T_2 estimation of downfield metabolites in human brain at 7T

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Purpose: Magnetic resonance spectroscopy benefits greatly from increases in field strength, including increases in SNR and spectral separation. Thus far, the upfield part of the spectrum has been well-characterized in human brain, especially at very high field strengths [1]; however, the downfield part at 5-10ppm remains less well characterized. Some information has been published on downfield metabolites in animal brain [2, 3], and some on exchange rates and T_1 values in human brain at 3T [4], but a thorough confirmation of metabolite identification and characterization is still needed, particularly in humans. This work aims to further this goal by calculating the T_2 values of several peaks in the downfield spectrum in grey matter at 7 T.

Materials and Methods: Spectra were acquired on a 7T Philips Achieva scanner (Philips Medical Systems, Best, The Netherlands) using a quadrature transmit/receive surface coil (Rapid Biomedical). The voxel of interest was located in the visual cortex of the brain and measured 20x40x20mm^3. Second-order local projection based B_0 shimming was applied. Data was acquired using a STEAM sequence (TR/TM = 4000/24.8ms) with an eight-pulse VAPOR scheme to minimize water sidebands. A series of TEs at 13, 23, 35, 47, and 60ms was acquired in six healthy subjects (age range 21-49yrs, mean age 30yrs), with the applied RF frequency in the downfield region at 7.5ppm. For each volunteer, 256 averages per TE were collected. One data set was excluded due to excessive line broadening. The five spectra with different TEs were modeled simultaneously in FiTAID [5]. Using the average of the five remaining data sets, prior knowledge was defined with seven peaks in the 5 to 9ppm region. The NAA and α-glucose (Glc) peaks were used as binary patterns, as modeled in VESPA based on the known spin systems. Subsequently the individual data sets were fitted.

Results: Fig. 1 presents the downfield region of the TE series of five volunteers summed together, with vertical lines indicating the evaluated peaks. The TE 13ms downfield spectrum, fit, and residuals from one subject are shown in Fig. 2. Average T_2 results across the five subjects are given in Table 1 for the seven peaks of interest, with error given as the standard deviation across the subjects; also included are the mean and standard deviation of the Cramér-Rao bounds (CRB).

Table 1: *T_2 values and corresponding CRB, determined with FitAID for seven peaks.*

	T_2 (mean ± std) [ms]	CRB (mean ± std) [ms]
Glc	46.2 (25.4)	17.2(20.6)
6.0 ppm	22.8 (4.7)	4.7 (2.5)
6.8 ppm	26.7 (1.9)	3.9 (1.3)
7.1 ppm	46.6 (9.5)	8.0 (5.9)
7.3 ppm	31.8 (1.7)	3.1 (0.7)
NAA	29.8 (1.5)	1.2 (0.3)
8.1 ppm	22.3 (3.1)	8.0 (2.9)

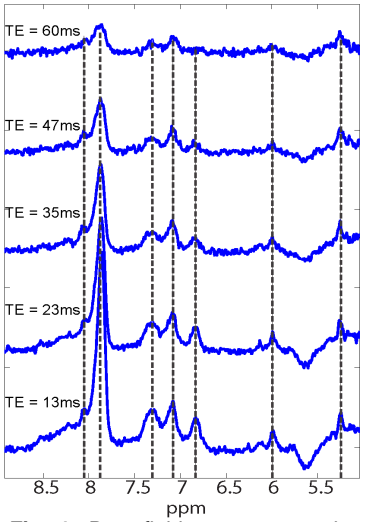

Fig. 1: *Downfield spectra at various TEs for brain grey matter, sum of five volunteers. Spectra are apodized by a 5Hz Gaussian filter. The artifact at ~5.7ppm was present in two volunteers' spectra and was accounted for in the model.*

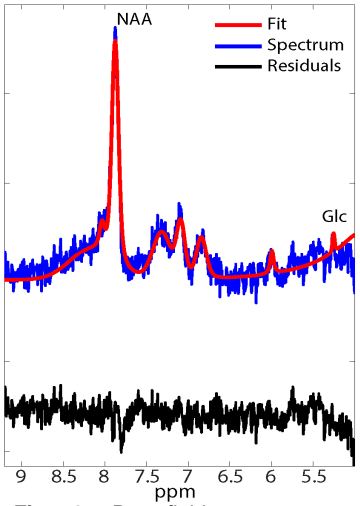

Fig. 2: *Downfield spectrum at TE=13ms for one volunteer, with the fit shown in red overlying the spectrum (blue), and the residuals shown below in black.*

Discussion: The initial fitting results indicate likely metabolite peaks at seven different locations, with fairly flat residuals (Fig. 2 shows a typical example) indicating a decent fitting result. The results for most metabolite peaks were very consistent between individuals, with low standard deviations. One exception with a very large standard deviation and CRB is the Glc T_2, which proved more difficult to model because of its proximity to residual water. It should be noted that other effects such as exchange or J-coupling might affect the T_2's obtained. Furthermore, for coupled peaks such as NAA, the TE decay depends critically on the TM chosen, due to zero-quantum evolution.

Peak assignment, based on chemical shifts of the metabolites and also as discussed in previous work [6, 7], is somewhat difficult, particularly as the use of VAPOR for water suppression might cause peaks that exchange moderately fast to be less visible. At 3T, for example, it has been shown that exchanging peaks exist at 8.2 and 8.5ppm [4], where one would expect the rapidly exchanging amide peaks; a decreased peak intensity due to their exchange might account for the broad shoulder to the left of the NAA. Effects from macromolecules on the baseline or peaks have yet to be verified.

The T_2's found for the various fitted peaks are all fairly similar, but significantly shorter than those reported for upfield peaks in the brain, which are approximately 70ms or longer depending on the structure [8]. The TE dependence of the various peaks seems similar to that previously shown at 3T [9]. Although in the 3T spectra the peak at approximately 8.4ppm appears more prominent even at TE=60ms, the lower magnitude here may be due to a field-dependent T_2 or more likely [4] exchange effects (longer water suppression module).

Conclusions: We have recorded downfield spectra at various echo times and determined the T_2 values for several peaks; while not all peaks have been identified, the quantification brings us closer to full characterization of the downfield spectrum and may aid peak assignment.

References:

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Acknowledgements: *This research was supported by the Swiss National Science Foundation.*