Repeatability of ^{1}H MRS: impact of the pulse sequence

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Introduction

Limited reproducibility of ^{1}H MRS measurements is one of the factors that has hampered widespread use of MRS techniques. While the impact of voxel repositioning and biological variability on data reproducibility are generally well understood [1], the importance of the choice of pulse sequence on measurement reproducibility has not been extensively studied yet. We present evidence suggesting that tailoring of the pulse sequence to measure a certain metabolite can significantly reduce MRS data variability for that particular metabolite. More precisely, we show that coefficients of variation (CV's) for the singlets acquired using TE averaged PRESS (PRESS-J) (a pulse sequence that simplifies spectra, leaving little else but singlets [2]) are much lower than for data acquired using a short TE PRESS pulse sequence.

Methods

All the scanning protocols described below were done on a 3T, whole body GE scanner. Four normal volunteers were scanned on four different days during the course of six months, three times each day. The scanning session was comprised of a whole brain localizer, followed by 2 spectroscopy acquisitions from the same voxel situated in the posterior cingulate gyrus. In the first acquisition, 128 spectra were acquired using PRESS (TE/TR=35/2000), and spectra were quantified using LCModel. In the subsequent PRESS-J acquisition, a total of 256 spectra were also collected, with TE varying from 35ms to 355ms in steps of 2.5ms (2 acquisitions per step). The repetition time for the sequence was 2s. The spectra were then averaged together, and also quantified using LCModel. The subjects were removed from the scanner between the three daily sessions, and the voxel was repositioned through an automatic algorithm [3] in subsequent scans.

Results and discussion

Figure 1 presents typical spectra (experimental data, as well as fitted spectra and fitted baselines) acquired from the same voxel of a normal volunteer: Figure 1a presents the PRESS spectrum, and 1b the PRESS-J spectrum, displayed between 1 and 4 ppm. As mentioned before, the complexity of the PRESS spectrum is greatly reduced in PRESS-J (only Cho, Cr, Glu, NAA, some mI and some lipids are visible). Additionally, a flatter baseline is noted (due to the filtering out of some of the macromolecule/lipid signals).

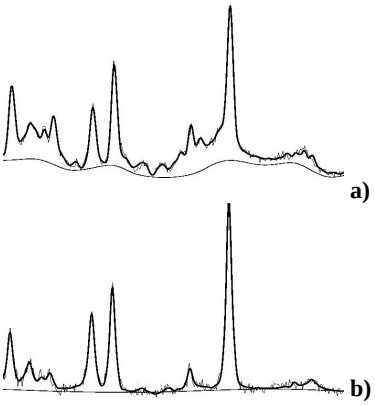

Figure1: **a)** *PRESS and* **b)** *PRESS-J spectra from the same voxel of a normal volunteer.*

Table 1 presents the average inter-day, intra-volunteer coefficient of variations for all the metabolite concentrations and concentration ratios measured in the study. Note that all the singlets and singlet ratios (boldface in Table 1) have consistently lower CV's when data is acquired using PRESS-J. At the same time, some precision has been lost in quantifying the complicated spectral pattern of mI. This was expected; by design, PRESS-J suppresses everything but the odd multiplicity spectral lines- including most of the mI spectrum. We hypothesize that the decreased CV's for the singlets in the PRESS-J spectrum is due to the simpler spectra, that leave less room for error when quantifying data through fitting. The reduced variability observed experimentally is also confirmed by the Cramer Rao lower bounds (CRLB's) reported by LCModel (Table 2). A very good agreement between the experimentally measured CV's and the CRLB's is also to be noted.

	Cr	**Glu**	**Glu/Cr**	**mI**	**mI/Cr**	**Cho**	**Cho/Cr**	**NAA**	**NAA/Cr**
PRESS CV [%]	**4.2**	6.6	8.5	6.2	5.9	**6.7**	**5.6**	**5.9**	**5.1**
PRESS-J CV [%]	**3.9**	8.1	8.0	13.7	13.3	**3.3**	**4.2**	**2.4**	**3.4**

Table 1: Inter-day, intra-volunteer coefficients of variation for data acquired using PRESS and PRESS-J

	Cr	**Glu**	**mI**	**Cho**	**NAA**
PRESS CRLB's [%]	3.9	7.8	8.3	5.9	4.0
PRESS-J CRLB's [%]	3.6	10.3	14.1	4.2	2.2

Table 2: Cramer Rao lower bounds (CRLB's) reported by LCModel for PRESS and PRESS-J data.

Conclusions

The evidence we presented showed that the choice of pulse sequence is very important when tight measurements are needed in ^{1}H MRS. Short TE PRESS is generally used in MRS exams, but crowded PRESS spectra make it more complicated for the fitting subroutines to give repeatable measurements. By comparison, the PRESS-J acquisition scheme filters out metabolites with complicated spectral patterns and produces spectra with lower signal to noise ratio. These spectra, however, are easier to fit due to their simplicity, leading to an opportunity to conduct more precise measurements of the singlets in the spectra. We suggest that, if precise measurements are needed for one particular metabolite in the spectrum, the pulse sequence should be optimized beforehand. However, this optimization for one metabolite might also lead to loss of precision in quantifying the other metabolites in the spectrum.

References

1. Brooks et al, Magn Res Med **41**, 193 (1999); **2.** Hurd et al, Magn Res Med, **51**, 435 (2004); **3.** Blezek et al, ISMRM 2005, submitted.