Does using a 16-element receive-array improve whole-liver ^{31}P metabolite ratio quantification at 7T?

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PURPOSE: Liver biopsy is invasive; it can produce pain and bleeding; and it has an undesirable sampling variability[1, 2]. This variability is evident, for example in studies of paired biopsies for chronic Hepatitis-C[1, 2] and has been blamed for causing "substantial misdiagnosis and staging inaccuracies" in non-alcoholic fatty liver disease (NAFLD)[3]. Liver metabolites containing ^{31}P have potential value as markers for staging many diseases of the liver, particularly NAFLD[4] and cirrhosis[5]. Nevertheless, the use of ^{31}P-MRS to quantify these metabolites has hitherto been limited by low signal-to-noise ratios (SNRs). Increasing field strength to 7T has been shown to improve SNR for ^{31}P-MRS in the liver[6] and to allow resolution of the PME and PDE peaks without ^{1}H decoupling. Receive arrays give better coverage and SNR than single-loop coils, but have not yet been used for ^{31}P-MRS in the liver at 7T. The aim of this abstract is to test whether the increased SNR from a receive array at 7T can be used to improve quantification of ^{31}P-MRS metabolite ratios in the liver.

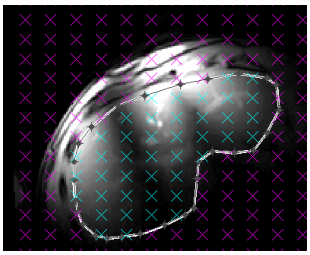

Figure 1: An example of a hand-drawn ROI superimposed on a typical ^{1}H localizer. The crosses show CSI voxel positions ('x' excluded and 'x' included).

METHODS: *Data Acquisition:* A 3D UTE-CSI sequence[7] was used to acquire liver spectra from 5 normal volunteers (4 male, 1 female, 25.8 ± 4.7 years, 77.2 ± 10.9 kg, recruited with ethical approval) using WSVD combination[8], a 16×16×8 matrix, acquisition weighting, 10 averages at k = 0, and a 1s T_R, giving a total acquisition duration of 28min. The excitation pulse covered all metabolites from phosphocholine (PC) to uridine diphosphoglucose (UDPG). One BISTRO saturation band was used to suppress skeletal muscle. Transverse and sagittal ^{1}H FLASH stacks of images were used for localization. Fiducial markers on the array were used to compute per-subject B_1^+s for saturation correction.

Data Processing: A region of interest (ROI) was drawn in each slice to select liver voxels (Fig. 1). Each liver voxel spectrum was fitted independently using linewidth-constrained AMARES[9] (Fig. 2) and corrected for partial saturation using literature T_1 values[10]. Any voxels having significant contamination from skeletal muscle (i.e. PCr > 0.3 × γATP), or bile (i.e. phosphatidylcholine peak > 0.5 × γATP), or poor quality spectra (γATP SNR <5) or where fitting failed (R^2 < 80%) was excluded from further analysis. In each subject, 10-44 "good" voxels of nominal volume 6.3mL each were obtained. The metabolite ratios in Table 1 were then computed.

RESULTS: The mean and standard deviation (SD) for several ratios that have been shown to be markers in NAFLD are shown in Table 1, together with corresponding literature values obtained with a single-element coil at 3T[4].

Mean Values: Glycerophosphorylcholine / total ester (GPC / TE) and gamma adenosine triphosphate / total phosphate (γATP / TP) are both higher in this study than reported by Abrigo et al. The consistency of the individual subjects can be seen when their values are plotted as a stacked histogram (see Fig. 3).

	PME/PDE	GPC/TE	PE / TE	γATP / TP
7T (N = 5) (this study)	36.4 ± 6.94	44.4 ± 3.93	12.6 ± 3.58	18.5 ± 1.04
3T Abrigo et al.[4] (N = 19)	41.67 ± 13.70	30.46 ± 6.31	15.42 ± 5.08	15.49 ± 2.76

Table 1: Comparison of liver 31P-MRS data quality at 3T and 7T. Total Ester (TE) is [PME] + [PDE], and total phosphate (TP) is the sum of all the phosphate peaks seen in the spectrum.

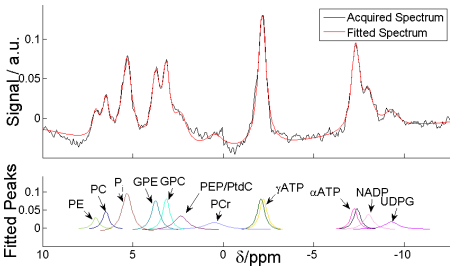

Figure 2: A typical liver spectrum and its linewidth-constrained AMARES fit.

Data Quality: The inter-subject SDs in this study are the smallest reported in the literature. However, the acquisition time was longer than the most protocols in the literature. We also compared the Cramér-Rao Lower Bounds (CRLBs) for the metabolite ratios from the fitting. Literature CRLBs using a 10cm loop at 7T for γATP amplitude are: 10.3% with 3D-CSI, 7.6% with 3D-ISIS[10]. Even including time-correction, the CRLBs in this study are significantly lower at 1.49% (P<0.01). This suggests that the receive array does indeed increase the sensitivity for liver ^{31}P-MRS.

DISCUSSION: The most important factor in the variation of number of usable voxels is subject size. The metabolite ratio CRLBs are greater than those of the individual peaks, as would be expected from propagation of error, especially for low SNR peaks. The intra-subject metabolite ratio coefficients of variation (CoVs) are greater than the mean CRLBs for every subject (Table 2). This suggests that there may be genuine physiological variation across the liver.

CONCLUSION: Using a 16-element receive array at 7T increases the precision of spectral quantification in individuals by 46% compared to values reported with a 10cm loop in (10). The use of a spatially-resolved method such as 3D UTE-CSI rather a single voxel spectroscopy sequence shows potential for evaluating focal disease and exploring heterogeneity (see Fig. 3 and Table 2). Metabolite quantification is consistent with the values at 3T, and confirms previous findings that ^{1}H-decoupling is not necessary at 7T. This work will be useful in future studies investigating metabolism in the diseased liver.

	γATP	PME/PDE	GPC/ [PME + PDE]	PE/ [PME + PDE]	γATP / TP
Mean Percentage CRLB	1.49	10.8	4.54	14.9	5.89
Mean Intra-subject CoVs	-	15.9	9.55	24.0	15.6
Inter-subject CoVs	-	19.1	8.8	28.5	5.61

Table 2: Mean Percentage Cramér-Rao lower bounds (CRLBs) and coefficients of variation (CoVs). γATP amplitudes have not been corrected for receive sensitivity, so they cannot be compared directly between voxels or between subjects.

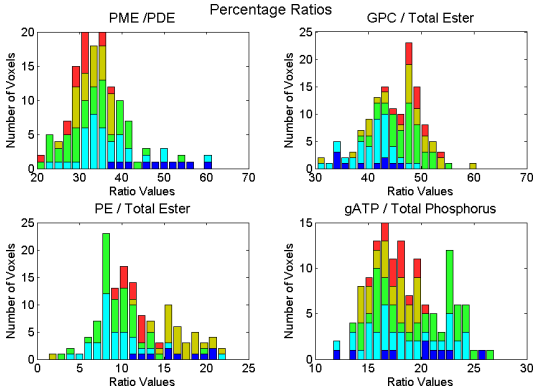

Figure 3: Stacked histograms of selected metabolite ratios. The data for each subject is plotted in a different colour.

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ACKNOWLEDGEMENTS: Funded by the Wellcome Trust and the Royal Society [098436/Z/12/Z] and the Medical Research Council. SN is supported by the Oxford NIHR Biomedical Research Centre.