Optimal Methodology for Glutamate and Glutamine Signal Quantification with Single Voxel MRS of the Human Brain

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Introduction

Proton magnetic resonance spectroscopy (1H-MRS) enables non-invasive in vivo metabolite measurement and quantification. There is increasing interest in differentiating glutamate and glutamine in various neurological and psychiatric disorders by using MRS [1,2]. Comparison of single voxel acquisition methods (short-TE PRESS and a PRESS based TE-averaged custom built pulse sequence) is presented here. The primary purpose of this study is to investigate which method is better for detecting both glutamate and glutamine in patients who have HIV-1 associated minor cognitive motor disorder (MCMD).

Methods

Scans were performed on subjects who have been diagnosed with HIV-1-associated MCMD, HIV-1 seropositive individuals without neuropsychological impairment and as well as HIV-1 seronegative controls. Subjects' serostatus and diagnosis are not unblinded for the evaluation of methodology reported here. 19 studies were done with short-TE PRESS method and 16 experiments were performed with TE-averaged method within the forward mentioned research population. TE-averaged data were acquired on a Siemens Trio 3T scanner with TR=1800, TE starting at 30 ms and ending at 150 ms with increment of 8 ms, voxel volume 10x15x20 mm^3, 1024 data points, scan time of 4 min. A water reference spectrum was also collected following each water suppressed acquisition. The scanning protocol also included a T1-weighted MPRAGE sequence for voxel positioning. The short-TE PRESS data was acquired with similar parameters as the TE-averaged data with TE value set at 30 ms. A 12-channel phased-array head coil was used for both acquisition methods. Spectral fitting was done with LC Model [3]. The FWHM and SNR level were selected as spectra quality control parameters, and any spectrum with greater than 0.1 FWHM or SNR lower than 4 was rejected for analysis. The Cramer Rao Lower Bound (CRLB) values for Glu, Gln and NAA were evaluated using unpaired t-test.

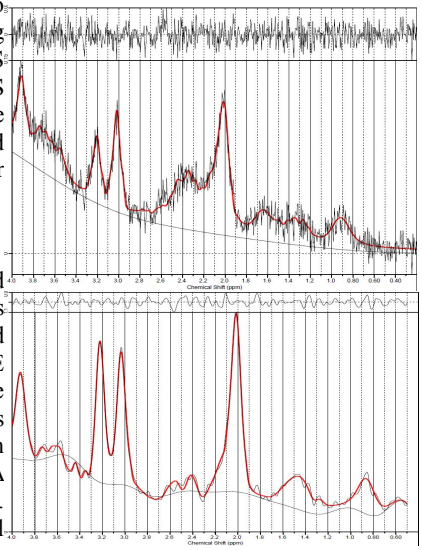

Figure 1: LC Model fitted TE 30 PRESS and TE-averaged spectra

Results

Sample spectra for TE 30 and TE-averaged acquisitions are shown in Fig. 1, and unpaired t-test results are shown in Fig. 2 for PRESS TE 30 and TE-averaged data. The SNR level is better for the TE-averaged data than the TE 30 PRESS data. Two outlier points (shown in Fig. 2) were not rejected due to fulfilling the forward mentioned quality control parameters. In analyzing the CRLB values for Gln, the mean and the standard deviation for PRESS TE 30 data is 61.973 and 60.368, and the values are 20.693 and 19.750 for the TE-averaged data. Group analysis has shown a p-value of 0.0175 for Gln when comparing the two sets of acquired data (shown in Table 1). However, our analysis has shown no significant differences in Glu and NAA detection with these two acquisition methods.

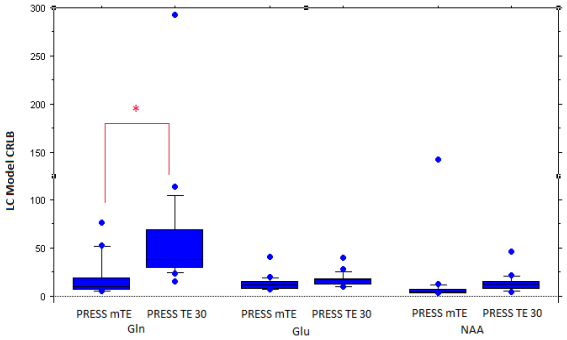

Figure 2: Group analysis summary for Gln, Glu and NAA

Conclusions

In our efforts to investigate whether the TE 30 PRESS or the TE-averaged acquisition method is more advantageous in detecting Glu and Gln for our HIV-1 associated MCMD study, we have found that the TE-averaged acquisition provides a better Gln detection than the TE 30 PRESS method, but no significant differences were found in their abilities detecting Glu and NAA.

Method	Mean LC Model CRLB
PRESS TE 30	61.97 ± 60.37 (n=19)
TE-averaged	20.69 ± 19.75 (n=16)

Table 1: Glutamine group analysis

References

1. Hattori et al., NeuroReport 2002; 13:183-186 **2.** Griffith et al., NMR Biomed. 2008; 21:381-387 **3.** Provencher, MRM 1993; 30:672-679