Multi-Echo Acquisition Based J-Resolved Spectroscopic Imaging on a Whole-Body 3T Scanner

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Introduction & Purpose: Two-Dimensional (2D) Magnetic Resonance Spectroscopic (MRS) schemes like J-Resolved Spectroscopy (JPRESS) can be used to resolve metabolites normally obscured through J-coupling interactions and overlap under 1D MRS (1). Combined with 2D spatial encoding, JPRESS is capable of detecting the spatial distribution of a wide variety of metabolites, at the expense of prohibitively long scan times. Multi-Echo (ME) based acquisition schemes have proven effective in reducing scan times in both imaging (2) and Magnetic Resonance Spectroscopic Imaging (MRSI) (3-5). By integrating ME-acquisition with a 2D spatially resolved JPRESS sequence, a fast MRSI sequence has been developed capable of generating 2D spectral maps over a 2D spatial array in clinically viable scan times. This novel sequence was then tested for performance and reproducibility in a series of brain phantom scans.

Materials & Methods: A brain phantom containing 16 metabolites at physiological concentrations was scanned using an ME-enhanced MRSI sequence with an 8-channel knee-array coil in a Tim Trio 3T whole-body scanner. The JPRESS sequence consisted of three slice-selective radio-frequency (RF) pulses (90°-180°-180°). Under the ME acquisition, the last 180° pulse was followed by a train of three more 180° pulses, each followed by an ADC pulse to record the signal echo. In this way, data from four voxels were acquired in a single repetition. Because this MRSI sequence operates over an 8x8 spatial array, an entire row of K-space data was acquired over two repetitions. The acquisition parameters were as follows: TE/TR = 30ms/1.5s, 64 $\Delta t1$ increments (extrapolated to 100 by linear prediction), 512 complex points, 2000 Hz bandwidth, 1 average and 1.5x1.5x1 cm3 voxels. The total scan time was 25.5 minutes.

Five scans with the knee-array coil and one with a 12-channel head coil were acquired and then post-processed using a custom-built MATLAB-based program. A 2D spatial Fourier transform was applied to the data to generate spatial profiles and spectral FFTs were applied to the t1 and t2 dimensions to generate the 2D spectra. A spatial Hamming filter and exponential spectral filters were also applied to the data.

Results and Discussion: Metabolite peaks due to creatine (Cr) (3.0 ppm, 3.9 ppm), choline (Cho) (3.2 ppm), N-acetyl aspartate (NAA) (2.0 ppm) as well as lactate (Lac) (1.3 ppm) were all visible in the spectral data (6). Figure 1 (left) shows the JPRESS spectra taken from the volume of excitation. Figure 1 (right) shows the spatial profile of the metabolite peak due to lactate superimposed over the entire 8x8 spatial array. The spatial profile of the lactate resembled a spherical shape, corresponding with the shape of the brain phantom. The concentration of lactate in this phantom was 0.5 mM.

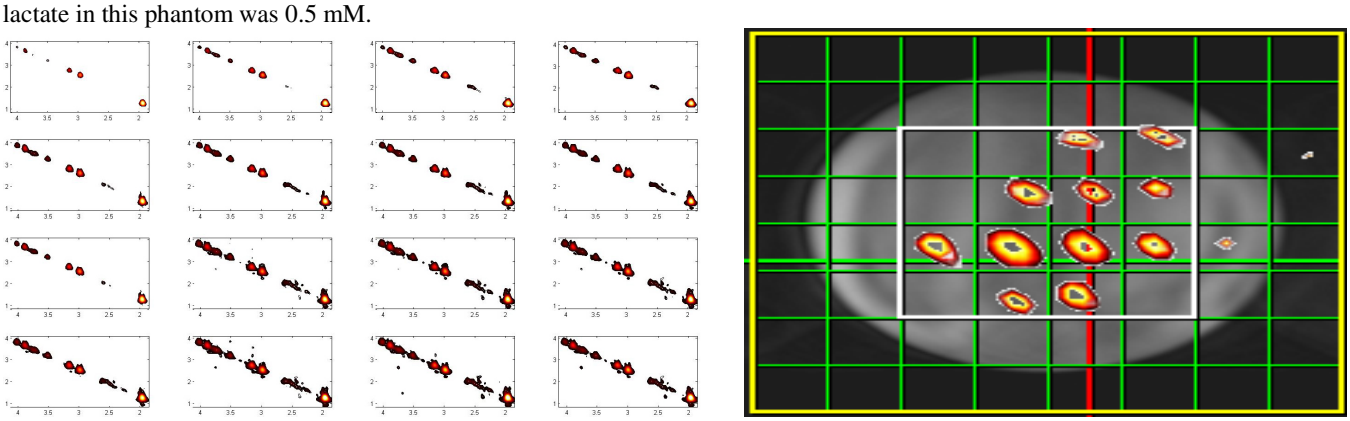

Figure1: MRSI data taken from a ME-based JPRESS scan of a brain phantom with an 8-channel knee-array coil. At left is JPRESS spectra in the 2.0-4.0 ppm range taken from the central 16 voxels of K-space. At right is a zoomed profile of Lactate (Lac) (1.3 ppm) superimposed over an image of the corresponding voxel localization.

Conclusion: 2D JPRESS data acquired from the brain phantom scans showed both the ability to detect metabolites at physiological concentrations and a spatial profile consistent with the spherical shape of the brain phantom. This pilot study demonstrates the viability and reproducibility of this ME-enhanced JPRESS MRSI sequence. Further improvements in signal acquisition, including the use of receive coils with a greater number of channels, could lead to improvements in the acquisition time.

References:

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