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HIGH QUALITY ^{1}H SPECTROSCOPY ON 3.0T MRI

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INTRODUCTION

The ^{1}H magnetic resonance spectroscopy have been known as the powerful tool to ex am in-vivo brain metabolites, especially for pathological leseion brain. However, more acc urate and higher resolved data sets are needed to investigate for reliable quantitative anal yses for it's clinical applications. We developed water suppressed STEAM(1) pulse sequen ce for 3.0T MRI system and this paper examined the efficiency and ability of high tesla MR Spectroscopy, and showed better accurate and high resolved results.

METHOD

All Data were acquired at a **3.0T** MRI systems equipped with a active shielded magn et(Oxford). STEAM pulse sequence were used for spetroscopy study, and water peak was suppressed by CHESS(2) pulse. Each spoiler were adjusted carefully to maximize water peak, and acquisition window was placed to correct phase. Gasusian sinc rf and Maximu m phase SLR rf selective pulse were tested for localization, and Maximum phase SLR rf pulse allowed good selectivity and more reliable stability at each different regions. Our r esult showed good agreement of Lawrence's flip angle effects of rf selectivity in STEAM and PRESS(3). Sinc was chosen to localize voxel, and Maximum phase SLR pulse for water suppression. A ^{1}H phantom was prepared to simulate the normal human brain. The phantom was composed of NAA, choline, chriatine, glutamate, glutamin, and Lactate with same concentration of human brain. For localized imaging, gradient echo pulse sequence was used with matrix size 256 x 256. RF pulse calibration and local shimming were pe rformed manually followed by automatic global shimming normally scoring 7-10 Hz, or 0. 05-0.08 ppm in the water peak. The CHESS pulse was optimized to suppress water peak up to 95% in the range of 2000 Hz.

For the phantom study, TR time was set to 2s and TE time 30ms. Voxel size was 20 x 20 x 20 mm^3, and at various off-centered regions voxel locations had been tested for the purpose of justification of the stability and selectivity. The acquired sample were proc essed using GIFA(4) software on a Pentium 133MHz PC Linux system. The data were ca lculated by using the Maximum Entropy Method algorithm for the baseline correction and each metabolite concentrations were determined by using the each peak areas following nonlinear least square curve fitting .

RESULT

The extended ppm interval and the good S/R ratio helped peak indexing and integrations In between 2 ppm and 3 ppm, galutamine and glutamate peaks can be distinguished cle arly and the concentration ratios were in good agreement.

DISCUSSION

Choline and creatine peaks were split so apparently that each peak integrations were very accurate. However, more accurate and higher resolved data sets are needed to investigate for reliable quantitative analyses for it's clinical applications.

CONCLUSION

In this report we have demonstrated that high resolved, high quality MR spectroscopy data at **3.0T** MRI. The result proves that **3.0T** MRI system produces higher resolution, g ood quality and S/R ratio spectroscopy results than **1.5T** machine.