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 $-\text{CH=CH-}$ 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).

**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 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).

**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.

**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:**