Regional variability in triglyceride composition of adipose tissue measured by ^{1}H MRS

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Introduction: The multi-peak structure of the adipose (^{1}H) proton MR spectrum (**Figure 1**) can characterize triglyceride type (**1**). We have previously reported the triglyceride composition of three different abdominal adipose tissue depots as estimated by ^{1}H MR Spectroscopy in a small patient group (**2**). We now examine, in a new larger patient group, triglyceride composition in terms of number of −CH=CH− double bonds per molecule (ndb), and number of double bonds separated by a single CH_2 per molecule (nmidb - number of methylene-interrupted double bonds) for a fixed the chain length (CL).

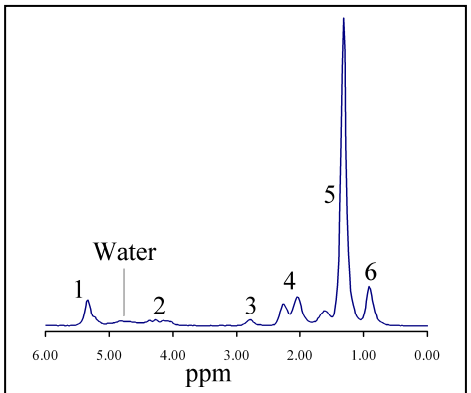

Figure 1: Typical subcutaneous adipose ^{1}H MR Spectrum.

Methods: The study was IRB and HIPAA complaint, with subjects giving written informed consent. STEAM spectra (TR 3500 ms, TE 10 ms, TM 5 ms) were acquired on 67 adult and pediatric human subjects at 3 Tesla (GE Signa EXCITE HD, GE Healthcare, Waukesha, WI) using an 8-channel torso array coil. After conventional imaging, 15 x 15 x 15 mm voxels were selected on the right side of the body in at least two of the following locations: 1) deep subcutaneous adipose tissue (dSCAT); 2) surface subcutaneous adipose tissue (sSCAT); and 3) retro-peritoneal visceral adipose tissue (VAT). All 67 subjects had spectra taken in dSCAT, with 52/67 subjects having spectra collected from dSCAT and 59/67 from VAT. The dSCAT and sSCAT voxels were placed at the same level with the minimal possible distance between voxels. Spectra were acquired in SCAT with 16 signal averages and 2 pre-acquisition excitations during free breathing. However the VAT spectra, being the more susceptible to breathing motion, were collected in a breath-hold with 6 signal averages and a single pre-acquisition excitation. Signals from different array elements were combined using an SVD technique (**2**). A single experienced observer analyzed the spectra using the AMARES algorithm (**3**) included in the MRUI software package (**4**). After the peak areas were corrected for T2 relaxation using previously established values (**Table 1**), the ndb and nmidb values were calculated by non-linearly minimizing the difference between the measured areas of peaks 1, 3, 4, 5 and 6 and that given by the theoretical model (**Table 1**). Peak 2 was not used in the calculation of ndb and nmidb, as it strongly coupled AB spin system (**5**). The chain length (CL) was fixed at 17.5. If more than one spectra was collected in a single location, the average ndb and nmidb were used. The ndb and nmidb values from the three fat depots were compared using paired Student t-test (two-tailed).

Table 1: 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	T2 (ms)	Expected Spectral Peak Area
1	5.29 ppm 5.19 ppm	-C**H**=C**H**- -C**H**-O-CO-	53	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-	54	2***nmidb**
4	2.20 ppm 2.02 ppm	-CO-C$\mathbf{H}_2$-CH_2- -C$\mathbf{H}_2$-CH=CH-C$\mathbf{H}_2$-	52	6 + (**ndb-nmidb**)*4
5	1.6 ppm 1.3 ppm	-CO-CH_2-C$\mathbf{H}_2$- -(C$\mathbf{H}_2$)$_n$-	69	(**CL**-3)*6 - **ndb***8 + **nmidb***2
6	0.90 ppm	-$(CH_2)_n$-C$\mathbf{H}_3$	93	9

Results: The mean (and standard deviation) of ndb and nmidb is shown in **Table 2**. There were significant differences in the ndb value for all cross comparisons of ndb ($p<0.0001$). There were also significant differences in nmidb between dSCAT and VAT ($p<0.002$). However there was no significant difference in nmidb between dSCAT and sSCAT or between sSCAT and VAT. On average VAT was the most saturated fat depot.

Table 2: Mean (and St Dev) of ndb and nmidb.

	ndb	nmidb
dSCAT	2.79 (0.16)	0.73 (0.11)
sSCAT	2.88 (0.16)	0.72 (0.12)
VAT	2.70 (0.16)	0.69 (0.12)

Conclusions: ^{1}H MR spectroscopy detects different triglyceride composition in the three abdominal adipose tissue depots examined, indicating there may be different biochemical processes in these fat depots.

Refs: 1. Ren J, Dimitrov I, Sherry AD, Malloy CR. *J Lipid Res* 49: 2055-2062, 2008. **2.** Middleton MS, Hamilton G, Bydder M, Yokoo T, Schroeder ME, Schwimmer JB, Sirlin CB. Proc RSNA Annual Meeting, Chicago, IL, 2010. **3.** Bydder M, Hamilton G, Yokoo T, Sirlin CB. *Magn Reson Imaging* 26: 847-850, 2008. **4.** Vanhamme L, van den Boogaart A, Van Huffel S. *J Magn Res* 129:35-43, 1997. **5.** Naressi A, Couturier C, Devos JM, Janssen M, Mangeat C, de Beer R, Graveron-Demilly D. *MAGMA* 12: 168-176, 2001**. 6.** Hamilton G, Yokoo T, Bydder M, Cruite I, Schroeder ME, Sirlin CB, Middleton MS. NMR Biomed, 2010 (Epub ahead of print).