Human Brain 1H MRS of GM and WM: a Comparison of BASE-SLIM and CSI Regression

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TARGET AUDIENCE: Scientists and technologists who are interested in non-Fourier based spectral localization methods for advanced *in vivo* ^{1}H MRS to measure neurochemicals in a region-specific and/or tissue type-specific manner.

INTRODUCTION: Neurochemical measurement shows significant concentration variations between tissue-types, e.g., gray (GM) and white matter (WM), as well as tissue-type specific alterations in neurological disorders. Current ^{1}H MRS acquisition strategies present significant challenges in ascertaining metabolite quantification of GM and WM. Regression analysis of CSI data with GM & WM tissue fractions [1] has been widely used to extrapolate metabolite concentrations from GM and WM. However, the accuracy of CSI regression analysis is hampered by a poor spread of tissue fraction values and inability to correct for B_0 and B_1 inhomogeneities in the analysis. Recently, we introduced BASE-SLIM [2], an advanced form of Spectral Localization by Imaging (SLIM) [3], which overcomes limitations of SLIM by incorporating B_0 and B_1 field corrections. In this study, we present 1H MRS of pure GM and WM using BASE-SLIM that incorporates anatomical contours of both GM and WM boundaries, and we compare the results with the regression analysis of CSI.

METHODS: Nine healthy subjects (31 ± 4 yrs, mean±SD) were studied, at 3 T (Skyra, Siemens) with a 16 channel head receive coil. The ^{1}H CSI was acquired using a semi-LASER sequence [4] (TE/TR=35/1600ms, matrix=16x16, FOV=20cm) with the slab positioned across the prefrontal to parietal lobes. B_0 and coil sensitivity (B_1) maps were acquired using gradient echo sequences (TE=4.92/7.38ms for B_0, TE=2.07ms for B_1). BASE-SLIM reconstruction was performed using the CSI k-space data, B_0 and B_1 maps, and high resolution GM and WM sementation masks. Coil combination of each ^{1}H MR spectrum from 16 channels was performed to maximize SNR with a maximal ratio combining scheme using the signal and noise spectral power estimates. Metabolite concentrations were quantified using LCModel [3] and non-suppressed water scan as a concentration reference. CSI voxels with greater than 75% tissue fraction were selected for the regression analysis. The GM and WM regions covered in BASE-SLIM were identical to the CSI ROI in the regression analysis. BASE-SLIM reconstruction was implemented as previously described [2], involving an expanded geometry matrix for multiple coil sensitivity profiles and a time-dependent solution for B_0 corrections.

RESULTS AND DISCUSSION: Distinct spectral patterns of GM and WM ^{1}H MRS of the human brain show high choline to creatine ratio in WM than GM, which is visible from the spectra in Fig. 1. GM and WM compartments used for BASE-SLIM reconstruction are shown in inset MR images above ^{1}H MR spectra. Metabolite concentrations of GM and WM from CSI acquisition were quantified from scatter plots of each metabolite using a linear regression fit. An example of total choline fit is shown in Fig. 2. Metabolite quantification from BASE-SLIM reconstruction was in agreement with the extrapolated CSI regression for GM and WM. For example, NAA, creatine, choline, myo-inositol concentrations between two methods were within 10% differences while quantification of glutamate (Glu), glutamine (Gln) and the sum (Glu+Gln) was more reliable using BASE-SLIM: Glu+Gln in GM (12.0±1.3 µmol/g) and in WM (6.7±2.3 µmol/g). Our results suggest that BASE-SLIM can provide accurate assessment of tissue type-specific as well as region-specific metabolite quantications that match or exceed the accuracy of the CSI regression method. In conclusion, BASE-SLIM based ^{1}H MRS may eliminate the need for Cartesian k-space acquisition and provides MR spectra from GM and WM with improved quality with minimum B0 and B1 inhomogeneity related errors.

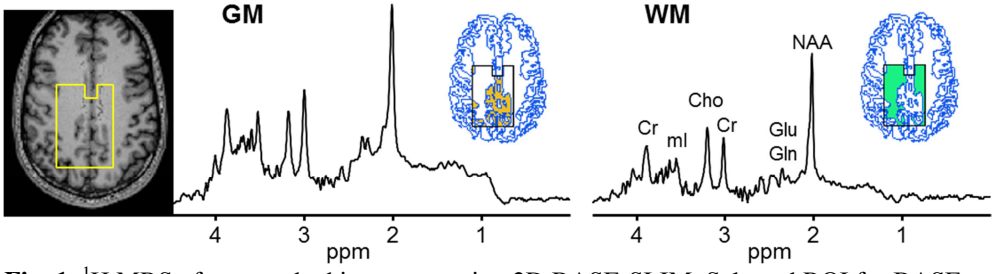

Fig. 1. ^{1}H MRS of gray and white matter using 3D BASE-SLIM. Selected ROI for BASE-SLIM and CSI analysis is shown in MRI (most left) and inset MRIs show GM (left) and WM (right) compartments where the corresponding ^{1}H MR spectra were measured.

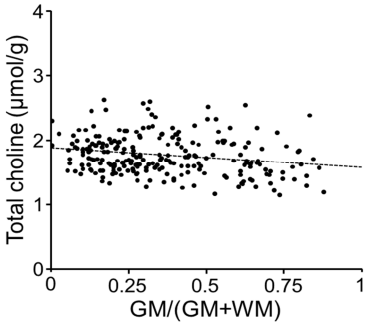

Fig. 2. Relationship between total choline and GM fraction (n=9).

REFERENCES: 1. Hetherington et al., *PNAS* 3115,1985. 2. Adany et al. *PISMRM* 3967, 2013. 3. Provencher, *MRM* 672, 1993. 4. Scheenen et al. *MRM* 1, 2008. This work is partly supported by the National Institutes of Health (S10RR29577, UL1TR000001) and the Hoglund Family Foundation.