Quantitative Short Echo ^{1}H Chemical Shift Imaging in Human Brain Incorporating Macromolecule Subtraction

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Introduction For *in-vivo* spectroscopy, chemical shift imaging (CSI) has three main advantages over single voxel spectroscopy (SVS): increased sensitivity (SNR/unit time), spatial information and post-acquisition alignment of voxels with pathology or anatomy of interest. However, few ^{1}H CSI techniques can acquire short echo-time (TE) spectra in human brain of the same caliber as those acquired from SVS. This paper presents a new ^{1}H CSI pulse sequence that incorporates Localization by Adiabatic Selective Refocusing (LASER)[1] and macromolecule subtraction, to obtain quantitative images of glutamate (Glu) and myo-inositol (Myo) in addition to N-acetyl-aspartate (NAA), Choline (Cho) and Creatine (Cr). The purpose of this study was to directly compare spectral quality and metabolite levels obtained with short-TE LASER-CSI and LASER-SVS.

Methods Data from five healthy volunteers were acquired using a 16-element quadrature hybrid birdcage RF coil on a 4.0 Tesla Varian whole-body MRI equipped with a Siemens Sonata gradient coil. LASER-CSI data were acquired (6cm x 6 cm x 1cm volume, 8x8 phase-encodes, nominal voxel size=0.56cm^3) in left posterior brain at the level of the ventricles. A k-space-dependent averaging scheme ((N_{av}=25*(0.5+0.5*cos(πk/k_{max}))+1) was employed during the water-suppressed acquisition. Total spectroscopic imaging time was 47 min. LASER-SVS (128 averages, TR/TE=2200/46ms (full spectrum), TI_1/TI_2/TR/TE=2200/700/4200/46ms (macromolecule spectrum) spectra[2] were acquired in a homogeneous region of white parietal matter from a volume equal to the effective voxel size of the spectroscopic imaging protocol (1.5 cm x 1.5 cm x 1cm based on the full width at half maximum of the point spread function). A CSI voxel was aligned with the SVS location during post-processing. After spatial reconstruction of the full, macromolecule and water spectra, the CSI spectra were processed identically to the SV spectra on a voxel-by-voxel basis. Spectra were lineshape corrected by QUECC[3], residual water subtracted, and the macromolecule baseline removed[2] prior to time domain fitting using prior knowledge of 19 metabolite lineshapes. Metabolite levels were normalized to the unsuppressed water signal from the same voxel after correcting for relaxation effects and water concentration to yield metabolite levels in absolute units[2]. CSI spectra were compared to SVS spectra on the basis of: linewidth of the unsuppressed-water signal, SNR (NAA/standard deviation of the noise) and absolute metabolite concentrations.

Figure 1

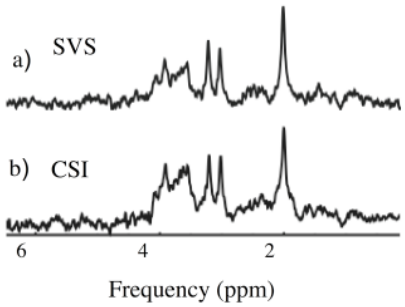
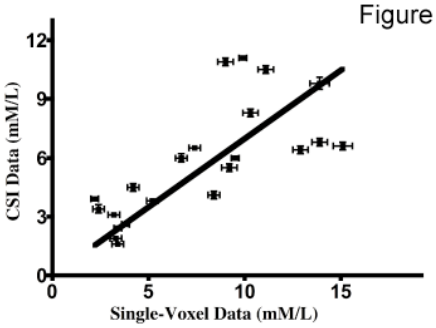
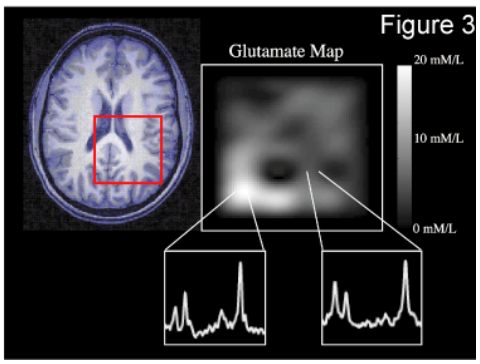


Figure 2



Results and Discussion Figure 1 shows typical matching SVS (a) and CSI (b) spectra. Average unsuppressed-water linewidths in SVS and the corresponding CSI voxels were 8 ± 1 Hz, and 10 ± 2 Hz respectively. Average SNR for SVS and CSI spectra were 10 ± 3 and 12 ± 4 respectively. Thus, CSI is on par with SVS. For quantitative comparisons, only metabolites with a standard deviation < 50% in single-voxel data were included (NAA, Glu, Cr, Myo, Cho) and individual cases with Cramer Rao minimum variance bounds > 50% were excluded. In two subjects, the myo-inositol data were excluded due to stimulated-echo artifacts. Further optimization of crusher gradients is expected to elminate spurious signals such as these and improve overall spectral quality of LASER-CSI. Figure 2 presents a linear-regression analysis of the concentration measurements, for all metabolites (slope=0.70±0.05, r^2=0.53). Some variability in quantified metabolite levels is likely due to the sampling of different tissue (due to the CSI point spread function) between methods, despite careful alignment of the CSI nominal voxel. A quantitative glutamate map is shown in Figure 3 alongside the corresponding anatomical image (CSI volume is outlined in red). The average concentration of glutamate for the entire map was 7.9 mM/L which is in good agreement with literature values[2]. Unsuppressed-water linewidths ranged between 3.1 and 11.4 Hz (mean = 7 ± 3 Hz).

Figure 3



Conclusion

A novel ^{1}H CSI sequence is presented which uses short-TE LASER for ROI pre-selection and incorporates macromolecule subtraction to produce high quality, quantitative metabolite maps in the human brain in a clinically feasible scan time. Therefore the combination of sharp volume selection provided by adiabatic localization, with rigorous spectral processing and macromolecule subtraction will allow a quantitative analysis of metabolic variation within cerebral lesions such as tumours.

Acknowledgements and References Funding provided by Robarts Research Insitute and CIHR/UWO Strategic Training Initiative in Cancer Research and Technology Transfer.(1) Garwood M, DelaBarre L. JMR. 153:155-177 (2001). (2) Kassem M, Bartha R. MRM. 49:918(2003). (3) Bartha R, Drost D, Menon R, Williamson P. MRM. 44:641-645 (2000).