

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

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Introduction: There have been many studies that have examined the regional distribution of adipose tissue depots. However, the regional distribution of triglyceride composition in adipose tissue has had limited study. Current techniques require an invasive biopsy, limiting most studies to analysis of the triglyceride composition at a single location. However, the multi-peak structure of the adipose (^1H) proton MR spectrum (**Figure 1**) allows the triglyceride composition to be estimated non-invasively (1). In this study, the variability in triglyceride composition in two locations in the same fat depot and in two different fat depots is explored.

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 40 human subjects at 3 Tesla (GE Signa EXCITE HD, GE Healthcare, Waukesha, WI) using 8-channel torso array coil. After conventional imaging, 15x15x15 mm voxels were selected in at least two of the following locations: 1) in the right rear subcutaneous adipose tissue (RSCAT); 2) in the left rear subcutaneous adipose tissue (LSCAT); and 3) in the right retro-peritoneal visceral adipose tissue (VAT). All 40 subjects had spectra taken in RSCAT, with 28/40 subjects having spectra collected from LSCAT and 35/40 from VAT. The LSCAT and RSCAT were taken at the same level with > 15 cm separation between the voxels. Spectra were acquired in the subcutaneous tissue 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 number of double bonds (ndb) per triglyceride molecule and number of methylene-interrupted double bonds (nmidb) per triglyceride molecule 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. The chain length (CL) was fixed at 17.5.

Results: The ndb and nmidb values for all the spectra acquired are compared in **Figure 2**. The range of ndb was 2.49 – 3.17 while the nmidb range was 0.56 – 0.95. There is no clear distinction between values obtained in SCAT, or VAT. **Figure 3** compares ndb values found in the RSCAT with those found LSCAT and with those found in VAT. While the values found in left and right SCAT are highly correlated, ($R^2 = 0.876$), there is more scatter when the VAT is compared with RSCAT ($R^2 = 0.429$). We see a similar pattern in **Figure 4**, which compares nmidb in LSCAT and VAT with the nmidb in RSCAT, with highly correlated LSCAT and RSCAT values ($R^2 = 0.731$) compared to lower correlation between VAT and RSCAT ($R^2 = 0.385$).

Conclusions: The high correlation between RSCAT and LSCAT indicates that there is little variation in triglyceride composition within subcutaneous adipose tissue, whereas there appears to be a larger variation in triglyceride composition between subcutaneous and visceral adipose tissue depots.

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