrus (gm PAC), nucleus caudate and in cerebrospinal fluid (CSF) by optimized single voxel MRS parameter series scan protocols.

MATERIAL AND METHODS All measurements were acquired on a 7T MR system (Philips Healthcare, Cleveland, USA) using a quadrature transmit head coil together with a 32-channel receive array (NOVA Medical, Wilmington, USA). Automatic volume based third order FASTERMAP shimming [12] and manual F0 adjustment was performed prior to each measurement. Nine healthy volunteers (median age 26 years, 3 female, 6 male) were measured and gave informed consent in line with local ethics regulations. SV-MRS: Unsuppressed single voxel water spectra using very small (0.343cm^3) voxel sizes with STEAM localization combined with flip angle-optimized outer volume suppression has been used. For T1 measurement an inversion recovery series with an adiabatic inversion pulse (TR=10-20s, 12 IR times, NSA =2-4, TA=6 to 10 minutes) and for T2 measurements an echo time series (TR=6-10s, 8 echo times, NSA=4-12, TA=5-9 minutes) were recorded. Voxel based flip angle optimization was applied to minimize B1 effects. The three parameter model $Mz(t)=M0-(M0-Mz(0))*\exp(-t/T1)$ was fitted to the areas of the water peak to determine T1, and the two parameter model $Mxy(TE)=Mxy(0)*\exp(-TE/T2)$ to determine T2 in the respective region. A biexponential fit was used in both cases in the PAC region - where gm and CSF was excited simultaneously - in order to account for partial volume effects. Imaging**:** For the Look-Locker sequence the following parameters were used: TR for Inversion=10s, TR=8.2ms, TE=4.9ms, readout flipangle = 7°, 5mm slice thickness, 30 images, TA= 4:50 minutes with an in plane resolution of 1 mm^2. A highly adiabatic inversion pulse (hypersecant, duration 22ms, amplitude 15μT) was used and the residual inversion imperfections due to B1 inhomogeneity (especially in parietal regions) were corrected by modifying the fitting model as follows: $M(t)=M0-(-\cos(\beta)+m\infty)*\exp(-\tau/T1^*)$, where $1/T1^*=1/T1 - \ln(\cos(\alpha)/\tau)$, β is the inversion prepulse and α the TFE readout flip angle. The already pre-implemented mixed sequence provides T1, T2 and rho maps simultaneously. Only the T2 maps are being validated with MRS in this study because T1 values from the mixed sequence (722ms (±94)) are underestimated due to the B1 sensitive 90° and 180° pulses in the sequence. Resolution parameters were kept identical as the Look-Locker.

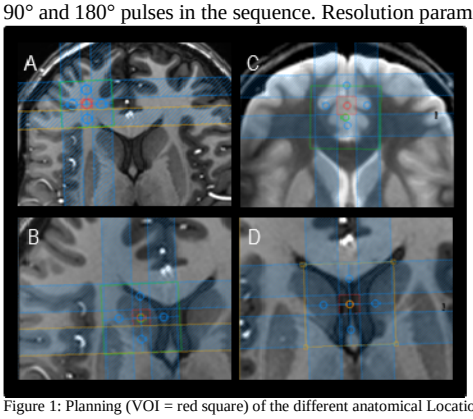

Figure 1: Planning (VOI = red square) of the different anatomical Locations A: White matter, B: caudate nucleus, C: grey matter, D: CSF.

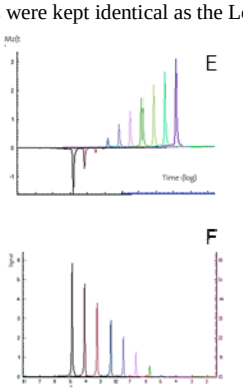

Figure 2: Waterspectra from IR-Serie (E) and Echotime-Serie (F).

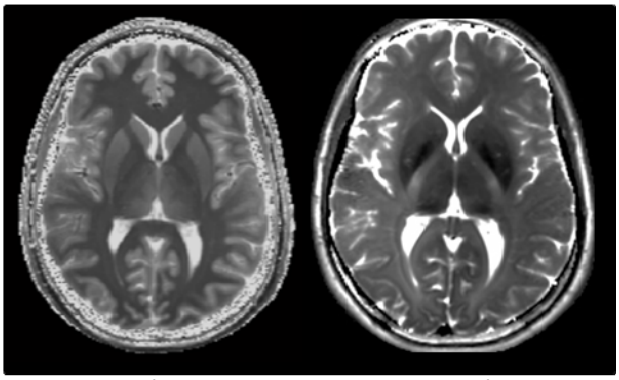

Figure 3: Examples of a T1 map with the Look-Locker sequence.

Figure 4: Example of a T2 map with the mixed sequence.

RESULTS AND DISCUSSION SV-MRS: Relaxation values from the spectroscopy experiments are summarized in Table 1. T1 values for wm lie approximately in the mean of the literature data [3-9], which vary significantly from 890-1500 ms. T1 values for nucleus caudate and gm are in a good agreement with published data. T2 values for wm, nucleus caudate and gm are in general lower than the few published data. The T1 values of the MRS experiments are, although no correction for B1+ errors was applied, fairly reliable because the flip angle optimization was limited to the VOI only. Additionally the fitting parameter $M_z(0)$ makes the estimation of T1 independent of the inversion accuracy. T2 estimation with the simple MRS echo time series method is independent of B1+ inaccuracy. Imaging: Except T1 values in wm, which were higher ($p < 0.05$) in the Look-Locker scan, T1 and T2 values in the caudate nucleus and gm as well as T2 values in wm from the imaging sequences (Table 2) were in an excellent agreement with the MRS data. Using the modified fitting model for T1 mapping (see methods) allows to a certain extent to correct for inversion imperfections, which occur when the adiabatic condition is not fulfilled anymore due to very low regional B1 field strength. The small readout flip angles (α) still suffer from B1 inhomogeneity. Therefore B1 correction would further improve the reliability of T1 maps at 7T. T2 mapping is only affected by B1 inhomogeneity if it leads to signal dropouts. Relaxation data from CSF need to be treated with caution. Non cardiac-triggered T2 measurements in CSF are not very reliable due to pulsation artifacts which results in phase shifts in the MR signal. T1 values are more robust because of the nonselective inversion which inverses also inflowing spins from the CSF. **CONCLUSION** We implemented a Look-Locker sequence at 7T with optimized adiabatic inversion and consideration of inversion imperfection during fitting and validated this with single voxel MRS. We compared the T2 map from the implemented mixed sequence with MRS echo time series and found an excellent agreement between the two methods. This enables relaxation parameter mapping at 7T for T1 and T2 without the use of technically challenging B1 correction methods. Additionally this study confirms mean published T1 values at 7T in most brain regions and provides accurate T2 data at selected brain regions. Nevertheless, to further improve the reliability of relaxation mapping at 7T, either B1 correction, based on acquired B1 maps or RF-shimming with multichannel transmit systems are needed.

Table 1: T1 and T2 values from Single Voxel MRS (mean, standard deviation)

	wm (n=6)	Caudate nucleus (n=4)	gm PAC (n=3)	CSF (n=4)
T1 [ms]	1063 (±64)	1658 (±54)	2144(±2)	3867(±838)
	wm (n=6)	Caudate nucleus (n=4)	gm PAC (n=4)	CSF (n=5)
T2 [ms]	37 (±2)	33 (±3)	45 (±2)	311(±86)

Table 2: T1 values from the Imaging sequences, T1= Look-Locker, T2 = mixed sequence, (mean, standard deviation)

	wm (n=6)	Caudate nucleus (n=4)	gm PAC (n=4)	CSF (n=3)
T1 [ms]	1285(±104)	1715(±58)	1954(±47)	3765(±337)
	wm (n=6)	Caudate nucleus (n=6)	gm PAC (n=6)	CSF (n=6)
T2 [ms]	38 (±2)	39 (±2)	49 (±3)	946 (±206)

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