

# High-resolution $^1\text{H}$ -FID-MRSI of the human brain at 7T

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## Introduction:

Proton magnetic resonance spectroscopic imaging ( $^1\text{H}$ -MRSI) is an essential tool with which to study specific biochemical aspects of brain tissue. This technique enables the non-invasive assessment of local changes in brain metabolism that underlie many brain diseases.

$^1\text{H}$ -MRSI at ultra-high magnetic field strengths (i.e.,  $\geq 7\text{ T}$ ) is particularly promising, but still limited considerably by several technical difficulties, including chemical shift displacement errors (CSDE),  $B_0/B_1$  inhomogeneities, a high specific absorption rate (SAR), and decreased  $T_2$  relaxation times.

## Methods and Materials:

This work describes a new approach for high spatial resolution  $^1\text{H}$ -MRSI of the human brain at 7 T *in vivo*, similar to that proposed by Henning et al. [1]. The presented method is based on free induction decay (FID) acquisition with an ultra-short echo time (TE) of 1.3 ms. This allows full signal detection with negligible  $T_2$  decay or J-modulation. CSDEs were reduced to below 5% per ppm in slice direction and were eliminated in-plane.  $B_1$  sensitivity was similar to that in standard gradient echo images.  $B_1+$  errors were corrected using flip angle maps. Metabolic ratio maps were additionally completely insensitive to receive  $B_1-$  inhomogeneities.

SAR requirements were well below the limit ( $\sim 20\%$  = 0.8 W/kg). The suppression of subcutaneous lipid signals was achieved by substantially improving the point spread function. In total six subjects were measured. Four reproducibility measurements were performed in one subject. A  $64 \times 64$  matrix was acquired within 30 min. A circular k-space was sampled using a spiral pattern, starting in the center of the k-space [2]. Spatial Hamming filtering was performed. First-order phase errors were incorporated into the metabolite basis set. All data were processed using LCModel software.

## Results:

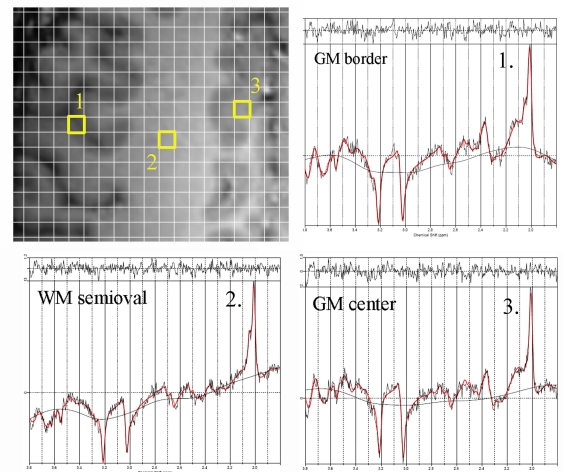
High quality metabolic mapping of several important brain metabolites (NAA, Cho, Cr, Ins, Glu) was achieved for a  $64 \times 64$  matrix with a  $3.4 \times 3.4 \times 12\text{ mm}$  voxel size in six healthy subjects (Fig.1, Fig.2). Subcutaneous lipids were suppressed by an additional factor of  $\sim 12$  compared to standard  $32 \times 32$  matrix (Fig.3). Most notably, the ultra-short TE increased the signal-to-noise ratio of J-coupled resonances, such as the important neurotransmitter, glutamate, by a factor of  $\sim 10$  compared to commonly used  $^1\text{H}$ -MRSI sequences. In addition to the increased SNR and spectral resolution at 7T, this enables reliable quantification of glutamate signals

Four measurement repetitions in one healthy volunteer provided proof of the good reproducibility of this method. With such a high resolution differences in white and grey matter for Glu/NAA can be easily distinguished. Homogeneous Cho/NAA maps were found. A characteristic Cho hotspot as previously found also by other studies was found in the mesial frontal brain region [3]. Also several other characteristic anatomical differences between grey and white matter were visible.

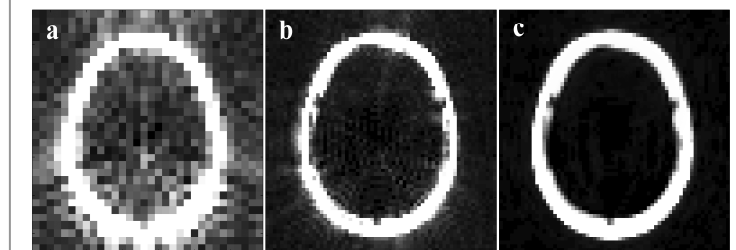
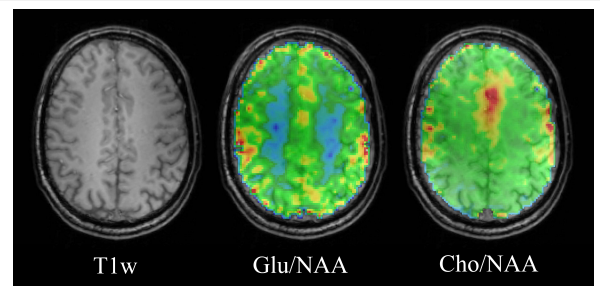
## Discussion and Conclusion:

FID-MRSI as presented in our study is insensitive to  $T_2$  decay, J-modulation,  $B_1$  inhomogeneities, CSDEs, and overcomes SAR restrictions at ultra-high magnetic fields. This makes it a promising method for high resolution  $^1\text{H}$ -MRSI at 7 T and above.

**Fig. 1:** shows sample spectra obtained from two grey matter and one white matter region of the brain with a nominal spatial resolution of  $3.4 \times 3.4 \times 12\text{ mm}$ .



**Fig. 2:** shows metabolic ratio maps of Glu/NAA and Cho/NAA which are completely insensitive to any  $B_1$  inhomogeneities with  $3.4 \times 3.4 \times 12\text{ mm}$  spatial resolution.



**Fig. 3:** comparison of lipid contamination (note: for display purpose enhanced by a factor of 10) for a (a)  $32 \times 32$ , (b)  $64 \times 64$ , and (c) hamming-filtered  $64 \times 64$  matrix.

## References:

- [1] Henning, et al. NMRBiomed 2009; 22:683-696
- [2] Haupt et al. MRM 1996; 35:678-687
- [3] Degaonkar, et al. JMRI 2005; 22:175-