Measuring T_2 in the liver. A comparison between ^{1}H spectroscopy and SE-EPI

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Introduction

There has been much recent interest in using MRI and MRS to replace liver biopsy to determine liver fibrosis [1], liver iron content [2] and liver fat fraction [3]. An important parameter is the transverse relaxation time, T_2; it can be combined with T_2* to estimate iron content and is used in correcting 1H spectra for T_2 decay when calculating fat fractions [4,5]. It has also been suggested as a parameter for staging liver fibrosis [6,7]. Currently ^{1}H liver spectra are corrected using literature T_2 values taken from MRI studies of bulk tissue, averaged over many individuals [8]. However, if fibrosis and iron content alter the tissue T_2 then it will be necessary to correct clinical spectra on an individual basis. The aim of this study was to compare liver tissue water T_2 measured using 1H spectroscopy with that measured using Spin-Echo (SE) EPI T_2 mapping to determine whether a small number of echo times can be used for the T_2 decay correction in MRS, and to investigate the variation of T_2 in patients with chronic liver disease.

Methods

The study was approved by the local NHS Ethics Committee and all patients gave written, informed consent. Patients (n=18, 13 male) with chronic liver disease confirmed by liver biopsy were scanned on a single occasion using a 1.5 T Philips Achieva scanner with body transmit and 5-element SENSE cardiac coil. MRS ^{1}H spectra were acquired from a 30x30x30 mm^3 voxel (positioned to minimise contributions from large blood vessels) using a varying TE PRESS sequence (90y-(TE_1/2)-180x-(TE_1/2+TE_2/2)-180z-(TE_2/2)-acq) with respiratory triggering (16 spectra at TE=30 ms, 8 at TE=40 ms, 8 at TE=60 ms and 8 at TE=80 ms where TE_1+TE_2=TE and with constant TE_1=10 ms), minimum TR was 3 s. MRI T_2 maps were generated from SE-EPI data (9 slices, 3x3x8 mm^3 voxels, 4mm slice gap, 96x96 image matrix, SENSE 2, SPIR fat saturation). Data were respiratory triggered and acquired during the expiration phase of the breathing cycle (minimum TR 3 s). 3 volumes were acquired at each of 6 TEs (27, 35, 42, 50, 60, 70 ms). Phantom data was also acquired from a 4 quadrant Gd-DTPA doped agar gel phantom which had T_2 vales of 35-90 ms, and T_1 values of 100-700 ms, across the quadrants. Data were acquired using the same protocol as for the liver patients using simulated respiratory triggering to give a TR of 6 s.

Data Analysis

Spectroscopy: All spectra were individually phase- and frequency-offset corrected before averaging spectra from the same TE. Areas under the water (and CH_2 fat peak if in-vivo data) were calculated in Matlab® (Mathsworks Inc, Natick, Mass.). T_2 was then calculated from the linear least squares fit of ln(area under peak) vs. TE.
Imaging: 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 region in a single TE volume (9 slices). All voxels from the SE-EPI data set within this mask were then fitted for T_2 using a weighted least squares fit, using 1/TE as the weighting factor to generate a 9 slice T_2 liver map. A histogram of the T_2 maps was then generated and the peak histogram value (which excludes most blood vessels), and mean T_2 value of the whole liver region (including blood vessels) were then calculated.

Results and Discussion

All patients tolerated the examination well as all the data was acquired under respiratory triggering. Water T_2 measured in liver tissue using SE-EPI and PRESS are shown in figure 1. There is good correlation between the mean MRI data (including vessels) and MRS T_2 data, whereas the MRS systematically measured a longer T_2 compared to the peak (mode) histogram T_2 which reflects solely tissue T_2. There is also significant variation between subjects which may be a result of iron deposition or fibrosis, or a combination of both. However, we are currently blinded to the liver biopsy data and can draw no conclusions about this spread in the data at present. The phantom data (figure 2) showed good correlation between MRI and MRS (R=0.9993); good agreement was found between imaging and spectroscopy for short T_2 (< 50 ms; range similar to liver tissue), however, as T_2 increases there is a trend for the spectroscopy to measure T_2 shorter than imaging. Therefore, the in vivo slight increase in T_2 measured from spectroscopy is most likely due to vessel contamination of the voxel (as reflected by the closer agreement when vessels are included in the estimation of the T_2 parameter). Although every effort was taken to place the spectroscopy voxel away from large blood vessels, the large voxel size of MRS, 30x30x30 mm^3 will result in the 'tissue' sample containing some blood vessels which have a corresponding long T_2 (50-80 ms) which may explain the longer T_2 measured when comparing the MRS T_2 with the peak (but not mean) of the MRI T_2 histogram. The main limitation of this study is that we are unable to compare the T_2 measurements for exactly the same tissue regions as the imaging technique has slice gaps of 4 mm (to cover the whole liver region in 9 slices) and some blood vessels in the T_2 maps appear bright and others dark depending on the orientation of the vessel in the slice. The close correspondence between MRS and MRI also suggests that 4 echo times are sufficient for measuring T_2 using spectroscopy when calculating individual T_2-corrected fat fractions [4].

Conclusions

There is considerable variation in T_2 of the liver of patients with chronic liver disease and therefore liver fat fractions measured using MRS require individual T_2 decay corrections. There is good agreement between liver water T_2 measured using MRS data acquired at 4 echo times and SE-EPI data, suggesting that T_2 can be accurately assessed from multiple TE MRS data (for MRS T_2 decay correction) using just 4 echo times.

References

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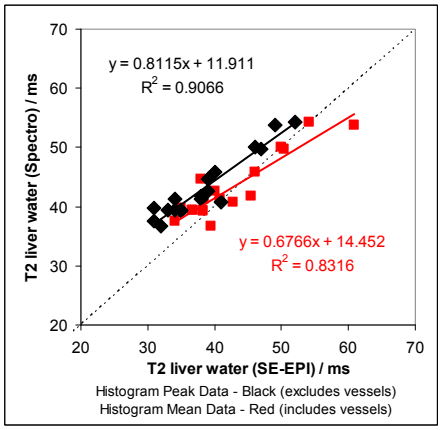

Figure 1. Chronic liver disease patient data comparing T_2 measurements made using MRI and MRS. Dashed line is line of identity.

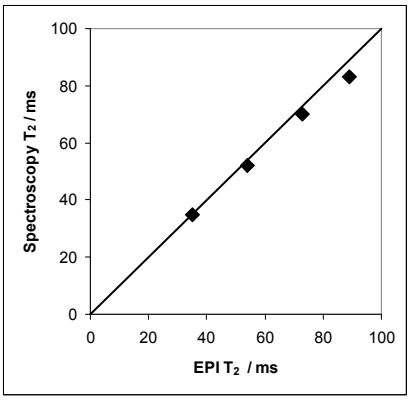

Figure 2. Phantom data comparing T_2 measurements made with MRI and MRS. Solid line is line of identity.