Comparison of Quantification of Clinical MR Spectra by LCModel and the Scanner System Software

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Introduction

Quantification of MR spectroscopy is frequently necessary in preparing reports of clinical examinations. Commercial MRI scanners have quantification software, and the results can be directly sent to PACS systems and become part of patient clinical records. On the other hand, LCModel [1] is a widely accepted MR spectroscopy analysis software package for research studies. We investigated how the results of the two quantification methods are correlated with each other by reviewing patient data that have been analyzed with both methods.

Materials and Methods

Proton brain MRS data were acquired from 1.5T Philips whole body clinical scanners (two Gyroscan Interas with Release 11.1.4 software and one Gyroscan Achieva with Release 1.5.4 software). Information about the patients and data are summarized in Table 1. Data with TE of 31 ms were all acquired with PRESS chemical shift imaging (FOV = 160 mm, NSA = 2, 16 phase encoding steps in each direction with 25% sampling reduction). Long TE spectra were acquired with either PRESS single voxel method or PRESS chemical shift imaging. In all studies, a water reference signal was acquired with a single voxel PRESS scan of the occipital lobe grey matter (VOI = 1.5x1.5x1.5cm^3, TR/TE = 5000/31, NSA = 4).

The scanner software allows analysis of single voxel data or CSI data. Multiple voxel data can be averaged for curve fitting. For short TE spectra, we used the parameters: baseline term = 1, 90% gaussian, spectra analysis range 4.2 to –0.7 ppm. For long TE spectra, we used baseline term = 11. The DSA filter was turned off. For CSI data, the average spectra of multiple voxels in specific brain areas were analyzed. The metabolites and peaks used for quantification are listed in Table 1. The results are expressed as peak area ratios relative to the Cr peak at 3.0 ppm. In Table 1, Glx from the scanner software corresponds to Glu+Gln by LCModel, and NAA corresponds to NAA+NAAG by LCModel.

LCModel version 6.1-4 was used for the study. The basis functions were provided by Provencher (TE = 30 and 135 ms for short and long echoes). The CSI data was first processed with SpecTool software from Philips Medical Systems. An average of multiple voxels in specific anatomical regions was taken, and the resulting time domain data was used as input to LCModel together with the water reference data. The LCModel analysis yields metabolite concentrations in millimolar units. In order to compare with the scanner software, all metabolite concentrations were normalized by that of creatine. Frequently, one anatomical region analyzed by the scanner software has been treated as two sub-regions in the LCModel analysis. In these cases, the average metabolite levels (weighted by the number of voxels of each spectrum) were obtained before normalization by creatine to obtain the concentration ratios of the combined region.

Results

The results are summarized in Table 2, which lists the conversion relationship (assuming $y = a \cdot x$), standard error of peak area ratios from the scanner software predicted by the metabolite ratios from LCModel through a linear relationship, the median and range of peak area ratios, and the coefficient of correlation between the two quantification methods.

Discussion and Conclusions

As expected, there are very strong correlations between the two quantification methods for long echo spectra. For short TE, the Cho/Cr quantified by the two methods remains well correlated (Figure 1). The correlations for other peaks are not as strong, due to overlapping of peaks and different ways of handling the baseline variation by the two methods. The correlation of mI peak may not be as strong as expected, due to contribution from other metabolites near the 3.56 ppm peak in LCModel.

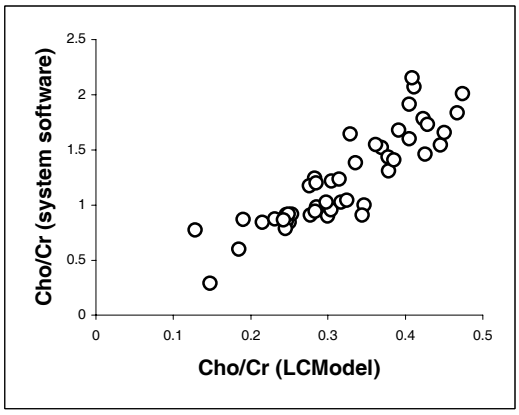

Figure 1. Correlation of Cho/Cr (TE = 31 ms) by the two quantification methods.

Reference: 1. Provencher SW, Magn Reson Med 1993: 30: 672-9.

Table 1. Summary of MRS data

	Long TE	Short TE
Number of patients	8	17
Age: median and range (years)	11.3 (0.4-16.8)	0.43 (0.01-10.1)
TR (ms)	1500 or 1550	1500
TE (ms)	135 or 144	31
Single voxel spectra	5	0
Averaged CSI spectra	8	49
Pathology	tumor 5, seizure 3	CCD 8, DD 2, WM 3, seizure 2, TBI 1, PA 1.
Metabolite peaks used for quantification by scanner	Cho (3.2 ppm), Cr (3.0 ppm), NAA (2.0 ppm)	Cho (3.2 ppm), Cr (3.0 ppm), NAA (2.0 ppm), Glx (2.1-2.5 ppm), mI (3.56 ppm)

CCD: congenital cardiac diseases; DD: developmental delay; WM: white matter diseases; TBI: traumatic brain injury; PA: propionic acidemia

Table 2. Conversion from metabolite molar concentration ratios of the LCModel (LC) to peak area ratios on scanners (S).

TE	Metab.	N[(a)]	Conversion relationship	Stand. error	S median (range)	r
Long	Cho/Cr	13	S = 2.90·LC	0.47	1.12 (0.67 – 4.65)	0.90
	NAA/Cr	13	S = 0.84·LC	0.21	1.20 (0.34 – 2.13)	0.93
Short	Cho/Cr	48	S = 3.87·LC	0.20	1.11 (0.29 – 2.15)	0.88
	NAA/Cr	48	S = 1.14·LC	0.33	1.51 (0.71 – 2.57)	0.56
	Glx/Cr	45	S = 1.42·LC	0.68	2.73 (0.22 – 5.23)	0.60
	mI/Cr	43	S = 1.15·LC	0.69	0.89 (0.14 – 4.83)	0.66

(a): number of spectra resulting in good fit for the metabolites by the scanner software that are included in statistical analysis