Whole Liver 31P Metabolite Mapping with 3D CSI

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Introduction

It has been shown that 3D ^{31}P CSI sequences can be used to enhance spatial coil coverage of the single-channel coil to aquire 3D ^{31}P spectrscopic data [1]. Furthermore, multi-channel ^{31}P phased-array coils can be used to acquire data from the entire abdominal slice using a 2D CSI sequence [2]. If the coil is large enough to wrap around the entire liver, 3D MR spectroscpic data can also be aquired for the entire liver by combining these two methods. However, lack of such coils and long scan times (long TR and large averages) for ^{31}P spectroscopy have prevented the acquition of such data in the past. In this abstarct we present ^{31}P in-vivo MRSI data collected from the entire liver using a 3D CSI sequence, allowing for whole liver metabolite mapping for the first time.

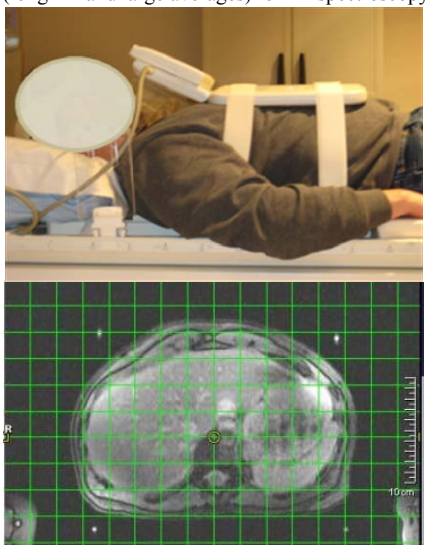

Figure 1: Coil coverage and Setup. Bright spots from the water filled fiduciary markers show the physical coil coverage.

Materials and Methods

In-vivo 3D spectroscopic data were acquired on a phantom and a healthy volunteer on a Siemens TIM Trio whole body scanner (Siemens Healthcare, Germany) using a dual tuned ^{31}P/^{1}H 8-channel phased array coil [1] and a 3D CSI-FID pulse sequence (TR/TE: 1000 ms/2.3 ms, bandwidth: 5000 Hz, 2048 data points/4096 with oversampling). A 400 mm x 400 mm x 200 mm field of view (FOV) was phase encoded to 16 x 16 x 8 matrix resulting in a nominal voxel size of 2.5 cm x 2.5 cm x 2.5 cm (15.625 cm^3). Weighted averaging (12 averages) and a100% Hamming filter were applied, for a total acquisition time of about 30 minutes. 3D volume data were segmented into 8 slices and corrected for coil sensitivity variations using the method described in [3]. Metabolite concentrations were quantified in jMRUI [4] using the AMARES algorithm in MRSI mode.

Results

Figure 1 shows the coil coverage and setup and 1H axial image of the subject acquired with the dual-tuned coil. Water filled fiduciary markers, which are wrapped around the coil perimeter, show up as bright dots on the corner of the images. These markers are used during the analysis to verify the extent of coil coverage. Figure 2 shows the ^{31}P spectroscopic data obtained for one of the 2D slices from the 3D MRS acquisition. Notice that no signal is seen in the voxels outside the bright spots because the bright spots correspond to the physical extent of the coil. Figure 3 shows the metabolite maps for 31P metabolites obtained for the entire liver. As expected the signal is strongest in slices centered on the liver and falls off as we move away. Furthermore, it can be seen that PCr mainly originates from muscle tissue, while Pi, alpha-ATP, and gamma-ATP are highly concentrated in the liver and spleen. A significant drop in the SNR observed for the slices close to the abdomen and heart because of signal loss from breathing.

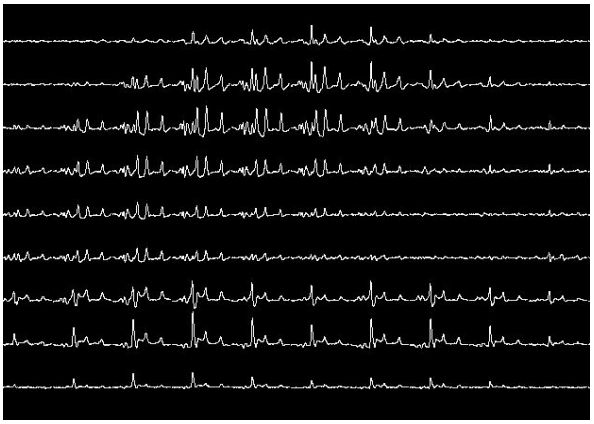

Figure 2: ^{31}P spectroscopic data is obtained from one slice of the 3D MRSI

Discussion

Original scan time for full 3D CSI data acquisition was well over an hour, which was reduced to 30 minutes by using weighted averaging. A 100% Hamming acquisition filter was applied to reduce side lobe amplitudes and minimize PCr signal leakage into liver voxels . The above results clearly show that a multi-channel ^{31}P coil enables quality spectra to be obtained from the entire liver in a single scan session. The acquisition time for the 3D data (~ 30 min, 12 weighted averages) is comparable with the acquisition time of a 2D CSI scan (~25 min, 30 weighted averges), yet the increase in volume (slices) and quality (SNR) of data acquired are increased by approximately eight and two fold, respectively. Implementation of GRAPPA data acquisition with 3D acquisition is currently being investigated, which may enable further reductions in scan time while maintaining acceptable levels of SNR [4].

References: [1] Chemlik M, AI Schmid, et. al., Magn Reson Med 2008; 60(4):796-802; [2] Panda A et. al., Proc. ISMRM, 2009; [3] Panda A et. al., Proc. ISMRM, 2010; [4] Vanhamme, L, et. al., J. Magn Reson., 1997;129:35-43; [5] Stefan D, et. al., MAGMA, 370, 15, 2002; [6] Raghavan RS et. al., Proc. ISMRM, 2009.

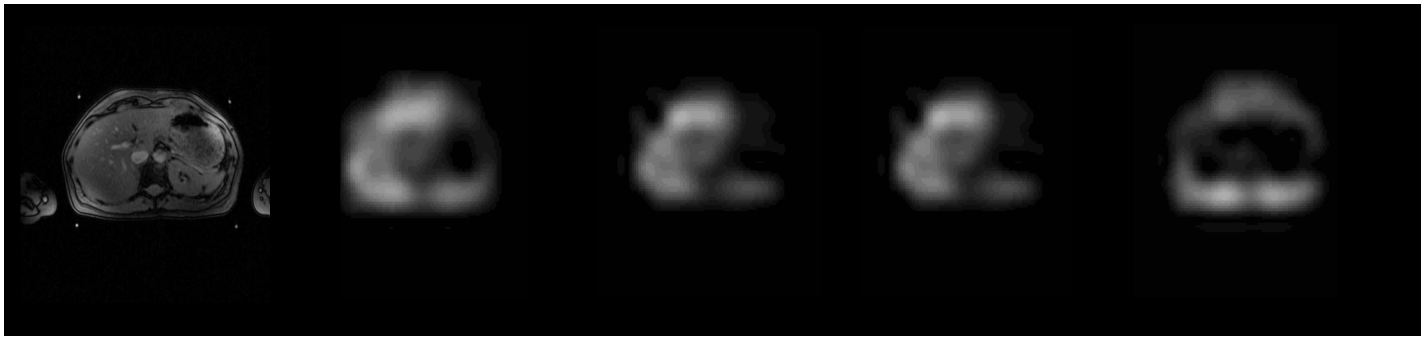

Figure 3: Metabolite Maps for β-ATP, α-ATP, □-ATP, and Phosphorcreatine