In vivo Characterization of Liver Fat Composition by ^{1}H MR Spectroscopy

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Introduction: *In vivo* ^{1}H MR spectroscopy at clinical field strengths may allow characterization of liver fat composition. Each of the resonance peaks present in the fat ^{1}H MR spectrum (**Figure 1**) represents a distinct proton moiety (**Table**). Although two fat peaks overlap the water peak, there exists enough information in the remaining four peaks to characterize triglyceride type in terms of the number of −CH=CH− double bonds per molecule (ndb), the number of double bonds separated by a single CH_2 (nmidb - number of methylene-interrupted double bonds) and the chain length (CL). We aim to compare repeatability of ndb and nmidb estimates produced by ^{1}H MR Spectroscopy for a fixed CL value acquired during respiratory gated and free breathing acquisition.

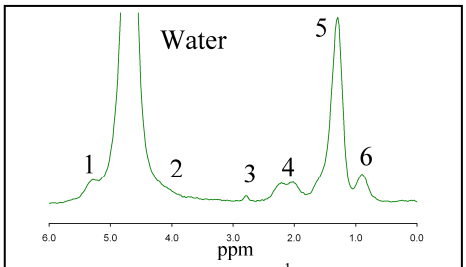

Figure 1: Unsaturated liver ^{1}H MR Spectrum.

Methods: The study was IRB and HIPAA compliant, and all subjects gave written informed consent. STEAM spectra were acquired on 46 human subjects with known or suspected NAFLD at 3 Tesla (GE Signa EXCITE HD, GE Healthcare, Waukesha, WI) using an 8-channel torso array coil. A 20 x 20 x 20 mm voxel was selected within the liver that avoided liver edges. Breath-held, non-water-saturated multi-TE spectroscopy was used to determine liver fat fraction (**1**). This multi-TE sequence had insufficient signal-to-noise to determine fat type, so one of two versions of the STEAM sequence (TE 10 ms, TM 5 ms) was also acquired to more accurately identify the individual fat peaks. In the first 27 consecutive subjects, water-saturated spectra were acquired during free breathing (TR 3500 ms) with 32 signal averages. In the last 19 subjects, respiratory gated water-saturated spectra were acquired with 16 signal averages. Gating parameters were set such that the TR was greater than 3500 ms. For both gated and free breathing sequences, the acquisition was repeated a further two times to give a total of three spectra to allow variability to be examined. Subjects with fat fraction lower than 4% were excluded from the study. No subjects had both free breathing and respiratory gated sequences performed. Signals from different array elements were combined using an SVD technique (**2**) and a single experienced observer analyzed the spectra using the AMARES algorithm (**3**) included in the MRUI software package (**4**). The relative areas of measureable fat peaks (peaks 3-6) were used in the theoretical model (**Table**) to generate ndb, and nmidb values, assuming a fixed chain length CL of 17.5. The coefficient of variation of ndb and nmidb in the three measurements was calculated and the values for free-breathing and gated acquisitions were compared.

Results: The fat fraction and range of fat fraction was similar for both acquisition groups (free breathing n = 22, mean FF 0.151, range 0.047-0.383; gated n = 18, mean FF 0.154, range 0.042-0.300). There was no statistically significant difference between ndb and nmidb in the two groups (free breathing: mean ndb 2.51, mean nmidb 0.62; gated: mean ndb 2.62, mean nmidb 0.67). The mean coefficient of variation of ndb was lower in the gated (4.2%) sequence compared to free breathing (5.8%). In nmidb, the difference in the mean coefficient of variation was more obvious (gated 10.7%, free breathing 18.1%). The nmidb estimate requires accurate determination of the area of peak 3, whereas ndb is mainly determined by peak 4. While both free breathing and gated sequences can accurately determine peak 4, accurate determination of peak 3 requires gating. This is demonstrated in **Figure 2** where for free breathing (left) and respiratory gating (right), the nmidb given by the first spectrum is compared to the second and third repeat spectra collected using the same sequence.

Table: Relative magnitude of triglyceride peaks given by theory. **ndb** – mean number double bonds, **nmidb** – mean number of methylene-interrupted double bonds and **CL** – mean chain length.

Peak	Location	Assignment	Expected Spectral Peak Area
1	5.29 ppm 5.19 ppm	-C**H**=C**H**- -C**H**-O-CO-	2***ndb** +1
2	4.2 ppm	-C$\mathbf{H}_2$-O-CO-	4
3	2.75 ppm	-CH=CH-C$\mathbf{H}_2$-CH=CH-	2***nmidb**
4	2.20 ppm 2.02 ppm	-CO-C$\mathbf{H}_2$-CH_2- -C$\mathbf{H}_2$-CH=CH-C$\mathbf{H}_2$-	6 + (**ndb-nmidb**)*4
5	1.6 ppm 1.3 ppm	-CO-CH_2-C$\mathbf{H}_2$- -(C$\mathbf{H}_2$)$_n$-	(**CL**-3)*6 - **ndb***8 + **nmidb***2
6	0.90 ppm	-$(CH_2)_n$-C$\mathbf{H}_3$	9

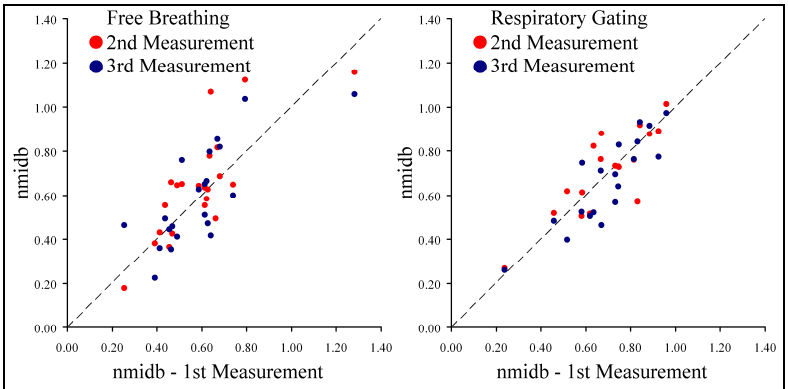

Figure 2: Comparison of nmidb measured by first spectral acquisition to that measured by 2nd and 3rd acquisitions. Dotted line indicates unity.

Conclusions: ^{1}H MR Spectroscopy can repeatably measure the composition of liver fat. Spectra collected with respiratory gating give a more repeatable characterization of the liver fat composition than spectra collected with free breathing.

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