Accelerated In-vivo Liver ^{31}P MRSI using GRAPPA

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Introduction: Regional changes in ^{31}P metabolite concentrations can be assessed across the whole liver using a multi-channel phased-array ^{31}P coil [1]. However, due to the lower sensitivity of ^{31}P nuclei in-vivo (low abundance and smaller gyromagnetic ratio) compared to ^{1}H, ^{31}P magnetic resonance spectroscopic imaging (MRSI) acquisition requires significantly longer scan times. Applying fast MRSI techniques based on fast k-space sampling to ^{31}P MRSI is challenging due to the short T_2 relaxation times of ^{31}P metabolites and the necessity to sample a large bandwidth. Parallel imaging techniques are another attractive approach to fast MRSI and have proven successful for acceleration of ^{1}H MRSI [2,3]. Furthermore, the potential of implementing GeneRalized Autocalibrating Partially Parallel Acquisitions (GRAPPA) [4] for ^{31}P MRSI has been shown with a high concentration ^{31}P phantom [5]. The aim of this work was to investigate the feasibility of accelerating in-vivo ^{31}P MRSI of the human liver using GRAPPA for clinical studies.

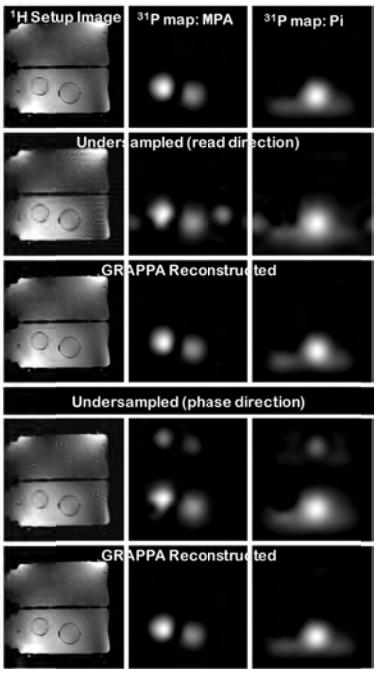

Figure 1: ^{31}P phantom MRSI with weighted, read and phase direction undersampled, and weighted GRAPPA acquisition

Methods: A dual tuned 8-channel ^{31}P/^{1}H coil was used for ^{31}P MRSI on a 3T whole body MRI scanner (MAGNETOM Trio, A Tim System, Siemens Healthcare, Germany). For the phantom validation experiment a stacked setup of two 10 liter plastic carboys was used. The top carboy was filled with a uniform solution of 10 mM potassium phosphate monobasic (Pi) solution and the bottom carboy was filled with a 25mM Pi solution. The bottom carboy also contained two plastic spheres filled a) with 300 mM methylphosphonic acid (MPA) and b) with 100 mM MPA plus 200 mM Pi solution. The in-vivo data were acquired from a healthy volunteer (male, 27 yrs).

The following parameters were used for both phantom and in-vivo data acquisition using a slice-selective MRSI sequence: TE 2.3 ms, TR 1 s, FOV 400x400x30 mm^3, nominal voxel size 25x25x30 mm^3. Each FID was acquired with 2048 points and a bandwidth of 5000 Hz. The normal weighted acquisition took 25.75 min for 30 weighted averages. For the GRAPPA acquisition, undersampling was performed for only one phase-encoding direction at a given time and took 15.17 min for 30 weighted averages. A 2x1 or 1x2 (depending on the undersampling direction) GRAPPA kernel was used to generate the weights for reconstruction. A central calibration region of 3x5 voxels (undersampling in phase encoding direction) or 5x3 (undersampling in readout direction) was retained for computing the coil weights. Data acquired by the top and bottom coil plates were reconstructed separately.

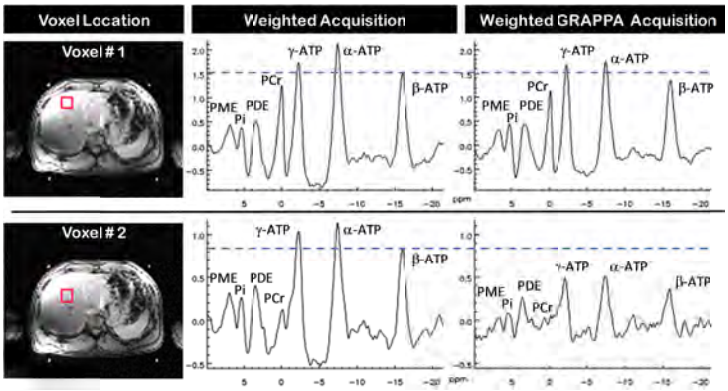

Figure 2: In-vivo liver ^{31}P spectra from two voxels acquired with weighted 2D MRSI and weighted GRAPPA MRSI (phase-direction undersampling).

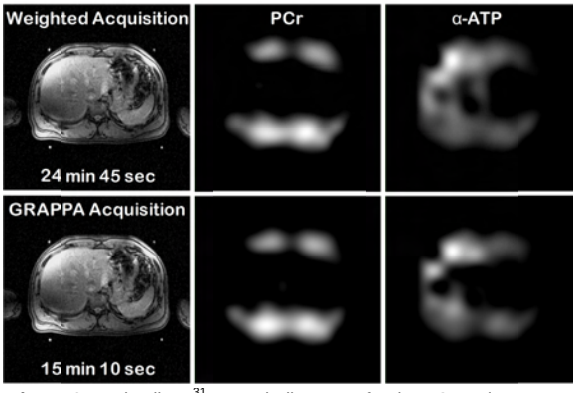

Figure 3: In-vivo liver ^{31}P metabolite maps for the PCr and α-ATP metabolites obtained from weighted acquisition and weighted GRAPPA acquisition.

Results/Discussions: Figure 1 shows the phantom setup and ^{31}P MRSI maps of two metabolites (Pi and MPA), showing that the GRAPPA reconstruction was able to remove aliasing. Figure 2 shows in-vivo ^{31}P spectra from two voxel locations in the liver acquired with a weighted 2D MRSI acquisition and a weighted GRAPPA acquisition (phase-direction undersampling). The dotted line denotes the amplitude of the β-ATP peak in the conventional acquisition. Figure 3 shows the PCr and α-ATP metabolite maps for an axial liver slice obtained from the same in-vivo conventional and GRAPPA acquisition. The ^{1}H images in the figure are provided as anatomical reference. It can be observed from both figures 2 and 3 that the GRAPPA reconstruction algorithm was able to reconstruct the in-vivo data with minimal loss of SNR for voxels close to the coil plates. However, more signal loss can be observed for voxels farther away (deeper in the liver). No aliasing was observed in the GRAPPA reconstructed images or spectra.

Conclusion: Acceleration of ^{31}P in-vivo liver MRSI is feasible using GRAPPA reconstruction. Successful implementation of ^{31}P GRAPPA MRSI on the scanner has allowed reducing the scan time of 2D ^{31}P MRSI data across a whole liver slice from 25.75 min to 15.17 min. A detailed SNR analysis has yet to be performed to investigate limitations of further acceleration. Future work also includes extending the GRAPPA acceleration implementation to a 3D MRSI protocol.

References: [1] Panda A et al., Proc. ISMRM 2009, 17:475; [2] Dydak U et al., MRM 2001, 46(4):713-22 ; [3] Breuer F et al., Proc. ISMRM 2006, 14:3653; [4] Griswold MA et al., MRM 2005, 54:1553-56; [5] Raghavan RS et al., Proc. ISMRM 2009, 17:4317

Acknowledgements: The authors would like to thank Siemens-IU pilot project grant for support.