Single Voxel MRS Measurements are not Influenced by Swirling Flow in Phantom Solution

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Introduction

The sensitivity of MRS results to the performance and stability of scanner hardware is well recognized and, therefore, regular quality control (QC) with phantom scans is strongly recommended for quantitative MRS [1]. Usually, a phantom containing a physiological solution of metabolites is used for this purpose. Because the measured metabolite concentrations can potentially be affected by the flow of solution after the phantom is transported and positioned in the scanner [2-3], two approaches are often taken to avoid such error. One is to allow enough time for the disturbance in the solution to settle before starting MRS QC data acquisition. This approach inevitably prolongs the MRS QC procedure. Another approach is to use a gel phantom [4]. However, the long-term stability of metabolites in a gel phantom may be less than that of a liquid solution. For this reason, a liquid phantom for MRS QC seems preferable, however, this would only be true if it could be demonstrated that swirling effects in a liquid phantom were immaterial. The purpose of this study was to test the hypothesis that the effect of phantom movement induced flow on measured metabolite concentrations is below the limit of detection of a typical single voxel MRS QC protocol.

Methods

We conducted experiments using a spherical MRS phantom of 22cm in diameter filled with a liquid solution of brain metabolites in physiological concentrations – i.e. "braino". The phantom was positioned consistently in the center of an 8-channel head coil on a 3T scanner during data acquisitions. Before the experiment, the solution phantom was left undisturbed in the scanner for more than 3 hours to allow the flow to settle completely. Figure 1a shows no obvious flow pattern in a transverse image acquired with a SE sequence of 17ms TE, 300ms TR, 15.6 KHz RBW and 20cm thickness.

To measure metabolite concentrations with and without flow, a PRESS MRS sequence with 30ms TE, 2000ms TR and 32 averages was used to acquired spectroscopy data from a single voxel of 2cm x 2cm x 2cm at the center of the phantom. The scan time was 1:23. The acquisition parameters such as transmitter and receiver gain were kept constant throughout the experiment after initial calibrations. Our experience is that, these parameters are identical whether the calibrations are performed when the phantom is stable or not. For the stable condition without flow, a series of eight measurements was made while the phantom remained undisturbed. For the next eight measurements with flow, the phantom was removed from the scanner and agitated vigorously for 15 seconds prior to each measurement. Figure 1c shows flow pattern after such agitation, and the signal intensity variation is much greater than the result of a typical phantom transportation and positioning shown in figure 1b. A typical spectrum acquired after agitation is shown in figure 2 and the metabolite concentrations of NAA, Cho, Cr, mI and Glu+Gln are quantified using LC Model software without water scaling.

Results and Discussion

Qualitatively, MRS spectra acquired under stable and agitated conditions are very similar. Table 1 is a summary of measured metabolite concentrations. Wilcoxon Rank sum tests indicate that there is no significant difference in metabolite measurements between the agitated versus stable conditions for each metabolite.

Typically, there are two mechanisms for flow related signal loss in MR. One is the time-of-flight effect when the excited spins flow out of the region of refocusing RF pulses. The magnitude of this effect is inversely proportional to voxel size and proportional to TE. Due to the large voxel size used in MRS and the short TE in our protocol, this effect is much less in MRS than in imaging. Another effect is intra-voxel phase dispersion due to incoherent motion. This effect is minimized when the pulse sequence is flow compensated. Since there is neither phase encoding nor readout gradients in a single voxel PRESS sequence, the first moment of gradients for all three axis is also nulled at the center of the echo, minimizing flow related signal loss. Therefore, the experimental results, although previously unexpected, are reasonable.

If internal water referencing is chosen for metabolite quantification, one may also use water scaling in MRS QC. If the delay between acquiring the non-water suppressed signal and water suppressed signal is much less than the time scale of flow settlement, then the flow effect should attenuate water and metabolite signals equally. In this case, the flow induced signal change, if any, will be cancelled by water scaling. However, using water scaling in MRS QC analysis can potentially mask out scanner performance changes.

Conclusion

The potential error in measured metabolite concentrations due to swirling flow of a liquid phantom solution is below the sensitivity of single voxel MRS. A liquid solution phantom maybe used for MRS QC without incorporating a delay for flow settling.

References

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[3] Pattany PM et al, AJNR 2002; **23**: 225-230
[4] Port JD, ISMRM 2004, "State of the Art Clinical MRS Techniques"

Figures and Tables

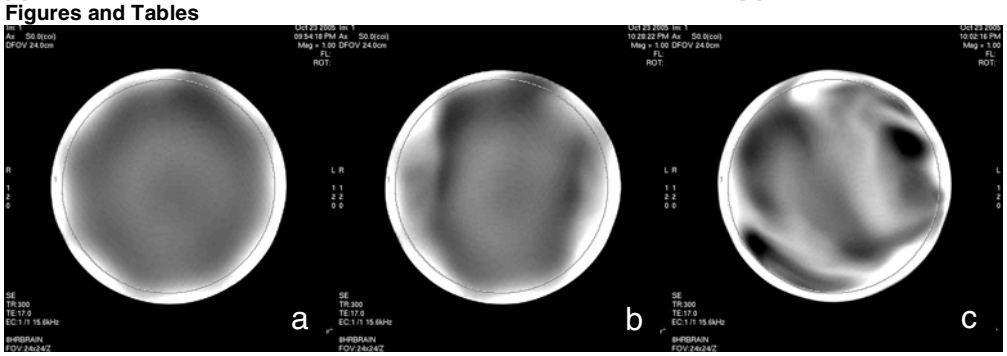

Figure 1. Signal intensity variation in SE images of a solution MRS phantom when it's stable (a), immediately after positioning in the scanner (b) and after 15s agitation (c). The grayscales are identical.

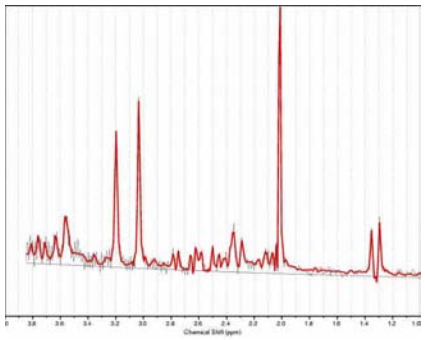

Figure 2. A typical spectrum of MRS solution phantom acquired under agitated condition.

Metabolite	NAA		Cho		Cr		mI		Glu+Gln	
	Stable	Agitated	Stable	Agitated	Stable	Agitated	Stable	Agitated	Stable	Agitated
Median	4.25	4.28	1.20	1.22	3.25	3.20	3.36	3.68	2.98	2.82
Min	4.01	4.20	1.09	1.11	2.94	2.98	3.00	2.91	2.64	2.31
Max	4.49	4.43	1.24	1.31	3.32	3.40	4.18	4.00	3.65	3.75
CV	4.22%	1.54%	4.55%	5.66%	4.34%	4.21%	10.05%	9.63%	10.64%	17.52%
P Value	0.87		0.34		1.00		0.22		0.43	

Table 1. The median, minimum and maximum values as well as the coefficient of variation of the metabolite concentrations in solution MRS phantom measured in the experiment and quantified by LC Model. The P values are calculated according to Wilcoxon / Kruskal-Wallis Rank Sums Tests.