Efficient Spectroscopic Imaging by an Optimized Encoding of pre-Targeted Brain Main Metabolic Resonances

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Target audience: MRI/MRSI sequence programmers, researchers interested metabolic imaging and mapping.

Purpose: Obtain MRSI information in a faster, more efficient way using Relaxation-Enhanced Chemical shift-Encoded Spectroscopically-Separated (RECESS) MRI.

Introduction: MRSI plays a crucial role in deciphering the intricate relationships between the brain's structure, function, and metabolism [1]. Recently, a "relaxation-enhanced" (RE) selective-excitation MRS approach could acquire *in vivo* localized spectra with flat baselines and excellent signal-to-noise ratios (SNR) in a single scan [2, 3]. This transforms an in-principle continuous spectral acquisition into a sparse, binned one, targeting only few resonances whose positions are *a priori* known – opening in turn new possibilities to acquire the MRSI information in a faster, more efficient manner. Indeed with evolution frequencies known, the images of the various targeted metabolite can in principle be resolved by collecting a series of conventional imaging echoes, with the chemical shifts of the different resonances encoded into the MR images as coherent phase modulations amenable to disentanglement by some form of post-processing –for instance Fourier or Hadamard analyses. The present study describes the principles, the implementation and the potential of one such new form or MRSI, based on what we denote as RECESS MRI.

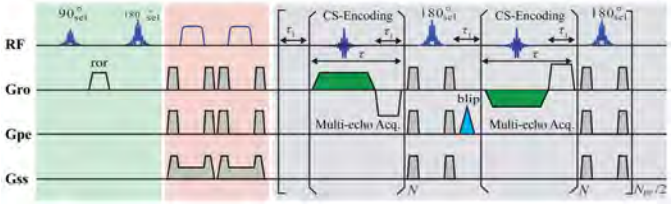

Fig. 1 Multi-echo RECESS sequence, delivering 2D images of *N a priori* defined peaks in a single scan.

Methods: A variant of RCESS MRI is shown in Fig. 1. The sequence begins with a multiband selective echo targeting solely resonances of interest [3]. The spectroscopic information is then extracted via N refocused readout gradients whose echoes are timed at intervals $\{\tau\}$ such as to enable –following the echoes fast FT along their k-evolution axes– a stable Fourier-based matrix inversion delivering each of the metabolites' images. A τ_1 delay is introduced to refocus the gradient-imposed evolution without disturbing the shift-encoding steps. The acquisition acquires a CPMG-based echo train that carries out a phase encoding of the remaining spatial dimensions (N_{pe} loops) in a single scan. The spatial encoding of the MRS information is assumed along only two axes, leaving a need for a 1D LASER block [4] to localize the remaining dimension. All experiments were done on a 7T Agilent MRI scanner.

Results & Discussion: A phantom, containing three tubes with different components (Fig. 2a, I: Methanol; II: Acetone; III: Cyclohexane) inside a water tube, was tested for the RECESS sequence. The water was unperturbed by a 40 ms 90˚ SLR multiband selective pulse. Spectroscopically-separated images mapping the resonances I, II, III, are obtained in 20 sec with good SNR and residual level performances (Fig. 2 b-d).

Figure 3 shows the metabolic-separated capabilities of RECESS MRI, on an *ex-vivo* mouse brain, involving a 40 ms 90˚ SLR pulse targeting solely the three prominent metabolites in the brain: Choline (Cho), Creatine (Cre), and N-Acetyl-Asparate (NAA) resonances. Figs 3d-f and 3g-i compare, respectively, the metabolic maps of Cho, Cre, NAA are arising upon using the RECESS method vs a conventional chemical shift imaging sequence. Very good agreement is obtained with a higher time effiency.

Conclusion: RECESS MRI provides new possibilities to acquire the MRSI information in a faster, more efficient manner, rendering MRSI a more widely used technique.

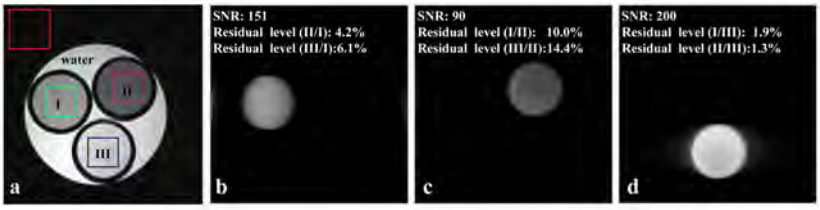

Fig. 2 Phantom test for the RECESS sequence. (a) Reference multi-shot spin-echo image. (b-d) Three spectroscopically-separated images acquired by RECESS sequence, corresponding to I, II, III components in (a), respectively. The SNR is measured as the average of the corresponding component signals within the related marker divided by the standard deviation of the noises (marked as red color). For each component, the residual levels are calculated by the average signals of the other two residual signals within the markers divided by the average signals of the component with the marker. Scan parameters: L_{ro} = 40 mm, L_{pe} = 40 mm, slice thickness = 2 mm, dummy scan =2, echo time = 50 ms, TR = 5 s, # averages = 1. RECESS parameters: τ = 1.002 ms, N = 6. the matrix size = 128 × 128, scan time is 20 sec.

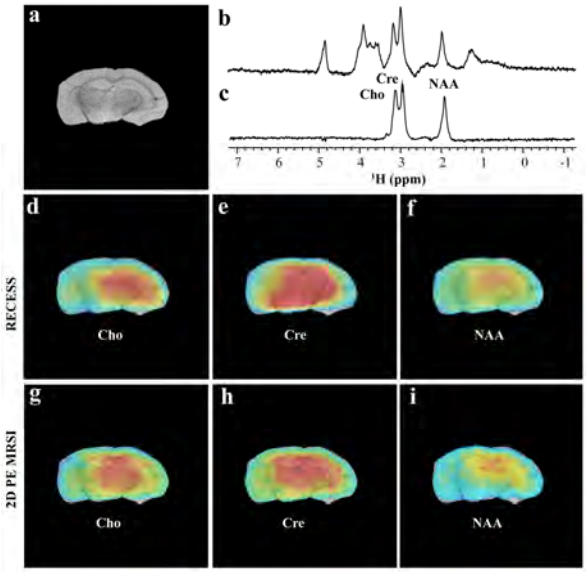

Fig. 3 Comparison of the *ex-vivo* mouse brain results obtained using the RECESS sequence (d-f) vs results arising from a chemical shift sequence using two phase-encoded gradients for imparting the spatial resolution. (a) Reference multi-shot spin-echo image. (b, c) Spectra acquired using PRESS sequence and LRE sequence [2] on a 16 × 16 × 4 mm^3 voxel with 32 averages. The LRE sequence uses 40 ms SLR pulse only exciting the Cho, Cre, NAA resonances. (d-f) 2D spatial Cho, Cre, NAA maps acquired by RECESS sequence. (g-i) Idem for Cho, Cre, NAA ratio maps by conventional CSI. Scan parameters: L_{ro} = 16 mm, L_{pe} = 16 mm, slice thickness = 4 mm, matrix size =32 × 32, echo time = 50 ms, TR = 2 s. τ = 1.524 ms, N = 8, # averages = 2048 for RECSS while 8 for the phased-encoded sequence. The experimental time of RECESS experiment was 2 h 16 m (including reference scanning) while that of regular experiment took 4 h 33 m.

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