Whole Liver $T_1$, $T_2$, and $T_2^*$ Relaxation Mapping using Echo Planar Imaging

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Introduction: Incidence of chronic liver disease is increasing in the UK with rising prevalence of risk factors such as alcohol excess and obesity in the population. Liver fibrosis, a pathological change in the liver tissue caused by chronic liver injury is currently diagnosed and monitored using liver biopsy, an invasive procedure with associated complications. There have been several recent studies investigating whether MRI and MRS can be used to replace liver biopsy for staging fibrosis [1,2], monitoring iron deposition [3] and estimating liver fat content [4].

Figure 1. Base SE liver images from a liver patient with $T_1$, $T_2$ and $T_2^*$ maps overlaid (3 slices of 9 slice data set shown). Corresponding histograms (black curve) from the 9 slice data set, and the Gaussian curve fitted to the central peak only (red curve). Colour overlay displays only pixel values where the red curve is non-zero.

Methods: For this study approved by the local NHS Ethics Committee and all patients gave written, informed consent. Patients (n=13, 9 male) who had chronic liver disease confirmed on liver biopsy were each scanned once on a 1.5 T Philips Achieva scanner with body transmit and a 5-element SENSE cardiac receive coil. All maps were generated from EPI data (9 slices, 3x3x8 mm voxels, 4 mm slice gap, 96x96 image matrix, SENSE 2, SPIR fat saturation ($T_2^*$) water only spectral excitation ($T_1$)). Data were acquired with respiratory triggering, during the expiration phase. The TR was set to 3 sec. After a 200-400 ms delay ($T_D$), for $T_2^*$ mapping, 3 volumes of SE-EPI data was acquired at each of 6 TEs (27, 35, 42, 50, 60, 70 ms). For $T_2^*$ mapping, 3 volumes of GE-EPI was collected at each of 5 TEs (12, 15, 20, 30, 40 ms). $T_1$ maps were formed from inversion recovery (IR) SE-EPI data collected at 10 TIs (100-1000 ms). A single inversion pulse was applied per volume (9 slices acquired in 432 ms), the acquisition was performed twice with the slice order reversed (acq1: slices 1-9; acq2: slices 9-1) resulting in all slices being acquired across 20 TIs ranging from 100 to 1484 ms. To ensure that for each TI the slices were acquired during the ‘stationary’ near-end expiration period, an additional variable delay (IV) was introduced into the respiratory trigger such that slices were collected at the time $T_v+T_I=1000$ ms. The total acquisition time of the complete mapping protocol was < 10 mins.

Data Analysis: If respiratory triggering was poor, some through-plane misalignment between slices occurred and these volumes were discarded from the analysis. A mask was drawn around the liver from a single TE/TI volume (9 slices) and each voxel fitted. For the SE-EPI/GE-EPI data, the signal from the voxels within this mask were fitted for $T_2^*$ using a weighted least squares fit, with 1/TE as the weighting factor to generate a 9 slice $T_2^*$/$T_1$ map. For the IR-EPI sets voxels were fitted to a 3 parameter model for M$_0$, $T_1$ and $T_2$ using a weighted least squares fit, with 1/TE as the weighting factor. For non-zero fitted values displayed as overlay maps. Histograms of $T_2^*$/$T_1$ were generated with a bin size of 1 ms and the peak histogram value, FWHM of the peak and the corresponding upper and lower parameter values of this FWHM were then calculated. For the histogram of $T_1$ data bin sizes of 10 and 20 ms were investigated. To test the reproducibility of histogram analysis a subset of 8 patients were investigated. Three different masks were drawn around each liver on separate occasions and the resulting peak, FWHM and boundary values of the FWHM data were compared. The mean and standard deviation between the 3 maps for each parameter were measured with this standard deviation being quoted as a % of mean.

Results and Discussion: Figure 1 shows an example SE-EPI image and mask, and the generated relaxation maps and the corresponding histograms. The overlay maps are shown for voxels which had a non-zero fit to the Gaussian, and clearly show that most vessels have been eliminated from the histograms $T_2^*$ and $T_1$ maps overlaid (3 slices of 9 slice data set shown). Corresponding histograms (black curve) from the 9 slice data set, and the Gaussian curve fitted to the central peak only (red curve). Colour overlay displays only pixel values where the red curve is non-zero.

Figure 2. Individual subjects peak histogram data, $T_1$ versus $T_2$ (black diamonds) and $T_1$ versus $T_2^*$ (red squares).

Conclusions: This study has shown it is possible to generate $T_2$, $T_2^*$ and $T_1$ maps covering the whole liver in a reasonable acquisition time. Histogram analysis of the relaxation time maps provided a robust method to separate liver tissue from vessels, with the peak histogram data arising from bulk tissue with minimal vessel contamination and the histogram data derived from the data showing minimal dependence on the shape of the mask. Our data shows a spread in measured peak relaxation times in chronic liver disease patients which exceeds the intra-subject variance.


Acknowledgements: This work was funded by a Strategic Funding Initiative from the Biomedical Research Committee at the University of Nottingham.