Effect of ^{1}H MRS Sequence on Absolute Quantification of Hepatic Lipid

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Introduction: Proton magnetic resonance spectroscopy (^{1}H MRS) is considered the most accurate non-invasive method of determining intrahepatocellular lipid levels (IHCL) in the liver. Both PRESS (Point Resolved Spectroscopy) and STEAM (Stimulated Echo Acquisition Mode) sequences are used, but the effect that the choice of sequence has on hepatic fat quantification has not been considered. These two sequences have different responses to j-coupling present in fat peaks, which may affect the peak area measured. We aimed to examine, in an animal fat phantom and *in vivo*, the effect that sequence choice makes on IHCL.

Methods: MR spectra were obtained on a 1.5T Symphony^{TM} scanner (Siemens Medical Solutions, Malvern, PA) from i) an animal fat phantom and ii) 49 patients (IRB approved). *In vivo* PRESS and STEAM sequences were collected with TR 1500ms, voxel size 20 x 20 x 20mm and 6 signal averages. For the PRESS sequence, spectra were acquired every 10ms in the range TE 30-70 ms; STEAM spectra were acquired every 10ms in the range TE 20-60ms. Spectra were collected from the fat phantom over the same range of TE, but every 5ms. The spectral quantification was performed in the time domain, using the AMARES algorithm (**1**) included in MRUI (**2**) The T_2-corrected peak area of the water, CH_2 (2.1 ppm), CH_2 (1.3 ppm) and CH_3 (0.9 ppm) peaks were calculated, by least squares linear fitting of the log of the peak area against TE. The T_2-corrected peak area of the composite fat peak, which treats the sum of the individual fat peaks in the range 0.5-3 ppm as single peak, was also calculated. Fat peak areas were expressed as a ratio of the water peak area.

Results: Figure 1 shows the change in peak area with TE for the fat phantom. This demonstrates that while for STEAM all the resonances displayed the expected exponential decay, in PRESS, both the CH_2 (2.1 ppm) and CH_3 (0.9 ppm) peaks showed non-exponential decay. Figure 2 compares the T_2-corrected peak area given by PRESS and that given by STEAM *in vivo*. PRESS overestimated the peak area compared to STEAM. This is most obvious in the CH_2 (1.3 ppm) and CH_3 (0.9 ppm) peaks. However, the overestimate appears systematic. This particularly true for the composite peak, where the 25% overestimate of the peak area measured by PRESS with respect to STEAM is a strongly correlated (r^2=0.986).

Conclusions: The IHCL measured is dependent on MRS sequence used, probably because j-coupling causes non-T_2 decay in the PRESS sequence, as shown in the phantom. *In vivo*, the j-coupling causes a systematic overestimate of peak area given by PRESS with respect to STEAM. However, the values given by PRESS and STEAM are correlated particularly in the case of the composite peak.

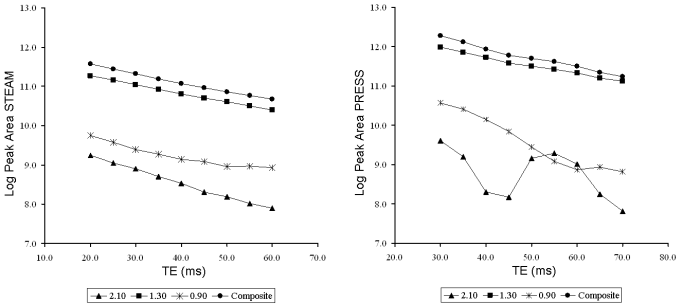

Figure 1: Change in Peak area with TE for animal fat phantom

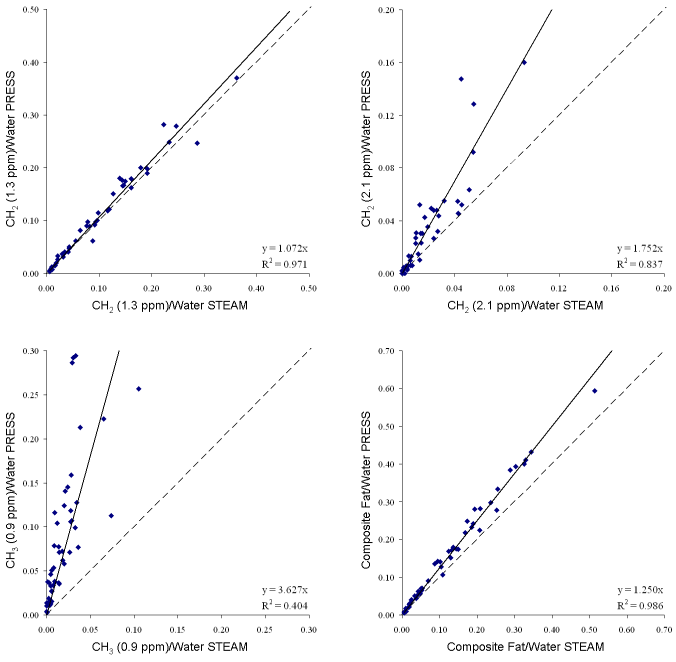

Figure 2: Comparison of the peak area by PRESS and STEAM *in vivo*. Dotted line indicates unity.

References:

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