Improved metabolite quantification using VAPOR water suppression

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Introduction

The availability of whole body MR scanners with field strengths of 7 Tesla offers the potential of higher SNR and better spectral resolution. This can be used to improve the spatial resolution or detection a larger number of metabolites. Despite the potential benefits, there are complications, such as increased sidebands from unsuppressed water that interfere with the evaluation of metabolites such as Cho and mI. Conventional water suppression uses CHESS RF pulses but the performance of this method is insufficient at 7 Tesla and results in gradient-induced water sidebands. One solution that has been proposed is to use variable power RF pulses with optimized relaxation delays (VAPOR) [1]. This was first designed for animal studies, where highly efficient water suppression and reduced sensitivity to B1 variation and water was demonstrated. The purpose of this study was to evaluate the efficacy of this approach in single-voxel short-echo MRS and to assess improvements in the accuracy of metabolite quantification compared to conventional water suppression.

Methods

All MR studies were performed using a commercial 8-channel receive-only array with a volume transmit head coil (NOVA Medical, Wilmington, MA) on a GE Excite 7T scanner. A phantom and 2 volunteers were scanned. To test the reproducibility of the data, we scanned the phantom a second time. The protocol consisted of a T1-weighted sagittal scout, T2*-weighted gradient recalled echo (GRE) and two spectroscopy acquisitions from the same 2x2x2 cm^3 voxel. The spectral data was obtained using PRESS for volume selection with an over-PRESS factor of 1.4, VSS pulses for outer volume suppression, and VAPOR or CHESS for water suppression, with TR/TE of 2000/35 ms and NEX of 64. The total acquisition time for each spectrum was around 2 minutes. The spectral data were acquired with 2048 spectral points and 5000 Hz spectral width. The 8 channels of data were combined as described previously [2], and then quantified using LcModel. Metabolite signals for the basis set, which included Cho, Cr, NAA, Glu, Gln, mI and Gly, were generated using GAMMA simulations with prior knowledge of chemical shift and J-coupling. Cramer-Rao lower bounds (CRLB) of LcModel analysis were created for the combined spectral data and the two channels with highest water signals to estimate the accuracy of quantification. The Spearman rank correlation coefficient was calculated to determine the association of CRLB between CHESS and VAPOR water suppression, and a nonparametric Wilcoxon signed-rank test was used to test for significance differences. The coefficient of variance (CV) for reproducibility was calculated for the phantom data using the standard deviation divided by the mean.

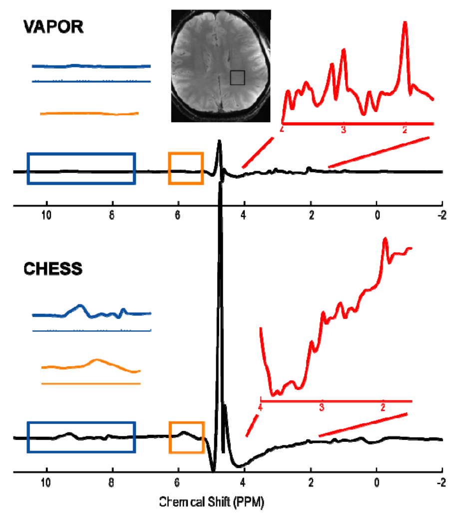

Figure 1. Single voxel MR spectra acquired with VAPOR (upper) and CHESS (lower) water suppression from a healthy volunteer. Note that the sideband in the orange box, distributed anti-symmetrically about the water peak, could affect the region of mI and Cho.

Results

An example of the spectra data acquired from a volunteer acquired using VAPOR and CHESS water suppression is shown in Figure 1. VAPOR reduces the residual water signal by a factor of 8 compared to CHESS water suppression, and significantly decreases gradient-induced water sidebands. The sidebands are distributed anti-symmetrically about the water peak, which could affect the interpretation of metabolites of interest in evaluating patients. The correlation of CRLB between VAPOR and CHESS water suppression is illustrated in Figure 2. The Spearman rank correction coefficient was 0.873 with P<0.001. The CRLB in VAPOR water suppression is significantly different from those using CHESS water suppression with P<0.001 (Table 1). The estimates of reproducibility obtained from the phantom are shown in the Table 2. The CVs were relatively smaller using VAPOR water suppression.

		Cho (%)	Cr (%)	NAA (%)	Glu (%)	mI (%)
Phantom	VAPOR	3.5±0.8	3.7±0.8	3.5±0.8	22.5±11.9	11.5±1.0
	CHESS	8.0±7.5	7.8±6.0	7.5±6.7	39.2±26.3	21.4±5.2
Volunteer	VAPOR	3.8±0.4	4.0±0.9	2.8±1.0	10.2±2.7	8.8±3.1
	CHESS	5.0±0.0	4.8±2.1	3.5±1.6	16.2±9.3	10.3±1.0

Table 1. The Cramer-Rao lower bound (CRLB) of metabolite concentrations using LcModel.

	Cho/Cr	NAA/Cr	Glu/Cr	mI/Cr	Cho/NAA
VAPOR	3.6%	0.2%	34.7%	7.7%	3.4%
CHESS	10.2%	7.3%	76%	9%	18.2%

Table 2. The coefficient of variation of metabolite concentration ratios in the phantom.

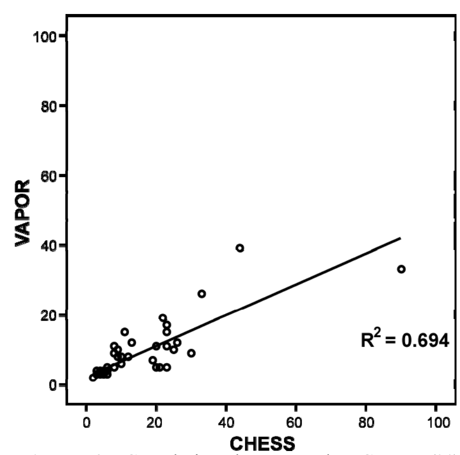

Figure 2. Correlation between the CRLB (%) acquired using VAPOR and CHESS water suppression.

Discussion

Improving the sensitivity of MRSI and increasing the number of metabolites that can be evaluated by using ultra high field whole body scanners would be an important advance for evaluating patients with glioma. The large residual water signals and gradient-induced water sidebands can overlap with regions of metabolite signals such as Cho and mI, which are important biomarkers in glioma. These can interfere with the estimation of metabolite levels and may impede the ability to distinguish between tumor and treatment effects. The data that we have acquired using VAPOR water suppression have smaller residual water signals, less gradient-induced water sidebands, lower CRLB and CVs compared to that acquired using CHESS. Thus VAPOR improves the accuracy of metabolite quantification but further investigation will be required to see whether similar findings can be observed in patients.

References

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