"Optimized magnetic resonance spectroscopy for metabolite quantification at 9.4 T"

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Proton (^{1}H) Magnetic Resonance Spectroscopy (MRS) enables non-invasive quantification of metabolites in tissue. Animal models of disease can be studied with high field animal magnetic resonance scanners such as 9.4 T. The high field offers the advantages of improved signal to noise ratio (SNR) and spectral resolution in MRS. However, even at 9.4 T quantification of some metabolites is challenging due to overlap of peaks. Spectral editing, where differences in J-coupling evolution of the different proton spin systems of metabolites are exploited, can be employed to resolve target spins of interest. The presentation describes how timings of a Point RESolved Spectroscopy (PRESS) MRS pulse sequence can be optimized for signal from metabolite protons of interest while suppressing that from contaminating spins. For example, the signal of the low concentration metabolite glycine is resolved from that of myo-inositol at 9.4 T by optimizing PRESS timings. Similarly, glutamate, glutamine and GABA (gamma aminobutyric acid) signals are resolved from each other so that the three can be quantified simultaneously at 9.4 T. The methods were developed on phantom solutions and their efficacy was verified in rat brain *in vivo*.

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