Comparison between 1.5T and 3T Single Voxel 31P MRS of Human Liver in Health and Disease

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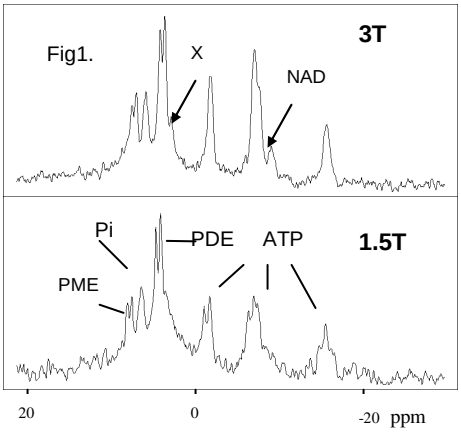
Introduction: With an increasing availability of high-field human MR scanners, the issue of optimal field strength for *in vivo* MR clinical studies has become a focus of discussion. For magnetic resonance spectroscopy (MRS), higher field strength should theoretically be advantageous, because improved sensitivity and chemical shift resolution are expected. To date, there have been few comparisons between 1.5T and 3T MRS measurements in clinical studies[1,2,3]. Those that are in the literature were mostly concerned with proton (^{1}H) MRS in human brain.

Phosphorus-31 (^{31}P) MRS has proved to be very useful in the assessment of chronic liver dysfunction[4] and, in particular, the phosphomonoester (PME) to phosphodiester (PDE) ratio, an index of cell membrane turnover, can provide a non-invasive index of disease severity and response to treatment.

Here we report the results of a direct comparison between single voxel ^{31}P MRS of human liver performed at both 1.5T and 3T in the same subjects using the same methodology. Comparisons were performed in terms of spectral resolution, signal to noise (S/N) of PME and PME/PDE ratios. We also investigated a broad background resonance, originating from immobile phospholipids in cells membranes and vesicle bilayers [5].

Methods: With the approval of local ethics committee, 15 healthy controls (C) and 15 patients (P) diagnosed with chronic liver disease were scanned as a part of a wider study. All MR studies were performed using 1.5T and 3T Philips Achieva^{TM} systems (Best, The Netherlands) both with software version (r2.1). In both scanners the Q-Body coil was used for MR imaging of the liver and a 14cm transmit/receive surface coil was used for ^{31}P MRS. A 7x7x7cm^3 spectroscopic volume of interest (VOI) was placed in the right lobe of the liver using T_1-weighted images in all three orthogonal planes. ^{31}P MR spectra were acquired using an ISIS technique[6] with broadband proton decoupling (WALTZ-4 scheme) [7]. The repetition time (TR=10s) and number of averages (NS=64) were kept the same on both scanners, while the spectral width was 3000Hz and 1500 Hz at 3T and 1.5T respectively. Using a phantom, the sequences were optimized on both scanners to ensure the same frequency profiles across the spectral width. Spectra were analysed in the time domain using the MRUI package (www.mrui.uab.es). Two approaches were used: one with the AMARES[8] algorithm, and one using QUEST[9]. For AMARES, the PME resonance was modelled by two components: phosphocholine (PC) and phosphoethanolamine(PE),while the PDE resonance was modelled by glycerophosphocholine (GPC) and glycerophosphoethanolamine (GPE) (see Figure 1) with prior knowledge as previously described[10]. Truncation of initial points (corresponding to 1.92ms) was applied to remove the broad component. For QUEST, inorganic phosphate (Pi), PE, PC, GPC, GPE, and adenosine triphosphate (ATP) were simulated with the NMR-SCOPE tool[11]. Here, the broad component was estimated and subtracted from the raw data in the procedure as previously described [7]. The signal from the broad component was divided by the total signal from the mobile metabolites and the area integrated.

Results: Examples of ^{31}P MR hepatic spectra at the two field strengths are shown in Figure 1. At both fields, PC, PE, GPE and GPC are resolved in the PME and PDE resonances, owing to ^{1}H decoupling. Improved spectral resolution at 3T is evident in two further resolved resonances: the NAD peak and an additional peak, X (most likely originating from biliary phospholipids), however the splitting in ATP looks smaller as J-coupling is field independent. The table presents results for the mean S/N measured for all subjects, the PME/PDE ratios with the mean (SD), for the (C) and (P) groups estimated with two analysis techniques. At both field strengths and with both analysis techniques, there was a significant increase in PME/PDE in the P, compared to the C group. Also PME/PDE ratios appear to be higher at 1.5T ($p<0.02$ and $p< 0.05$ paired t-test) in both P and C groups respectively with QUEST analysis, while for AMARES it was only significant for the P group. There was a good correlation between PME/PDE values in the P group, measured at both field strengths (correlation coefficient r=0.806 (AMARES) and r=0.735 (QUEST)). Background signal relative to total signal from mobile metabolites appeared to be slightly lower at 3T by ~14%.



B_0	S/N	PME/PDE (AMARES)		PME/PDE(QUEST)	
		Healthy controls	Chronic liver disease	Healthy controls	Chronic liver disease
1.5T	4.3	0.390(0.064)	0.500 (0.139) p<0.001	0.410 (0.055)	0.508 (0.116) p<0.01
3T	5.2	0.352(0.086)	0.456 (0.112) p<0.01	0.379 (0.057)	0.455 (0.059) p<0.01

Discussion and Conclusions: ^{1}H decoupling in ^{31}P MR spectra improved resolution at both field strengths (particularly PME and PDE resolution into their components). Further improvement in resolution was evident at 3T. There was an improvement in S/N (~21%) at 3T. There was a good correlation between the two field strengths, but a small difference in PME/PDE ratios between 1.5T and 3T using the paired test. The analysis methods used influenced the calculated ratios. The reduced broad hump at 3T may be related to line-broadening of phospholipids bilayer signal at higher fields, as previously described [5]. Further investigation of the broad hump and its clinical importance is still needed.

References: 1 Kantarci et.al Am.J.Neurorad.2003,24:843 2.Ethofer et.al MRM 2003,50,1296 **3.**.Baker P et.al.MRM 2001, 45,765; **4**.Lim AK et al Hepatology 2003:37:788; **5**.Murphy et al. MRM 1989;12:282;**6**.Ordidge et al MRM 1988;8:323 **7**.Widmaier et al.MRI 1998; 16 845 **8**. Vanhamme L et al JMR 1997,129 :35. **9**.Ratiney et al NMR Biomed 2005:18:1 **10**. Hamilton et al.NMR in Biomed 2003;16:168.**11** Graveron-Demilly et al . JMR 1993 A101:233 **Acknowlegements** Authors would like to acknowledge Dr Bill Vennart for helpful discussion and support.