A Pilot Comparison of 2D and 1D MR Spectroscopic Quantitation of Metabolites in Healthy Human Brain at 3T

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Introduction: Due to the added second dimension, 2D MR spectroscopy (MRS) offers better spectral dispersion of metabolite resonances minimizing the overlap in the spectral domain, which may improve the overall quantitation accuracy [1]. 2D JPRESS can be easily implemented by modifying the conventional PRESS sequence by encoding the J evolution around the last 180^0 rf pulse [2]. Localized 2D shift correlated spectroscopy (L-COSY) was proposed as a way to further improve the spectral dispersion along the second spectral dimension [1,3]. The goal of this pilot project was to compare the specificity of metabolite quantitation offered by ProFit [4] processed 2D JPRESS and L-COSY data with 1D PRESS processed by LC-Model.

Method and Materials: The 2D JPRESS and L-COSY sequences were implemented on a Siemens 3T Trio-Tim scanner (Siemens Medical Systems, Germany) running on the VB13 and VB15 platforms. Eight healthy volunteers have been scanned so far using the following parameters for 2D MRS: TR/TE=2.0s/30ms, voxel size of 3x3x3 cm^3, 8 averages per $\Delta t1$ and 100 $\Delta t1$ increments. The parameters used for 1D PRESS were as follows: TR/TE=2.0s/30ms, voxel size of 3x3x3 cm^3 and 256 averages. Also, a white matter brain phantom containing fifteen metabolites (pH=7.3) was used for recording more than 10 in-vitro measurements. Profit [4] was originally developed in MATLAB (Mathworks, Natlick, MA, USA, ver. 7.3) for processing JPRESS signals, and the necessary changes were introduced for processing 2D COSY data. The 2D spectra were quantified using ProFit on a 2.8GHz Intel processor with Windows XP. Prior knowledge generated for JPRESS and L-COSY using the GAMMA library [5] included 20 metabolites: creatine (Cr), N-acetylaspartate (NAA), glycerylphosphocholine (GPC), phosphorylcholine (PCh), free choline (Cho), alanine (Ala), aspartate (Asp), γ-aminobutyric acid (GABA), glucose (Glc), glutamine (Gln), glutamate (Glu), glycine (Gly), glutathione (GSH), lactate (Lac), myo-inositol (mI), N-acetylaspartylglutamate (NAAG), phosphoethanolamine (PE), taurine (Tau), scyllo-inositol (Scy) and ascorbate (Asc). The 1D PRESS spectra were processed using LC-Model [6]. The accuracy of the quantitation was characterized using Cramer-Rao lower bounds (CRLB) [7]. For JPRESS and COSY, only values with CRLB<20% were considered valid.

Results: Table I presents, for a selected group of metabolites, the average concentration of each metabolite (expressed as a ratio to creatine) with its standard deviation, and the average Cramer-Row Lower Bound (CRLB) [7] for 1D PRESS-LCModel, 2D JPRESS-ProFit and 2D COSY-ProFit obtained from the *in vivo* measurements. 1D PRESS in combination with LCModel was able to quantify 10 out of the 20 metabolites previously listed (the ones presented in Table I), even though some of them had higher CRLB values that 20%; 2D JPRESS-ProFit was able to detect 18 out of those 20 metabolites, all of them except PCh and Cho; and 2D COSY-ProFit was able to identify the 20 metabolites considered. The concentrations obtained, for the best part, agree with the concentrations reported in the literature [4]. Regarding the CRLB, 2D spectroscopy combined with ProFit showed a reduction in the average CRLB when compared to 1D PRESS and LCModel. Preliminary comparison of the two 2D MRS techniques indicates that 2D COSY-ProFit enables the individual quantitation of GPC, PCh and Cho, which was not possible when using JPRESS-ProFit; and that COSY-ProFit reduces CRLBs in 18 of the 20 metabolites when compared to JPRESS-ProFit (only GABA and Gln had lower CRLB in JPRESS-Profit). These results were reproduced after analyzing the phantom data.

Conclusion: Preliminary results indicate that 2D MRS data processed using ProFit increases the number of detected metabolites and reduces the CRLBs when compared to 1D MRS processed by LCModel and also, that 2D COSY-ProFit reduces the average CRLB of the detected metabolites when compared to 2D JPRESS-ProFit. We acknowledge that none of these metabolites concentrations are corrected for T_1 and T_2 losses.

Table I. Summary of ratios calculated using 1D MRS and 2D MRS data.

	1D PRESS-LCModel		**2D JPRESS-ProFit**		**2D COSY-ProFit**	
	Cr Ratio±SD	**CRLB**	**Cr Ratio±SD**	**CRLB**	**Cr Ratio±SD**	**CRLB**
NAA	1.36±0.18	13	1.42±0.15	0.82	1.27±0.22	0.55
GPC	0.14±0.03	22	0.17±0.03	8.62	0.101±0.02	4.54
Asp	0.55±0.09	16	0.56±0.12	5.9	0.43±0.09	4.68
GABA	0.23±0.14	60	0.33±0.09	5.5	0.41±0.28	8.2
Glc	0.05±0.1	18	0.68±0.12	4.5	0.31±0.1	4.2
Gln	0.12±0.12	99	0.42±0.06	6.56	0.43±0.00	18
Glu	1.2±0.21	16	1.24±0.12	2.52	1.48±0.31	1.42
Lac	0.038±0.01	31	0.12±0.03	9.9	0.14±0.05	4.5
NAAG	0.06±0.08	137	0.31±0.03	5	0.33±0.09	1.97
Tau	0.25±0.05	19	0.11±0.00	17.5	0.21±0.08	5.12

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