# Regional difference in glycine concentrations in human brain as measured by 1H-MRS at 7T in vivo

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## INTRODUCTION

Glycine (Gly), an inhibitory neurotransmitter and coagonist at excitatory N-methyl-D-aspartate receptors in the human brain, may be associated with several neuropsychiatric disorders [1,2]. Although the Gly concentration in the human brain is not very low (0.5 – 1 mM), detection of the Gly singlet at 3.55 ppm is not straightforward primarily due to the spectral overlap with *myo*-inositol (mIns), which is present at much higher concentrations. Recently, a PRESS (point-resolved spectroscopy) acquisition strategy at 7T has been reported for differentiation between Gly and mIns in the human brain [3]. Here, we report an *in vivo* result from the prefrontal and left frontal brain regions, obtained with the reported method. The preliminary data indicate that regional difference in Gly levels may exist in human brain.

## METHODS

An *in vivo* $^1$H-MRS study was carried out on a whole-body 7T scanner (Philips Medical Systems, Cleveland, OH, USA), using a birdcage head RF coil with a 16-channel phased-array coil. Proton MRS spectra were obtained from the prefrontal and left frontal cortices of a healthy volunteer (male; 47 years old), using the reported PRESS echo times, ($TE_1$, $TE_2$) = (100, 50) ms [3]. The voxel size was 25×30×30 mm$^3$. Spatial localization RF pulses included an 8.8 ms 90° RF pulse (BW = 4.7 kHz) and an 11.9 ms 180° RF pulses (BW = 1.4 kHz), at an RF field intensity of 15 μT. First and second-order shimming for the selected volume was carried out using FASTMAP. Data acquisition parameters included a TR 2.5 s, a sweep width 5 kHz, and 4096 sampling points. Spectra were acquired in 16 blocks, each with 4 averages (scan time 2.7 min). A four-pulse variable-flip-angle scheme was used for water suppression [4]. The carrier of the volume selective RF pulses was set to 3.0 ppm. Artifacts due to residual eddy currents were removed using brain water signals acquired with an identical gradient scheme. The data were corrected for frequency drift and phase individually prior to the summation of the data. LCModel software [5] was employed to analyze the *in vivo* spectra, using numerically-calculated spectra of 21 metabolites as basis spectra. The spectral fitting range was set to 1.0 – 4.1 ppm.

## RESULTS AND DISCUSSION

Fig. 1 presents LCModel spectral fitting results of proton spectra from the prefrontal and left frontal cortices of a healthy adult brain, together with voxel positioning. *In vivo* brain spectra were well reproduced by fits, with residuals at the noise levels. Normalizing the spectra with respect to the brain water signals obtained at TE = 14 ms (STEAM), the Gly signal at 3.55 ppm was observed to be ~2-fold greater in prefrontal (PFC) than in left frontal (LF). Using published gray and white matter ratio of 3:1 for PFC, and 1:3 for LF [6], the observed Gly signal ratio of 2:1 between PFC and LF gives a GM-to-WM Gly concentration ratio of 5:1, implying that the detected Gly signal is largely attributable to GM and the Gly level in WM may be very low. For comparison, the myo-inositol (mIns) level was observed to be about the same in PFC and LF. In addition, the data show higher concentration of N-acetyl-aspartyl-glutamate (NAAG) in WM than in GM while glutamate (Glu), and creatine (Cr) show higher concentrations in GM than in WM, in agreement with published results [6,7]. It is premature to conclude higher Gly levels in GM than in WM based on the data from a single subject. Further study will be required to determine the reliability and reproducibility of the measures in small voxels with predominantly gray or white matter content of multiple subjects.

## REFERENCES

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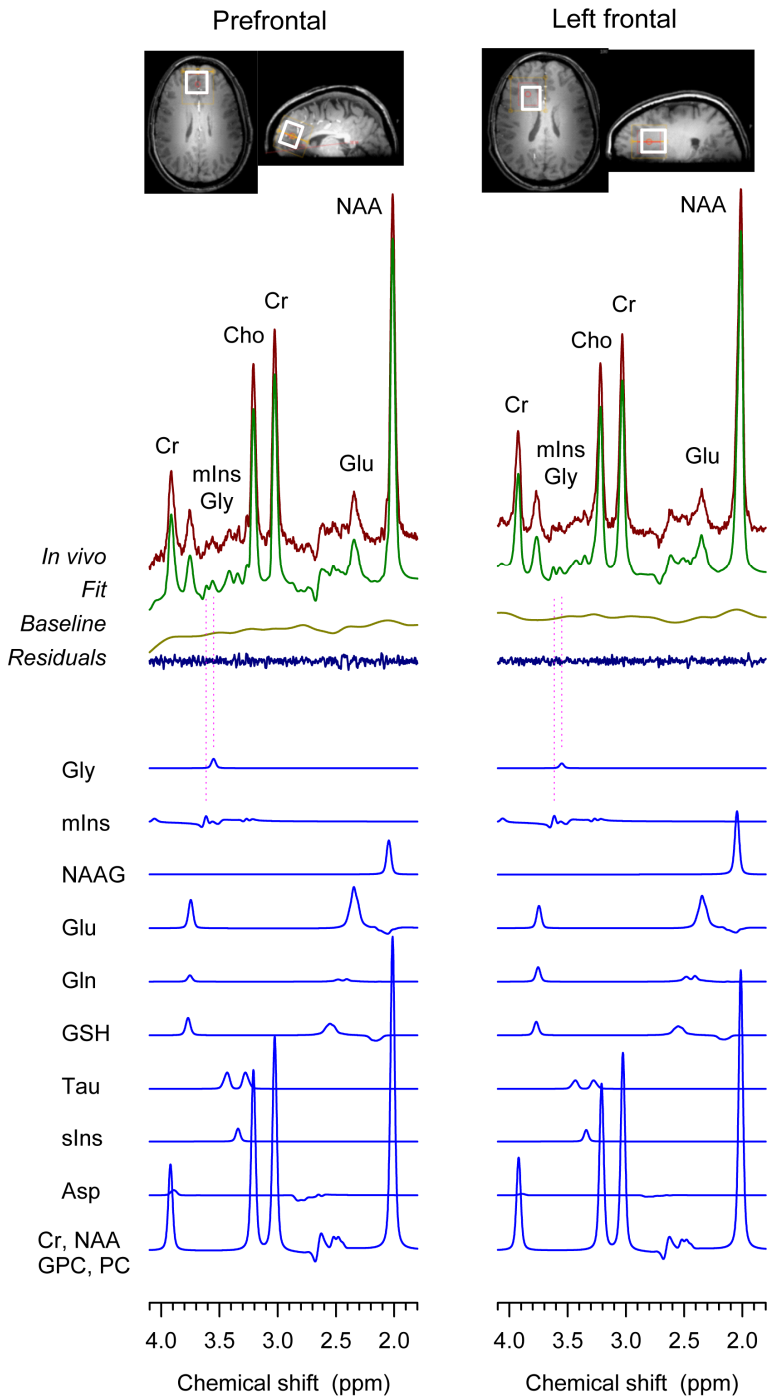


FIG. 1. LCModel fitting results of spectra from the prefrontal and left frontal cortices of a healthy volunteer (voxel size 25x30x30 mm$^3$ for both regions) are shown together with individual metabolite components. The spectra were obtained with PRESS ($TE_1$, $TE_2$) = (100, 50) ms at 7T (TR = 2.5 s; NEX = 64). Spectra are normalized with respect to the brain water. Individual metabolite spectra were broadened using a 5-Hz exponential and 10-Hz Gaussian function, giving singlet lineshape and linewidth (13 Hz), similar to *in vivo*.