Comparison of white matter and gray matter macromolecule resonances between 3 and 7 Tesla

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Target audience: Research and clinical spectroscopists concerned with metabolite and macromolecule (MM) quantitation in the human brain.

Purpose: In ^{1}H spectra of the human brain, relatively broad MM resonances complicate the estimation of metabolite concentrations, particularly in very short echo time (TE) acquisitions. They may also contain interesting information in their own right and have been used to characterize several diseases[1, 2]. We report on the MM quantitation in healthy human brain at 3 T and 7 T in two cerebral regions: the centrum semiovale (CSO), a reference region composed predominantly of white matter (WM), and in the anterior cingulate cortex (ACC), a mostly grey matter (GM) region.

Methods: All spectra were recorded on Philips 'Achieva' scanners using 32-channel receive head coils, operating at 3 T and 7 T. A CHESS water-suppressed inversion-recovery scheme based on the semi-LASER[3] pulse sequence was designed to acquire MM spectra free from longer T_1 metabolite signals. An adiabatic inversion pulse, designed to invert the resonances upfield from water, was used with a bandwidth of 600 Hz at 3 T and of 1400 Hz at 7 T. The inversion times (for metabolite nulling) and the repetition times were respectively 600 ms and 1559 ms at 3T, and 900 ms and 3000 ms at 7 T. The echo time and the scan time were 31 ms and 13 min at both magnetic field strengths. The numbers of averages were 512 and 256 respectively at 3 T and 7 T. 20 normal volunteers (5 for each cerebral region and at each field strength, aged 33 ± 4 years, 9 male) participated. The voxel volumes in the CSO and in the ACC were 18 and 16 cm^3 respectively. The MM peaks, labelled M1 to M7 according to reference 4, were fitted with a sum-of-Gaussians function (Figure 1) and integrated using in-house software. The water signal, acquired separately but within the same experiments, was used for calibration of MM concentrations. The corresponding voxel water content was determined by segmenting the brain tissues into WM, GM and cerebrospinal fluid contributions. No corrections for relaxation time effects were applied. A univariate ANOVA was performed with field strength and voxel location as fixed factors and MM peak integral as dependent factor. Differences between regions and field strengths were subsequently tested for each MM peak.

Results: The linewidth value of M1 was 13.0 ± 0.5 Hz at 3 T and 29.0 ± 0.5 Hz at 7 T. The MM proton concentration values (mM) are displayed in figure 2 (means ± standard deviations); MM proton concentration values were in the range of 5 mM to 20 mM, in general agreement with a previous study[5]. No significant differences were found between the MM proton concentrations by region ($p \approx 0.8$), nor by field strength ($p \approx 0.5$).

Discussion: The absence of differences in MM concentrations between white and grey matter implies that a general macromolecule 'baseline' may be adequate for spectral fitting of multiple brain regions when determining metabolite concentrations, at least in subjects with normal brain. Note this result is different from a previous 1.5T study[6] which did find significant differences in some MM peak concentrations between WM and GM. It also appears that there are no significant differences in MM profiles between 3 T and 7 T, other than the increased linewidths (as measured in Hz) at 7T.

1. Mader et al. *Brain* 2001 124:953-961. 2. Seeger et al. *MRM* 2003 49(1):19-28. 3. Scheenen et al. *MRM* 2008 59(1):1-6. 4. Behar et al. *MRM* 1994 32(3):294-302. 5 Gottschalk et al. *NMR Biomed* 2008 21(5):507-517. 6. Hoffman et al. *MRM* 2001 46: 855-863. This work was funded in part by NIH P41EB015909 and R01MH096263.

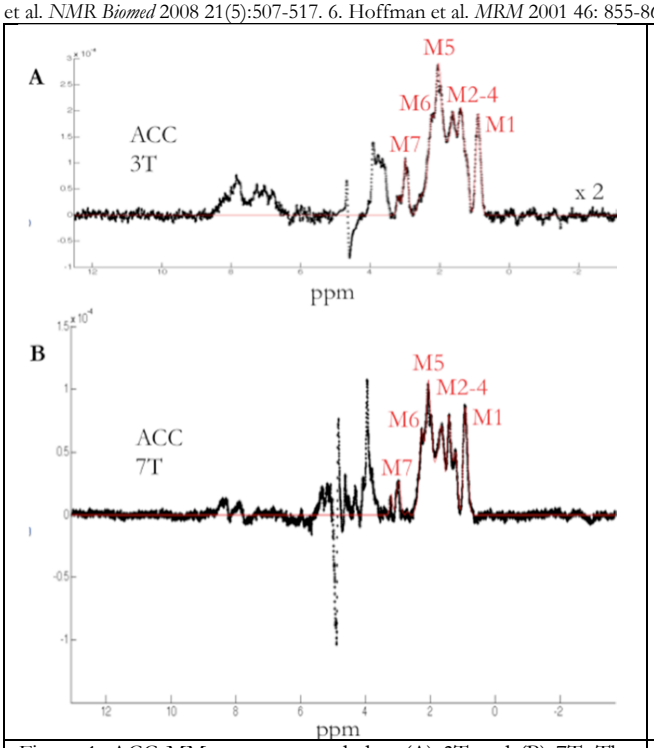

Figure 1. ACC MM spectra recorded at (A) 3T and (B) 7T. The MM peak clusters (M1-M7) were fitted using multiple Gaussian lineshapes.

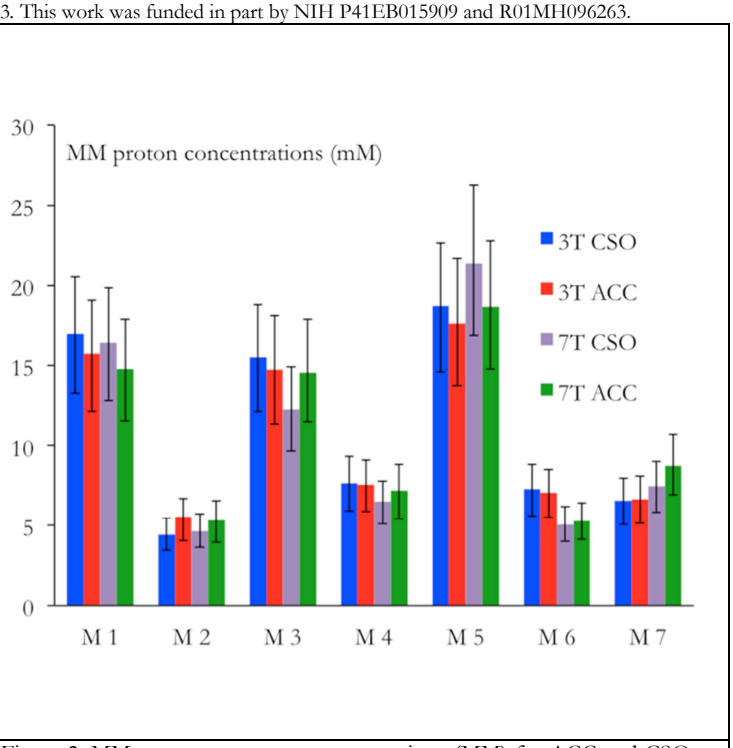

Figure 2. MM resonance proton concentrations (MM) for ACC and CSO at 3T and 7T (mean ± st.dev).