Diffusion weighted spectroscopy: A novel approach to determine macromolecule resonances at 14T

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Introduction

The quantification of the neurochemical profile by ^{1}H-MRS critically depends on the estimation of the contribution of macromolecule (MM) resonances to the spectrum. As the linewidth of macromolecules does not increase with B_0, the resonances attributed to MM are increasingly difficult to distinguish from those of coupled spin systems. Due to heterogeneity of T_1, in the metabolite-nulled spectra small residuals attributed to metabolites continue to be observed. With conventional technique, these residuals can be removed only by post-processing [1,2]. Pfeuffer et al. showed in an in-vivo study that MM have a diffusion coefficient 10 to 20 times lower than the metabolites (ADC_{MM} = 0.006 and ADC_{met} = 0.09 to 0.18 $\mu m^2/s$) which would allow to reduce the metabolite signal without altering the MM one. The aim of the study was to assess the feasibility to acquire MM signals using an inversion recovery ^{1}H-MRS sequence combined with diffusion weighted gradients to remove the remaining metabolite contributions.

Materials and Method

All experiments were performed on a 14.1T/26cm scanner (Varian/Magnex Scientific) with 12 cm gradients (400 mT/m in 120 µs). Localized spectroscopy was performed with a short echo time STEAM sequence with asymmetric RF pulses for slice selection as previously published [3] (TE/TM/TR = 8/200/2500 ms). Inversion recovery was performed using an adiabatic hyperbolic RF pulse (2ms, 8kHz BW) with an inversion time of 740 ms. A 4.5x5.5x5.5 mm^3 VOI was used (c.f. Figure 1). Signal from the outer volume was suppressed by four blocks of slice selective pulses as well as the water signal by the VAPOR. A 14 mm diameter two-loop quadrature transceiver coil was used. Field homogeneity was adjusted using FASTMAP. Diffusion weighting was applied as previously published [4] with a δ/Δ = 1.5/200 ms and the gradient strength was from 0 to 370 mT/m giving b-value from 0 to 13.19 $ms/\mu m^2$.

Results and discussion

The spectra acquired at b = 0 ms/um^2 (c.f. figure 1) shows clearly sharp residuals ascribed to several metabolites, specifically the CH_2 group of creatine resonating at 3.9ppm and the inverted signal of taurine at 3.24 and 3.42 ppm. Increasing the diffusion gradient to 13 affected the amplitude of the M09, M12 and M14 macromolecules peaks by less than 5%, as in [4], whereas the small metabolite residuals show a 3-fold reduction in signal intensity (dotted lines in Figure 1). The attenuation of the metabolite is clearly visible with the CH_2 group of creatine, the signal of which completely disappeared at b>9ms/um^2. The difference spectrum (top trace in figure 1) highlights the metabolites signal still present at b = 0 attributed to NAA, Cr, Gly, Cho and Glx, among others. The figure 2 shows the MM resonances acquired at a b = 12 $ms/\mu m^2$.

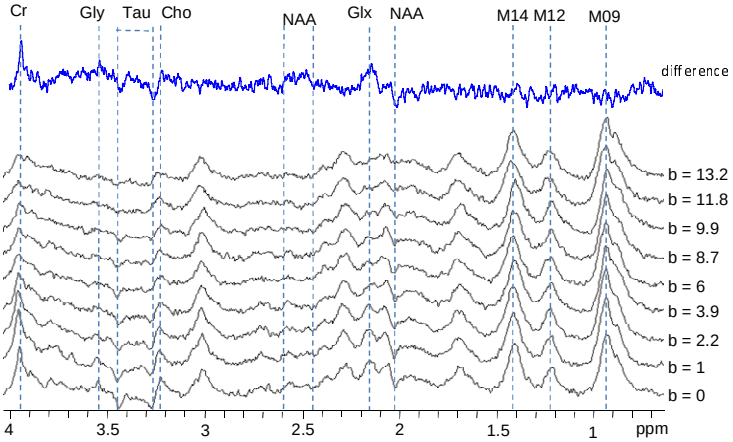

Figure 1: diffusion weighted spectra with b-value from 0 to 13.2 $ms/\mu m^2$ (nt = 720, LB = 10 Hz). The spectra on top in blue represent the difference between b = 0 and b = 11.8 $ms/\mu m^2$ spectra.

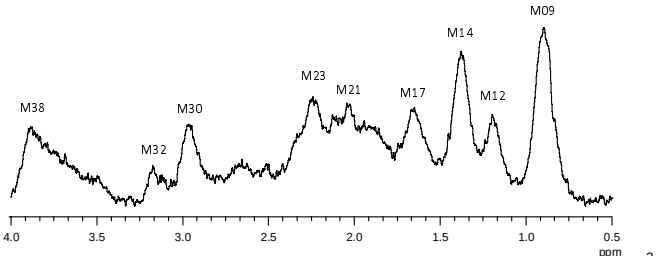

Figure 2: MM resonances at 14T acquired at b-value = 11.8 $ms/\mu m^2$ (LB = 3 Hz) with 1920 averages (acquisition time: 80mn) form one rat

We conclude that it is feasible to assess the macromolecules resonances using a diffusion-weighted spectroscopy sequence combined with inversion-recovery avoiding the need for additional post-processing removal of metabolite resonances.

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References

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