Getting more out of ^{31}P MRS of the human liver moving from 1.5T to 3T

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Introduction

At high fields, ^{31}P MRS is a powerful tool to study liver metabolism in-vivo (1-3). In spite of the potential of ^{31}P MRS for assessment of any disease that has an impact on the liver energy metabolism ^{31}P MRS has not gained much foothold as a clinical application. One of the reasons is that the more detailed metabolic information available with ^{31}P MRS in animal studies at higher fields is not accessible at the lower field strengths of most clinical MR scanners. In human subjects at 1.5T, even with ^{1}H-decoupling, the phospho-monoester (PME) signals, consisting of phospho-choline (PC) and phospho-ethanolamine (PE) are usually not resolved (2,3). Moreover, nicotinamide-adenine dinucleotide (NAD) and uridine 5'-diphosphate (UDP) are seldom separately quantifiable at 1.5 T because NAD and α-ATP signals are not resolved and the UDP signal intensity is too low.

The goal of our study was to compare ISIS-localized and ^{1}H-decoupled ^{31}P MR spectra recorded with nearly identical acquisition parameters and localized volume at 1.5T and 3T. Our aim was to achieve a high compatibility between the data at the two field strengths and to improve quantitation of detected metabolites at 3T.

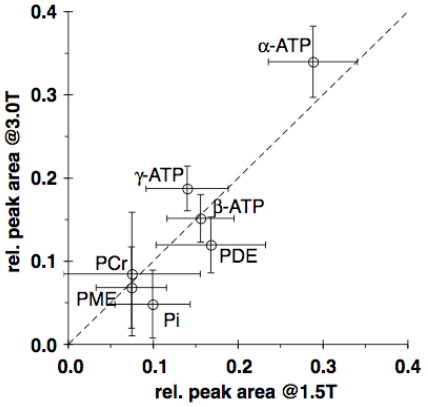

Fig 1 *Metabolite peak areas over total phosphates: means and SD 3T vs 1.5T*

Methods

Eleven adult subjects (5 healthy and 6 obese patients with type 2 diabetes enrolled in the Look AHEAD trial at Johns Hopkins) were examined with 1.5T Intera and 3T Achieva Philips scanners on the same day with no more than three hours between the two exams. A 14 cm Tx/Rx ^{31}P surface coil was placed laterally over the right liver lobe. After acquiring localizer images, ^{1}H-decoupled (0.7W), 5x5x6cm^3 ISIS-localized, ^{31}P spectra were recorded with TR=4s and 128 averages. At 3T localized second order shimming was applied based on an acquired field map and ISIS pulses were 10ms optimized adiabatic inversions with 6kHz BW. The voxels were carefully positioned to be as much alike in the 1.5T and 3T as possible. MRS data from both 1.5T and 3T were analyzed with CircleFIT (4). The 3T data were also analyzed with an eighteen peak fit using Amares (5,6). Chemical shift values were referenced to the γ-ATP signal (-2.36ppm). Intracellular pH was calculated from the γ-ATP-Pi and α-ATP-Pi chemical shift differences (7).

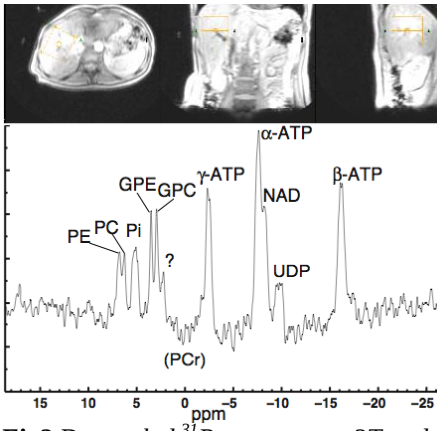

Fig2 *Decoupled ^{31}P spectrum at 3T and three plane scout*

Results and discussion

Relative signal intensities (normalized to total phosphorus signal) of same day studies on 1.5T and 3T are shown in fig.1. Significant differences (unpaired t-test $p<0.05$) in relative peak areas between 1.5T and 3T were observed for α–,γ– but not β-ATP, also for PDE, Pi but not for PME. A 3T liver spectrum is shown in fig. 2. Absence of the PCr signal confirms localization within the liver tissue. All spectra showed the UDP signal, not readily detected at 1.5 T. At 3T, quantitation with Amares of PE, PC, Pi, GPE, GPC, UDP, NAD, and γ-, α-, and β-ATP resonances was possible in all subjects. A very small amount of PCr was found in two subjects. Fig. 3 shows the detected signal at 3T for all subjects as peak area (normalized to total ATP area) vs. chemical shift (using γ-ATP as a reference at -2.36ppm). While a reliable evaluation of intracellular pH at 1.5T was difficult due to low resolution of the spectra, calculation of pH at 3T was feasible in 10 subjects using the chemical shift difference of Pi to γ-ATP (7.56±0.05, pH = 7.32±0.05), or Pi to α-ATP (12.67±0.08, pH = 7.33±0.09). The 3T spectra substantially improved on the results published earlier for 1.5T (3) and quantification of NAD, UDP and individual PME peaks now seems feasible. Also of great importance is the very tight range found for the Pi chemical shift difference with γ-ATP. This enables a far more reliable determination of intracellular pH in liver.

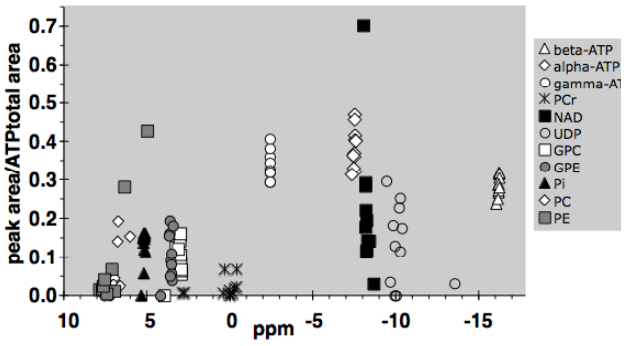

Fig 3 *Fitted peak areas versus chemical shift. Shift corrected to γ-ATP=-2.36ppm, area rel. to total ATP.*

References

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