Multi-echo Echo-planar J-resolved spectroscopy of human brain using semi-LASER pulses

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Target audience: Scientists interested in spectroscopic imaging, adiabatic pulses and multi echo sequences.

Purpose/Introduction: Echo-planar (EP)-based *J*-resolved spectroscopic imaging (JRESI) combines the speed advantage of echo-planar spectroscopic imaging (EPSI) readout with the increased spectral dispersion offered by 2D JPRESS and is capable of recording better-resolved 2D spectra from multiple region[1]. Multi-Echo (ME) based technique has been used to further reduce total scan time of 4D EP-JRESI, where two bipolar echo-planar imaging (EPI) read-out trains are used to collect dual phase encoded lines within a single TR[2]. Like other point-resolved spectroscopy (PRESS) based *in vivo* MRSI techniques with conventional pulses, the ME-EP-JRESI pulse sequence also suffers from large chemical shift displacement error (CSDE), non-uniform excitation, lipid contamination on the boundary and additional J-refocused artifactual peaks from spatially dependent J-coupling evolution[3, 4]. It has been demonstrated that by adopting semi-localized by adiabatic selective refocusing (sLASER) MRSI where adiabatic pulses having relatively high bandwidth are used, these artifacts can be minimized[4, 5]. In this study a sLASER based ME-EP-JRESI sequence is implemented and evaluated in phantoms and human brains. To demonstrate the feasibility and strength of the new sequence, a quantitative analysis was also done. We hypothesized that the sLASER-based ME-EP-JRESI sequence will be more reliable and accurate spatial distribution of metabolites in the human brain than the standard ME-EP-JRESI sequence.

Materials and Methods: The basic 4D ME-EP-JRESI sequence (Fig. 1) which uses a 90°–180°-Δt_1-180° scheme for localization was modified by employing two pairs of adiabatic fast passage pulses (AFP) in place of the refocusing 180° pulses (shown by arrows in Fig. 1); an optimized slice-selective 90° pulse was used for excitation. Also, the slice selective refocusing 180° pulse between the two bipolar EPSI read-out trains was kept same. In this way, only two pairs of AFP pulses were used to keep the RF power within the SAR limits and TE relatively short. A non-adiabatic version was used for comparison. All 4D data were collected on a 3T Skyra MRI scanner using the Siemens VD13a compiler using a 16-channel head 'receive' coils. A gray matter (GM) brain phantom containing sixteen metabolites (pH=7.3) was used for acquiring 10 *in vitro* measurements each for ME-EP-JRESI with and without sLASER. After obtaining written consent under local IRB approval, 5 healthy subjects (age 23-59 years) were scanned. The following parameters were used for both sLASER based and standard ME-EP-JRES phantom data: TR/TE = 2s/41ms, 1x1x2 cm^3 voxel for VOI localization, 64 Δt1 increments, 256 bipolar echo pair, FOV= 16x16cm^2, F1 and F2 bandwidths of 1250 Hz and 1190 Hz. Scan time for fully sampled data was ~17 min and NUS was ~8.5min respectively. A non-water-suppressed ME-EP-JRESI data with t_1=1 were also recorded. For *in-vivo* NUS data TR was 1.5s with scan time ~6.5 min. Other scan parameters were as of phantom.

Acquired data were extracted and post-processed with a library of custom developed MATLAB-based program, which sorted out the data first from the two EPSI read-out trains and then applied spatial Hamming filter[2]. This was followed by post-processing through a series of steps including scaling by a constant value, combining echoes, resolving averages and oversampling, coil combination and Eddy current correction. Modified Profit[6] algorithm was applied to process the extracted data and to calculate metabolite ratios with respect to the creatine (Cr) peak at 3.0 ppm.

Results and Discussion: Feasibility of 2D J-resolved LASER and sLASER sequences was first verified using the GM phantom. As shown in Fig. 2(c), ME-EP-JRESI sLASER sequences produced very similar 2D J-resolved spectra with the ME-EP-JRESI with standard coil. Fig. 2(a) shows a comparison of metabolite ratios with respect to Cr from a voxel away from center calculated by the ProFit quantiation. The metabolite ratios from sLASER based ME-EP-JRESI matched ME-EP-JRESI data and were in good agreement with original true values of the phantom metabolites. Fig. 2(b) shows the metabolite maps, as measured by peak area integration, of the 2D diagonal peaks of Cr/Cho, and NAA from ME-EP-JRESI with and without sLASER. In sLASER based ME-EP-JRESI peaks were localized within the PRESS excitation volume better with minimal leakage.

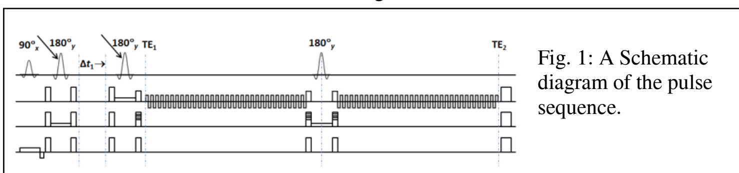
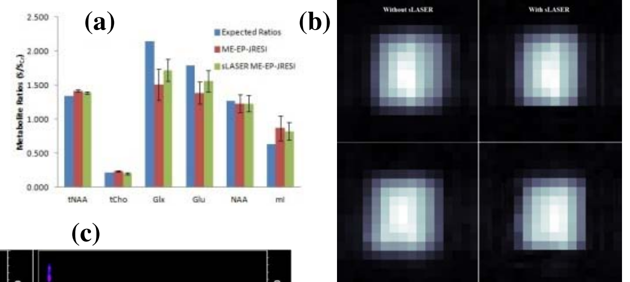


Fig. 1: A Schematic diagram of the pulse sequence.



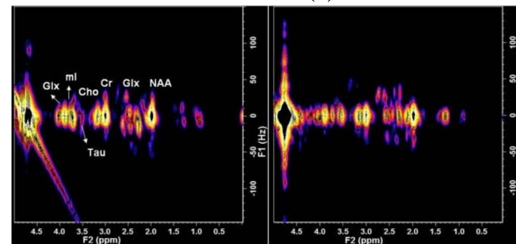


Fig. 2: Comparison of (a) mean metabolite ratios (±SD) with expected values, (b) metabolite maps, and (c) spectra extracted from the center of the phantom between ME-EP-JRESI without and with sLASER.

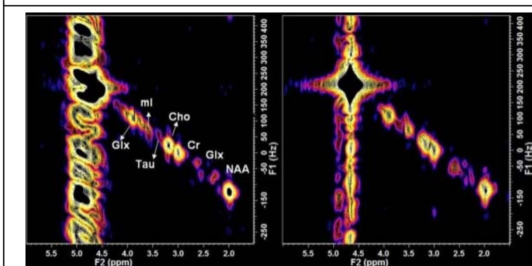


Fig. 3: ME-EP-JRESI spectra from occipital GM/white matter (WM) regions of a 37 years healthy male for: (a) without sLASER (left), (b) with sLASER (right). To show residual water effect spectra are displayed tilted (COSY-like).

Figure 3 shows 2D spectra acquired from a voxel in the occipital GM/WM of a healthy volunteer using the two sequences at same TE. The residual water peak, which is most prominent in ME-EP-JRESI reduced in sLASER version. This observation is consistent with a recent report[4]. Decrease in residual water signals will benefit the spectral quantification, especially for those metabolites with resonances close to the strong "phase-twisted" water peak.

Conclusion: In the present work, ME-EPJRESI sLASER spectroscopy was successfully implemented and after testing with the phantom, human brain spectra were recorded. Compared with ME-EP-JRESI using conventional pulses, sLASER based ME-EP-JRESI significantly suppressed the additional J-refocused artifactual peaks and reduced the CSDE. This technique is expected to advance the application of in vivo 2D MR spectroscopy at 3T and higher field strengths for more reliable and accurate quantification of metabolites. **Acknowledgement:** This research was partially supported by a NIH R01 grant (NINR 013693).

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