Fast Measurement of T2 Decay for Absolute MRS Quantitation

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Introduction:

Absolute concentration measurement is vital for single voxel proton MR spectroscopy studies of the brain. One of the more common and robust approaches is the use of the water signal as an internal concentration reference. After acquiring the un-suppressed brain water signal at multiple echo times, the water signal amplitude is computed at the extrapolated TE=0 using a bi-exponential T2 decay fit. At long TR, no correction for T1 relaxation of the water signals is needed. ; however, this results in a long data acquisition time (several minutes). Here, we demonstrate on both simulated and in vivo data that it is possible to acquire a multiple-TE data set with relatively short TR and still obtain the water signal amplitude to within the error of data acquired with long TR.

Methods:

Three multiple-TE data sets of un-suppressed water spectra were acquired on a 3T Siemens scanner from parietal grey matter of two human subjects. The first set was the long acquisition scheme, with a TR of 10 sec, and eight different TE values (TE = 35, 45, 55, 65, 75,125, 515 and 1000 msec). This data set fully relaxed, and the water signal amplitude was treated as the true value. Total acquisition time was 1.5 minutes. The second set was collected at a TR of 2 sec with the same set of 8 TE values, with a total acquisition time of 16 sec. The third set was acquired at a TR of 5 sec with only three TE values of 35, 65 and 515 msec. Total acquisition time for this scheme is 15 sec. The second and third data sets comprised the fast acquisition scheme with total acquisition time of 31 sec.

We assume there are two types of water present in the brain, the fast T2 component of the brain tissue and the slow T2 component of the CSF. The bi-exponential T2 decay equation is then:

$$W = Wb*(\exp(-TE/T2b)*(1-\exp(-TR/T1b))) + Wcsf*(\exp(-TE/T2csf)*(1-\exp(-TR/T1csf)));$$

where Wb is the brain water amplitude, and Wcsf is the CSF water amplitude.

Five different sets of simulated data, composed of different T1 and T2 for both brain tissue and CSF and different amount of brain and CSF water contribution, were used. The IDL's POWELL minimization procedure was used to determine a local minimum for a given set of T1, T2 and water content of brain and CSF. The TE and TR used were the same as in the actual subject scanned. For the in vivo optimization, the actual water signals from fast acquisition scheme were used as input values to the minimization routine, and the true water signal amplitudes were measured from the bi-exponential T2 fit of the slow scheme.

Results and Discussion:

The simulation results are shown in the Table.

T1b,t	T1b,cal	T1csf,t	T1csf,cal	T2b,t	T2b,cal	T2csf,t	T2csf,cal	Wb,t	Wb,cal	Wcsf,t	Wcsf,cal
1.1	1.1	3	3.03	0.08	0.08	1.5	1.49	0.7	0.69	0.3	0.31
1	1.1	3	3.18	0.07	0.07	1.8	1.49	0.75	0.74	0.25	0.26
1.1	1.11	2.5	2.64	0.07	0.07	1.8	1.69	0.85	0.84	0.15	0.15
1	1.01	2.8	2.98	0.08	0.08	1.7	1.69	0.9	0.89	0.1	0.1
0.9	0.92	2.5	2.66	0.08	0.08	1.6	1.6	0.95	0.95	0.05	0.05

where t means the true value given in the simulation and cal means the calculated value after fitting. The brain water signal amplitude from the fast acquisition is within 1% of the true values.

For the two human data sets, the brain water signal amplitude or the true brain water content (measured from the slow acquisition scheme) was also within 1% of that of the fast acquisition scheme.

Conclusions:

We demonstrate that it is possible to acquire multiple TE data with shorter TR and still recover the water signal amplitude within 1%. Therefore, this acquisition scheme is suitable for absolute quantitation of proton spectra.

Acknowledgement: We acknowledge support from Siemens Medical Solutions.