3D GABA imaging with high spatial resolution at 3T using a navigated MEGA-LASER MRSI sequence

Wolfgang Bogner[1], Borjan Gagoski[2], Aaron T Hess[3], Bernhard Strasser[1], Himanshu Bhat[4], Dylan Tisdall[5], Andre J.W. van der Kouwe[5], Ellen Grant[2], Siegfried Trattnig[1], Bruce Rosen[5], and Ovidiu C Andronesi[5]

[1]High-field MR Center, Department of Biomedical Imaging and Image-guided Therapy, Medical University Vienna, Vienna, Vienna, Austria, [2]Fetal-Neonatal Neuroimaging & Developmental Science Center, Boston Children's Hospital, Harvard Medical School, Boston, United States, [3]Department of Cardiovascular Medicine, John Radcliffe Hospital, University of Oxford Centre for Clinical Magnetic Resonance Research, Oxford, United Kingdom, [4]Siemens Healthcare, Charlestown, United States, [5]Athinoula A. Martinos Center for Biomedical Imaging, Department of Radiology, Massachusetts General Hospital, Harvard Medical School, Charlestown, United States

Target Audience:

Developers of MR sequences (MRS, motion correction, imaging acceleration);Neuroscientists and clinicians interested in neurotransmitters GABA and Glx.

Purpose:

Alterations in gamma amino butyric acid (GABA) - the major inhibitory neurotransmitter in the brain - are relevant in many neuro-psychiatric disorders. MRS is the only way to measure GABA non-invasively *in vivo*. However, measuring GABA is challenging due to its low concentration and signal overlap with more abundant brain metabolites. The most popular MRS technique for unambiguous GABA detection is MEscher-GArwood (MEGA) editing [1], which provides the highest retained signal compared to other techniques. However, MEGA editing is a subtraction technique, and is therefore prone to scanner instabilities and motion artifacts. In addition to chemical shift displacement errors (CSDE) that reduce editing efficiency, other technical limitations exist [2]. Most commonly, the measurements are limited to rather large single-voxel placed in the brain region of interest [2]. So far, only one group published MEGA editing data on 2D-MRSI [3]. Consecutive measurements of several single-voxels in different locations are inefficient and clinically not feasible. Moreover, the brain coverage of 2D-MRSI is limited as well. Nevertheless, to obtain neurotransmitter profiles from different brain regions is highly desirable. We designed a new 3D-MRSI sequence for robust and efficient GABA imaging by integrating three highly optimized modules: i) adiabatic J-difference MEGA-LASER [4], ii) spiral spectroscopic imaging, and iii) real-time motion and shim correction [5].

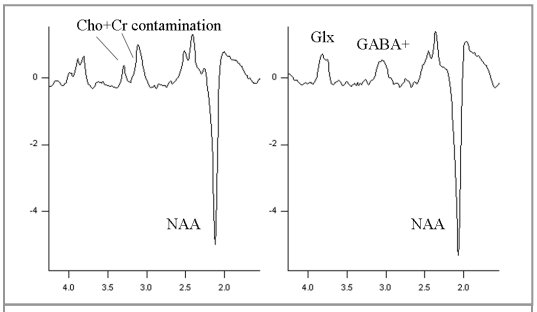

Fig. 1: Subtraction spectra obtained by MEGA-LASER 3D-MRSI in the frontal lobe: (left) w/o ReShMoCo severe subtraction artifacts bias GABA+ quantification. (right) ReShMoCo reduces subtraction artifacts significantly.

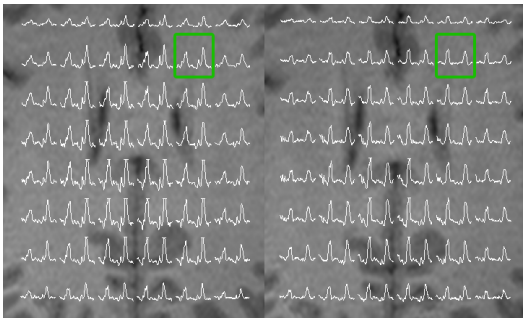

Fig. 2: Difference spectra in an axial slice: (left) without correction movement results in strong subtraction artifacts particularly in the frontal lobe. (right) Subtraction artifacts are eliminated by ReShMoCo. The GABA-Glx range is shown.

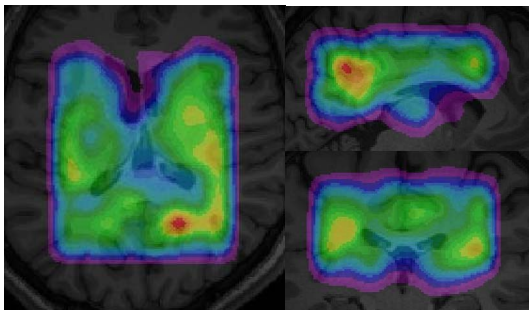

Fig. 3: 3D-GABA+ map obtained by LCmodel quantification using MEGA-LASER 3D-MRSI with ReShMoCo (16x16x10 matrix, 1cc isotropic resolution in ~24min)

Methods:

Phantoms and volunteers (n=5) were scanned on a 3T TIM Trio MR Scanner (Siemens, Erlangen, Germany) using a 32-channel head coil. Phantom measurements (i.e., sphere filled with GABA, Glu, Cre and other brain metabolites, surrounded by lipids) were evaluated for editing efficiency and the performance of correction algorithms. In order to minimize subtraction errors we implemented a combination of Reacquisition, Shim, frequency, and Motion Correction (ReShMoCo). Simulations to find the optimum MEGA-LASER editing scheme/timing were performed.

Gradient Offset Independent Adiabatic GOIA-W(16,4) pulses, with 3.5 ms duration and 20 kHz bandwidth were used for LASER, excitation and two 65 Hz Gauss refocusing pulses were used for MEGA editing [4]. A dual-contrast, multi-shot 3D-EPI navigator was inserted prior to water suppression to provide real-time motion, shim, and frequency correction [5]. Any data which happened to be corrupted by motion in between the updating of two consecutive navigators were selectively discarded and reacquired. *In vivo* MRSI parameters were: TR/TE 1600/68ms; 8cc isotropic; matrix size of 10×10×10 interpolated to 16×16×16; FOV 20×20×20cm; VOI 9×7×5cm; spectral bandwidth 1.1kHz; 20 averages (acquisition weighted in z-direction); TA 9:55min. Additional high-resolution scans were acquired in one volunteer (16×16×10, 1cc isotropic in ~24min). Standardized movement patterns (i.e. repeated ~10° right-left head rotation and up-down head translation) were tracked and corrected in real-time. Localization and spectral quality were evaluated qualitatively and quantitatively (i.e. linewidth, SNR, contamination) for MEGA-OFF and difference spectra.

In vivo data from five MRSI scans were compared: (a) static scan w/o MoCo; (b) static scan with ReShMoCo; (c) motion scan w/o MoCo; (d) motion scan with ShMoCo; and (e) motion scan with ReShMoCo.

Results:

The weighted stack-of-spirals MEGA-LASER 3D-MRSI sequence provided accurate localization, high spectral quality, and editing efficiency in phantoms and volunteers (Fig. 1-3). Motion during the scans caused significant subtraction artifacts (16±6%) that biased GABA quantification, even if MEGA-OFF spectra looked relatively normal (Fig 1,2). The use of ShMoCo improved data quality, but some residual subtraction artifacts remained. However, additional reacquisition of corrupted TRs successfully eliminated major subtraction errors and possible bias in GABA quantification (Fig. 1,2).

Discussion/Conclusions:

Combined spiral accelerated MEGA-LASER 3D-MRSI with real-time ReShMoCo significantly improved editing efficiency and spectral *in vivo* quality in the presence of motion and/or scanner instabilities. Therefore, with ~10 min acquisition time, this sequence allows clinically feasible and robust 3D mapping of GABA and Glutamate in the brain at 3T.

References:

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