Supplement

MRI-M Acquisition.

Multi-echo spoiled gradient-recalled echo images were acquired with a 10° flip angle and TR = 125 - 270 ms (adjusted to individual breath-hold capacity) to minimize T1 effects. In a single 18 - 30 s breath-hold, six fractional-echo magnitude images were obtained at serial, nominally in- and out-of-phase echo times (TEs) of 1.15, 2.3, 3.45, 4.6, 5.75 and 6.9 ms. These TEs permitted simultaneous modeling of fat-water signal interference, and estimation of T2*. Other imaging parameters were 8-mm slice sickness, 0-mm interslice gap, ± 142 kHz receiver bandwidth, 0.8 fractional echo sampling, 192 × 192 base matrix, one signal average and rectangular field-of-view (FOV) adjusted to habitus and subject breath-hold capability. Number of slices varied from 14 - 26 depending on TR and phase FOV. Images at each of the six TEs were transferred offline for analysis **[15]** as described in the main manuscript.

MRI-C Acquisition

An investigational version of a water-fat separation method (Iterative Decomposition of water and fat with Echo Asymmetry and Least-squares estimation [IDEAL]) was implemented as a multi-echo three-dimensional (3D) spoiled gradient-echo acquisition with a TR of **7** ms. Six echoes at TEs of 1.0, 1.8, 2.6, 3.4, 4.2, and 5.1 ms were acquired per TR, and a two-dimensional (2D) parallel imaging acceleration method (Autocalibrating Reconstruction for Cartesian imaging [ARC]) with an effective net acceleration of 2.2 was used to reduce imaging time to 21 s. Other imaging parameters were a flip angle of 3° to minimize T1 effects, 10-mm slice thickness, 0.8 fractional echo sampling, ± 125 kHz receiver bandwidth, 256 x 160 base matrix, and rectangular field-of-view (FOV) adjusted to habitus and subject breath-hold capability.

MRS Acquisition

Using a long TR of 3,500 ms to minimize T1 weighting, stimulated-echo acquisition mode (STEAM) proton spectroscopy was performed. A single pre-acquisition excitation pulse was acquired to balance T1 saturation on subsequent excitations. Five STEAM spectra were acquired at TEs of 10, 15, 20, 25 and 30 ms in a single 21-s breath-hold. This range of TE values permitted reliable T2 estimation while minimizing confounding effects of fat-peak j-coupling. The shortest possible mixing time (TM) of 5 ms was used to minimize both j-coupling and T1 weighting. No water, fat, or spatial saturation was applied. Signals recorded at eight array elements were combined by singular value decomposition and saved for offline analysis **[9]**.

Spectral Model used in MRI-M and MRI-C

To correct for the multi-frequency interference effects of signals from triglyceride fat protons, the same spectral model was applied by the MRI-M and MRI-C reconstruction algorithms. In this model, the water peak is modeled as a single 4.7 ppm frequency signal, and composite fat signal is modeled as the sum of six individual frequency signals at 5.3, 4.2, 2.75, 2.1, 1.3, and 0.9 ppm, with weights of 0.047, 0.039, 0.006, 0.120, 0.700, and 0.088, respectively **[15, 24]**.

MRS Analysis

Peaks corresponding to water (4.7 ppm) and fat (2.1, 1.3, 0.9 ppm) were modeled as Gaussian resonances and measured. Nonlinear least-square fitting was used to calculate spectral peak T2 values and T2-corrected peak areas. Fat peaks at 4.2 and 5.3 ppm, obscured by the water peak and not visible at *in vivo* field strengths in human liver, were estimated from visible fat peaks based on the known biochemical structure of human liver triglyceride. MRS PDFF was calculated separately for each MRS acquisition as the integrated sum of T2-corrected fat peaks divided by the sum of T2-corrected fat and water peaks.