Proton density fat fraction and liver water and fat T2 as measured by multi-TR, multi-TE ^{1}H MRS compared to multi-TE ^{1}H MRS.

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Target Audience: Radiologists and physicists with an interest in liver fat quantification and characterization.

Introduction: We have developed a rapid multi-TR, multi-TE ^{1}H MRS sequence for *in vivo* hepatic fat quantification and characterization that acquires 32 distinct spectra in a single breath-hold (**Table 1**), allowing estimation of liver proton density fat fraction (PDFF), and water and fat T1 and T2 values. Here we compare the estimates of water and fat T2 and PDFF given by the multi-TR-TE sequence with those given by the current MRS standard: a long-TR, multi-TE sequence that allows estimation of PDFF, and water and fat T2 values, but not T1 values.

Methods: *In vivo* liver ^{1}H MR spectra were acquired without contrast at 3 Tesla (GE Signa EXCITE HDxt, GE Healthcare, Waukesha, WI) using an 8-channel torso array coil in 51 adult subjects between January 2014 and September 2014. A 20 x 20 x 20 mm voxel was selected within the liver, avoiding liver edges and major blood vessels. The selected voxel was shimmed during free breathing. Thirty-two spectra (including four preparatory acquisitions) were acquired in a 21 s breath-hold using a modified Stimulated Echo Acquisition Mode (STEAM) sequence (timings in **Table 1**). For comparison a STEAM long-TR multi-TE acquisition (the current MRS standard) was performed at the same location with five spectra and a single preparatory excitation acquired with a TR of 3,500 ms consecutively at progressively longer TEs of 10, 15, 20, 25 and 30 ms in a 21 s breath-hold; the long TR was required to minimize T1 effects. For both sequences, a minimum mixing time (5 ms) was used to reduce j-coupling effects and the bandwidth was 5,000 Hz with 256 data points per spectrum for multi-TR-TE and 2,048 data points per spectrum for the multi-TE. Spectra were acquired with no water or spatial saturation.

Table 1: Sequence timing of the multi TR-TE sequence. P1-P4 are pre-pulse excitations. Scan time 20.95 s.

Spect No.	**P1**	**P2**	**P3**	**P4**	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**
TR (ms)	150	150	150	150	150	225	300	400	600	900	2000	1500	700	450	325	250
TE (ms)	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10
Spect No.	**13**	**14**	**15**	**16**	**17**	**18**	**19**	**20**	**21**	**22**	**23**	**24**	**25**	**26**	**27**	**28**
TR (ms)	175	200	275	350	500	800	1250	1000	1000	1000	1000	1000	1000	1000	1000	1000
TE (ms)	10	10	10	10	10	10	10	10	15	20	25	30	50	70	90	110

Spectra from the individual channels were combined using singular value decomposition (**1**). A single experienced observer analyzed the spectra using the AMARES algorithm (**2**) included in the MRUI software package (**3**). The multi-TR-TE results were analyzed with a custom Matlab routine that non-linearly fitted the measured peaks area to the standard equation $S = S_0\left(1 - \exp\left(-\frac{TR}{T1}\right)\right).\exp\left(-\frac{TE}{T2}\right)$. The multi-TE results were non-linear fitted to give the T2 and T2-corrected peak areas of fat and water assuming T2 decay was monoexponential. T2 was calculated for 'water' (4-6 ppm) and fat (0-3 ppm); PDFF was corrected for fat included in the 'water' peak from a previously-established standard liver spectrum (**4**). For fat T2, only values from subjects with PDFF > 5% (n = 32) were used in the comparisons.

Results: **Figure 1** compares the PDFF estimated by the multi-TR, multi-TE sequence to that estimated by the long-TR, multi-TE sequence, while **Figures 2 and 3** show the same for water T2 and fat T2. In all figures the dotted line indicates unity. PDFF estimates by the two methods show strong agreement (slope 0.997; intercept -0.03; R = 0.997). There is weaker agreement for water T2 values estimated by the two methods (slope 0.830; intercept 4.2; R = 0.815). The poorest agreement is for the estimates for fat T2 (slope 0.30; intercept 36.6; R = 0.711)

Discussion: The multi-TR, multi-TE and standard long-TR, multi-TE sequences show good to excellent agreement for estimating PDFF and water T2 but modest agreement for estimating fat T2. The long-TR multi-TE sequence uses a short TE range to minimize j-coupling. This minimizes the ability of the multi-TE sequence to measure fat T2, which is significantly longer than water T2, whereas the greater TE range of the multi-TR-TE sequence may allow better estimation of fat T2.

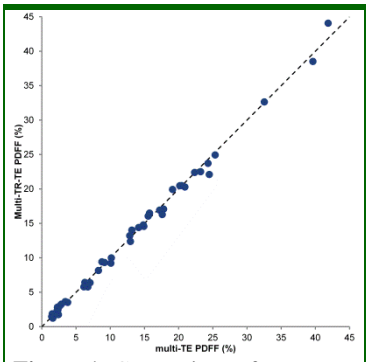

Figure 1: Comparison of PDFF estimated by multi-TR-TE and multi-TE sequences

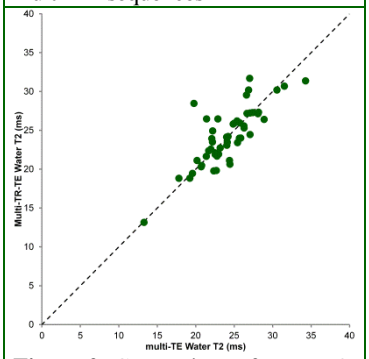

Figure 2: Comparison of water T2 estimated by multi-TR-TE and multi-TE sequences

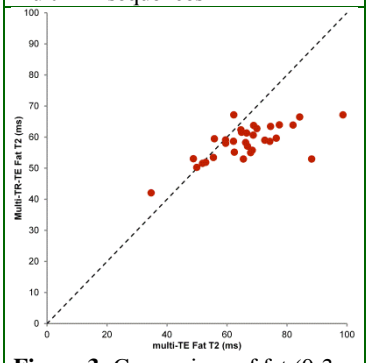

Figure 3: Comparison of fat (0-3 ppm) T2 estimated by multi-TR-TE and multi-TE sequences

Refs: 1) Bydder M, Magn Reson Imaging 2008; 26: 847-850. **2)** Vanhamme L, J Magn Reson 1997; 129: 35-43. **3)** Naressi A. MAGMA 2001; 12: 168-76. **4)** Hamilton G, NMR Biomed 2011; 24: 784-790