Spectroscopic Imaging of Glycine of Human Brain at 7.0 T

Sandeep K Ganji[1,2], Abhishek Banerjee[1], Elizabeth Maher[3,4], and Changho Choi[1,2]

[1]*Advanced Imaging Research Center, University of Texas Southwestern Medical Center, Dallas, Texas, United States,* [2]*Radiology, University of Texas Southwestern Medical Center, Dallas, Texas, United States,* [3]*Internal Medicine, University of Texas Southwestern Medical Center, Dallas, Texas, United States,* [4]*Neurology and Neurotherapeutics, University of Texas Southwestern Medical Center, Dallas, Texas, United States*

INTRODUCTION

Glycine (Gly) is an inhibitory neurotransmitter and its abnormal levels have been observed in several brain disorders like gliomas [1-4]. Major difficulty for *in vivo* detection of Gly arises from the presence of overlapping complex signal from myo-inositol (mIns). We present a spectroscopic imaging (SI) method of *in vivo* Gly imaging at 7T. Preliminary results from healthy and brain tumors subjects are reported.

METHODS

To discriminate Gly from mIns, we performed density matrix simulations of PRESS, incorporating the 90˚ and 180˚ slice-selective RF pulses and gradient profiles. Based on these simulations subecho times of TE_1 = 100 and TE_1 = 50 ms (total TE = 150 ms) were obtained [5]. Pixel localization was performed applying phase encoding gradients within the PRESS sequence. A single PRESS-prescribed slab (VOI) was positioned along the transverse direction to cover the region of interest with a spatial resolution of 10 x 10 mm^2 and slab thickness of 15 mm. Typically a 200 x 160 mm^2 field of view (FOV) in the phase encoding directions was used for acquisition. Number of averages was set to 2; spectral width of acquisition was 5000 Hz and 2048 complex points per FID. Outer volume suppression bands (REST slabs) were placed in the subcutaneous regions to minimize the lipid signal contamination from brain meninges. The PRESS RF carrier was set to 3.55 ppm (Gly resonance) to avoid chemical artifacts in Gly estimation. On average VOI covered 90 x 80 mm^2, which was positioned to cover the central brain regions in healthy volunteers and/or FLAIR enhancing regions in brain tumor patients. Written informed consent was obtained from subjects before scans. To reduce the acquisition times on the scanner only 70% to 80% portion of the k-space is acquired around the center of the k-space, while rest of points were zero filled. The residual water suppression was performed using HL-SVD algorithm in jMRUI [6]. Water SI was also acquired under similar conditions and used to minimize the eddy current artifacts. Frequency drift and eddy current correction was performed on individual spectra using in-house custom programs in Matlab. An exponential filter of 3Hz was applied prior to Fourier transformation, which removed artifact signals at the end of FID's and increased the SNR without compromising the spectral resolution. The time domain data was zero filled to 4096 points. LCModel [7] was used for metabolite estimation using basis sets created with published chemical shift and coupling constants [8]. Metabolite concentrations were estimated with reference to Cr of 8 mM in normal-brain gray matter.

RESULTS AND DISCUSSION

Fig. 1 displays SI spectra from the healthy volunteer. The spectral pattern observed was consistent with the reported simulated spectrum at TE = 150 ms [5]. The mean Gly over the entire brain was estimated to be 0.6 mM, in agreement with the previous studies [5]. Figure 2 shows the axial images and spectra from a glioblastoma (GBM) patient. The spectra from normal brain region in figure 2 are similar to those in figure 1. In a GBM patient, the Gly concentration was found to be high up to ~5 mM (spectra 4-6, figure 2), with CRLBs less than 5%. A Gly estimate of ~0.7 mM was obtained from non-FLAIR regions (spectra 1 and 2, figure 2), with CRLBs less than 10%. Figure 3 shows Gly and choline (Cho) concentration maps for the region shown in figure 2. The map shows the elevated Gly in the tumor region clearly. In conclusion, the optimized-TE SI method can be used for obtaining the regional distribution of abnormal Gly levels in disease conditions.

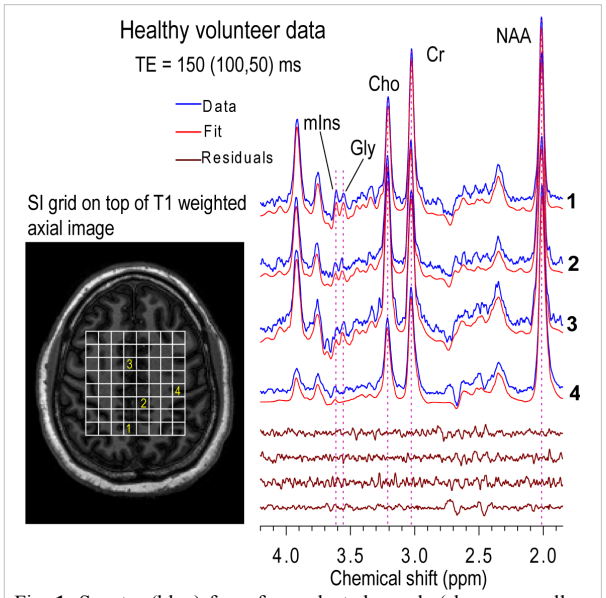

Fig. **1**: Spectra (blue) from four selected voxels (shown as yellow numbers) along with LCModel fits (red) and residuals (brown).

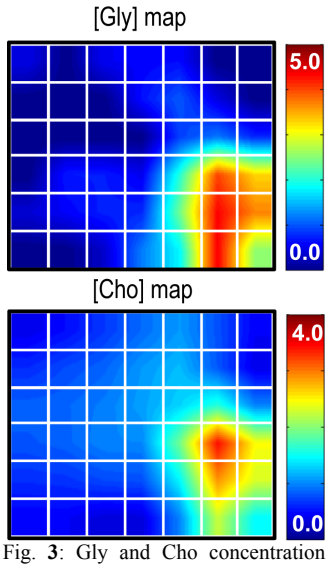

Fig. **3**: Gly and Cho concentration maps of SI data from patient shown in figure 2.

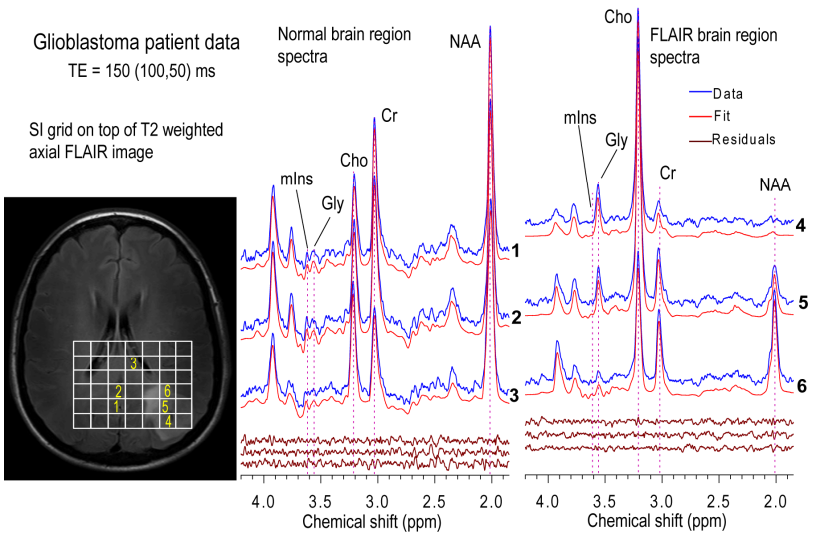

Fig. **2**: Spectra (blue) from six selected voxels (shown as yellow numbers) along with LCModel fits (red) and residuals (brown). Spectra 1 through 3 are from normal brain region and show mIns and Gly signals similar to figure 1 spectra. Spectra 4 through 6 are from tumor region, showing elevated Gly signal at 3.55 ppm.

ACKNOWLEDGEMENTS

This study was supported by *NIH CA159128* and *MH093959*, and *CPRIT RP101243*.

REFERENCES

1. Hattingen E *et al*. MAGMA 2009;22:33-41. **2**. Bruhn H *et al*. NMR Biomed 1992;5:253-258. **3**. Davies NP *et al*. NMR Biomed 2010;23:80-87. **4**. Ganji S *et al*. ISMRM 2011. Montreal. p. 3329. **5**. Choi C *et al*. Magn Reson Med 2009;62:1305-10 **6**. Naressi A. *et al*. MAGMA 2001;12:141–152. **7**. Provencher SW Magn Reson Med 1993;30:672-679. **8**. Govindaraju V *et al*. NMR Biomed 2000;13:129-153.