

## Short-echo spin-echo localization MRSI in gliomas at 7 Tesla

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### Introduction

The availability of MR scanners with a field strength of 7 Tesla offers the potential of higher SNR and better spectral resolution, which can be used to improve the spatial resolution or detection of J-coupled metabolites such as mI, Glu and Gln. The most widely used method for localizing *in vivo* 1H MRSI to a specific region of the body is PRESS. This is based on RF pre-selection of a volume-of-interest (VOI), which is important for avoiding contamination of water and lipid that originate outside the VOI. Although the PRESS volume selection is beneficial in terms of eliminating unwanted signals, it results in field-dependent spatial variations in metabolite ratios on the edges of the selected volume and is susceptible to inhomogeneities in the B0 and B1 magnetic fields. An alternative spectral localization method that uses a spin-echo (SE) sequence [1] for a single slice excitation offers higher SNR and shorter TE. The purpose of this study was to implement short echo MRSI using spin echo localization at 7 Tesla in patients with gliomas.

### Methods

All MR studies were performed using a commercial 8-channel receive-only array with a volume transmit head coil (NOVA Medical, Wilmington, MA) on a GE Excite 7T scanner (GE Healthcare, Waukesha, WI). A standard phantom (3 mM Cho, 3 mM Cr, 12.5 mM NAA, 12.5 mM Glu, 8 mM ml and 5 mM Lac), 2 healthy volunteers and 2 patients with gliomas were scanned. Anatomical imaging consisted of a T1-weighted sagittal scout, T2\*-weighted gradient recalled echo (GRE), and T2-weighted fast spin echo (FSE). The 2D H-1 MRSI was localized using the spin echo sequence for slice selection with TE/TR = 30/2000 ms, spectra array = 20x20, FOV = 20 cm and the effective slice thickness after application of the VSS being 10 mm. The nominal voxel size was 1 cm<sup>3</sup>. Six graphic prescribed VSS pulses were applied adjacent to the subcutaneous lipid layer for suppression (Figure 2). The total acquisition time was 13 min. The spectral data was acquired with 2048 spectral points and 5000 Hz spectral width. The 8 channels of data were combined and processed as described previously [2], and then quantified using LCModel. Metabolite signals for the basis set, which included Cho, Cr, NAA, Glu, Gln, ml and Gly, were generated using GAMMA simulations with prior knowledge of chemical shift and J-coupling.

### Results

Figure 1 illustrates the result of 2D MRSI data acquired from a phantom without outer volume suppression. With mean±standard deviation of 0.82±0.13 for Cho/NAA (147 voxels), the spectra were markedly uniform in the spectral array. *In vivo* MRSI data were obtained with good quality over the entire spectral array. An example of MRSI data from a healthy volunteer is given in Figure 2. Noted that the baseline was not removed in the spectra. Figure 3 shows the MRSI data before and after quantification using LCModel from a glioma patient. The lipid contamination was observed on the edge of FOV.

### Discussion

Improving the sensitivity of MRSI and increasing the number of metabolites that can be assessed using ultra high field scanners would be an important advance for evaluating patients with glioma. This study has successfully demonstrated a short echo spin echo MRSI acquisition at 7 Tesla and applied it to volunteers and patients with gliomas. Very spatially selective suppression pulses were used to suppress contamination from subcutaneous lipid. We will incorporate fast spectroscopic imaging techniques, such as flyback trajectories, SENSE and GRAPPA into the sequence in order to shorten the total acquisition time and to provide greater coverage in the slice dimension. This method could be applied in a larger study of patients with gliomas to assess whether it provides additional information compared to the conventional MRSI acquisitions at 3T and 7T.

### References

1. Otazo, R., Magn Reson Med, 2006;56(6):1200-10;
2. Nelson, SJ. Magn Reson Med, 2001;46(2):228-39.

### Acknowledgements

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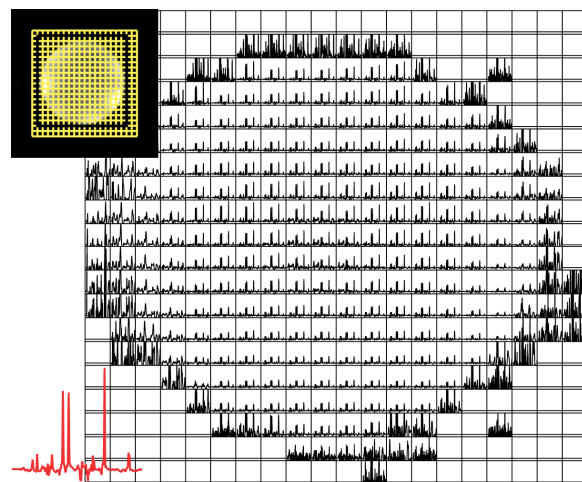


Figure 1. MRSI data from a phantom without OVS

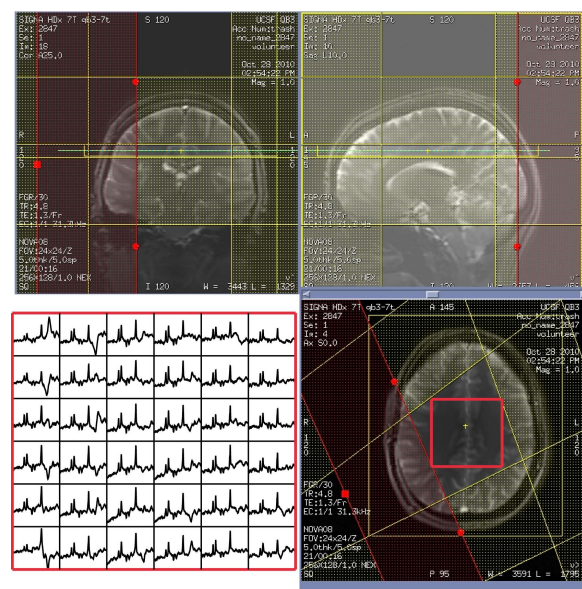


Figure 2. MRSI data (with baseline) corresponding to the location from a healthy volunteer.

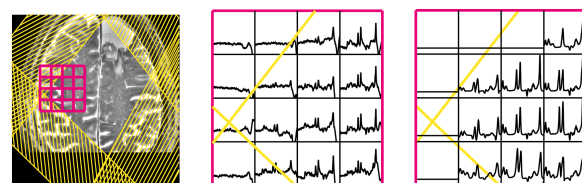


Figure 3. MRSI data with baseline (middle) and quantified using LCModel (right) corresponding to the image (left) from a patient with glioma.