High resolution spectroscopic imaging with ultra short TE in patients with multiple sclerosis and brain tumors at 7T

Gilbert Hangel[1], Bernhard Strasser[1], Michal Považan[1], Stephan Gruber[1], Marek Chmelik[1], Georg Widhalm[2], Engelbert Knosp[2], Assunta Dal-Bianco[3], Fritz Leutmezer[3], Siegfried Trattnig[1], and Wolfgang Bogner[1]

[1]MCRE, Department of Biomedical Imaging and Image-guided Therapy, Medical University of Vienna, Wien, Vienna, Austria, [2]Department of Neurosurgery, Medical University of Vienna, Wien, Vienna, Austria, [3]Department of Neurology, Medical University of Vienna, Wien, Vienna, Austria

Target Audience:

Scientists with interest in the application ofMRS/MRSIfor MS and tumor diagnostics

Purpose:

To our knowledge, there are no prior reports of the application of high-resolution MRSI at 7T for the research of multiple sclerosis (MS) and brain tumors. With this work, we demonstrate the feasibility of using accelerated free induction decay (FID) 2D- and 3D-MRSI with ultra-short acquisition delay (AD)[1] to detect metabolic differences in MS lesions and low grade glioma.

Methods:

Our MRSI sequence was used in a single slice (SSL) and a Hadamard-encoded four slice (4SL) version[2], both using a 64×64 matrix with elliptical weighting, FOV of 220mm and 8mm slice thickness. The sequence used direct FID acquisition after an AD of 1.3 ms for the SSL measurement and ADs of 1.3/2.3/3.3/4.3 ms for the 4SL-measurement.The sequences were accelerated using in-plane CAIPIRINHA[3,4] or a combination of in-plane (2D) and slice-accelerated CAIPIRINHA (2D+1D) with an effective acceleration factor of 5 for the SSL- and 8.3 for the 4SL-sequence, resulting in measurement times of 6:00 and 22:38 minutes.

We successfully performed measurements of two MS patients (male, 43 y and 31 y) and two low grade glioma patients (WHO grade 2, male, 46y and 35 y) using a 7T Siemens Magnetom scanner (32 channel head coil in array coil mode) as part of a conventional imaging protocol. Institutional board of review approval and informed consent were obtained for this study.

Measurement data were Hadamard-decoded, CAIPIRINHA-reconstructed, and signals from coil elements were combined using image-based pre-scan reference data[5].The resulting spectra were processed with LCModel software. Maps of metabolic concentrations, ratios, CRLB, linewidths… were created and displayed as color-coded overlays after interpolation to 128×128.

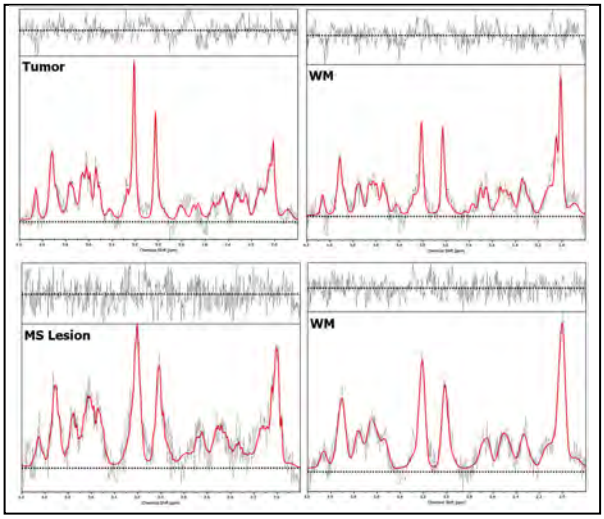

Fig.1: *Example spectra of SSL measurements in a tumor and a MS patient, with regular WM spectra as comparison [nominal voxel size: 3.4×3.4×8 mm]*

Results:

The average SNR values for tNAA were found to be over 5 in all measurements, indicating sufficient SNR for reliable spectral quantification.

The spectra in Fig.1 illustrate the differences between lesions and healthy white matter. MS lesions show very well as hypointense clusters in tNAA maps comparable to anatomical imaging (Fig.2 and Fig.3). In particular, focal regions of low NAA were found even in areas without corresponding changes visible on conventional T1 or T2-weighted MRI. In the glioma measurements, especially tCho/tNAA maps highlight the tumor location (Fig.4 and Fig.5) with elevated Cho in particular indicating focal areas of highly metabolically active tumor tissue.

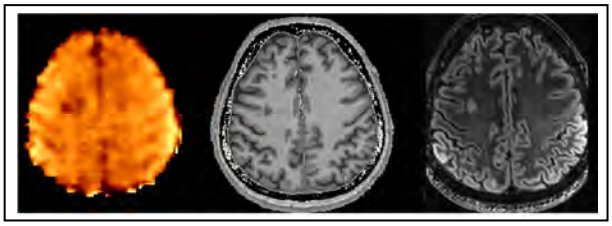

Fig.2: *SSL tNAA map of an MS patient compared with T_1-weighted and FLAIR images; in addition to the lesion visible on the anatomical scans, another NAA signal drop is visible next to it*

Discussion/Conclusion:

The presented MRSI sequence was shown to clearly display metabolic differences in tumors and MS lesions as metabolite or metabolite ratio maps with high spatial resolution. It may be possible that MS lesions could be visible on NAA maps even before they show on conventional imaging methods, which is an interesting target for future research.

Limitations include that even with parallel imaging accelerated MRSI, the measurement protocol for multi-slice acquisitions may not be feasible in all patients. Due to B0 shimming limitations, only regions at the level of the upper ventricles and above can be measured with good data quality. Further hardware and sequence improvements will be necessary to overcome these limitations.

High-resolution 3D-MRSI of the brain with ultra-short TE will be a powerful tool for neuroscientific studies even well beyond these two clinical examples.

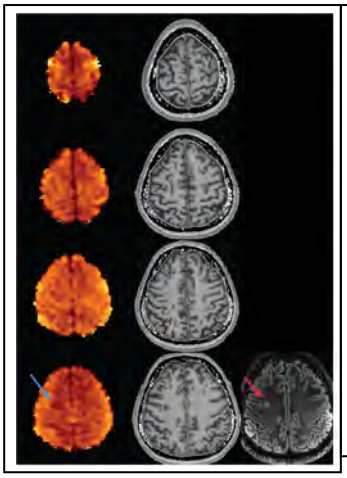

Fig.3: *tNAA maps of all four slices in a MS patient, the same lesion as in Fig.2 is clearly*

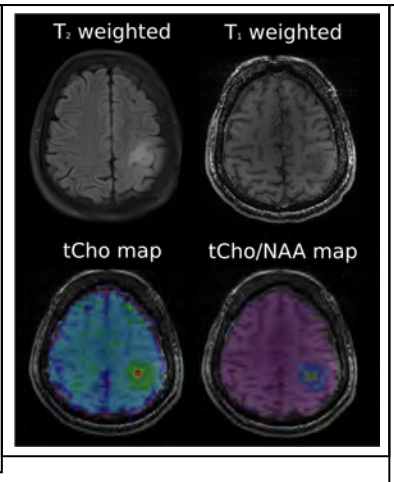

Fig.4: *Maps of a glioma in the parietal lobe*

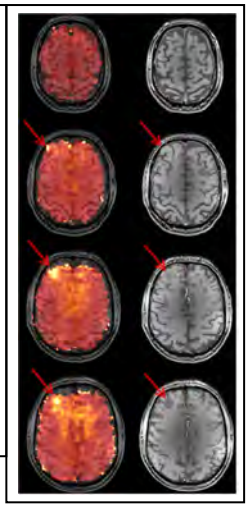

Fig.5: *tCho to tNAA ratio maps and T_1-weighted images of all four slices for a glioma in the frontal lobe*

References:

[1] Bogner et al., NMR Biomed 2012; 25(6):873-82
[2]Hangel et al., Proc. Intl. Soc. MRM 22 (2014):3728
[3]Strasser et al., Proc. Intl. Soc. MRM 21 (2013):201
[4]Strasser et al., Proc. Intl. Soc. MRM 22 (2014):5048
[5]Strasser et al., NMR Biomed 2013; 26(12):1796-805