Efficient Spectroscopic Imaging by an Optimized Encoding of Pre-targeted Resonances

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Introduction

MRSI plays important roles 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 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 analyses. The present study describes the principles, the implementation and the potential of one such new form of MRSI, based on what we denote as Spectroscopically-Encoded Chemical Shift Imaging (SECSI).

Methods

A variant of SECSI MRSI is shown in Fig. 1a. The sequence begins with a multiband SLR selective pulse 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 (Fig.1 b) 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. Figures 1c and d show the data procedure.

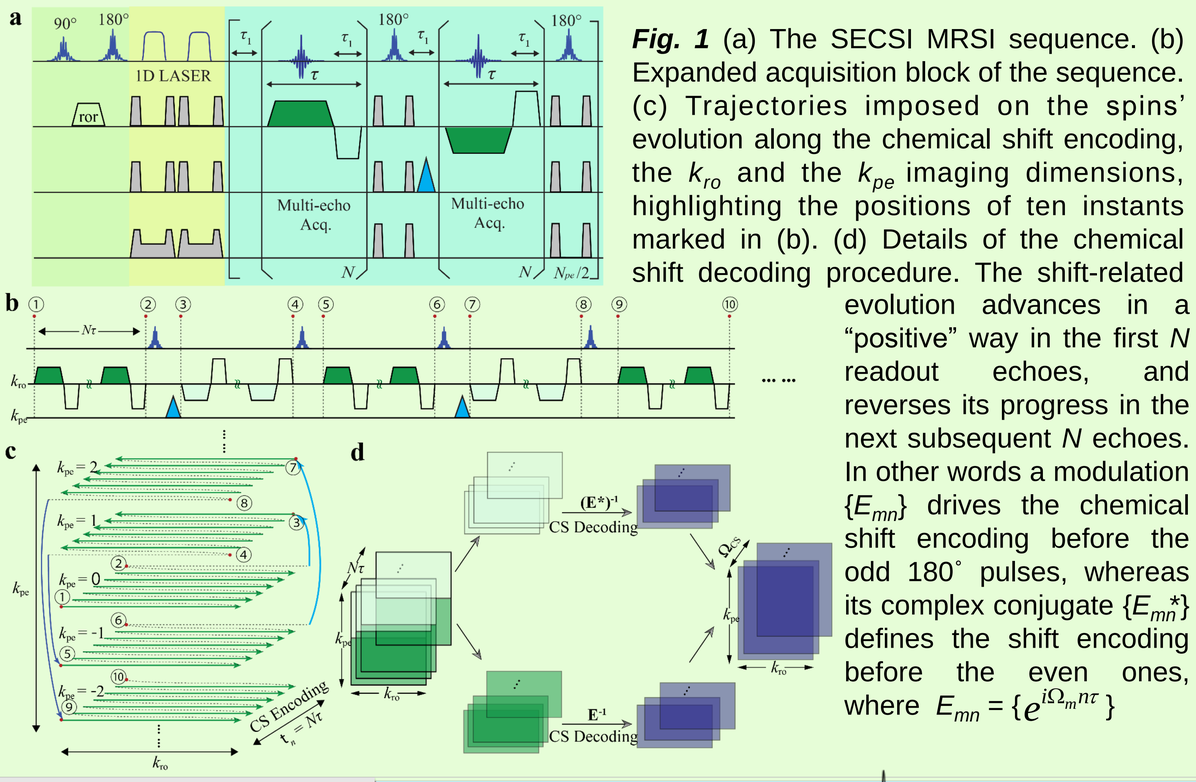

Fig. 1 (a) The SECSI MRSI sequence. (b) Expanded acquisition block of the sequence. (c) Trajectories imposed on the spins' evolution along the chemical shift encoding, the k_{ro} and the k_{pe} imaging dimensions, highlighting the positions of ten instants marked in (b). (d) Details of the chemical shift decoding procedure. The shift-related evolution advances in a "positive" way in the first *N* readout echoes, and reverses its progress in the next subsequent *N* echoes. In other words a modulation $\{E_{mn}\}$ drives the chemical shift encoding before the odd 180˚ pulses, whereas its complex conjugate $\{E_{mn}^*\}$ defines the shift encoding before the even ones, where $E_{mn} = \{e^{i\Omega_m n\tau}\}$

Results

The usefulness of this SECSI MRSI approach is demonstrated on a chemical phantom (Fig. 2), on an ex-vivo mouse brain for metabolic mapping (Figs. 3) and in vivo water-fat separation imaging at 7 T (Figs. 4). (See captions for details). The phantom contains three tubes with different components (I: Methanol; II: Acetone; III: Cyclohexane) inside a water tube. All experiments were done on a 7T Agilent MRI scanner.

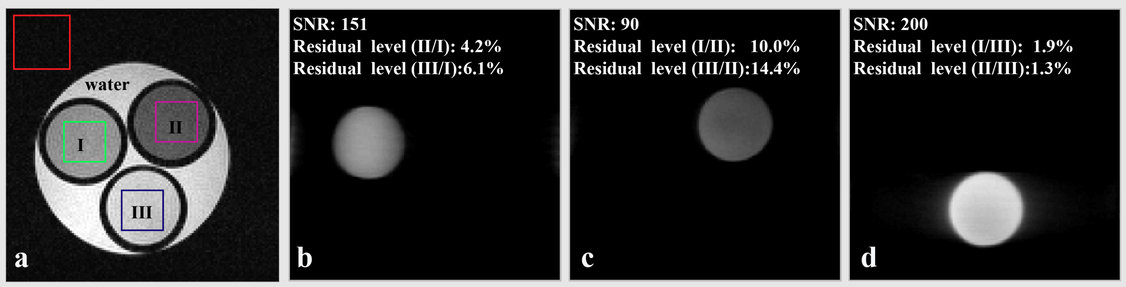

Fig. 2 Phantom test for the SECSI MRSI sequence. (a) Reference multi-shot spin-echo image. (b-d) Three spectroscopically-separated images acquired by SECSI MRSI sequence, corresponding to I, II, III components in (a), respectively. The SNR is measured as the average of the corresponding component signals 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: FOV = 40×40 mm^2, matrix size = 128×128, slice thickness = 2 mm, echo time = 50 ms, TR = 5 s, # averages = 1. RECESS parameters: τ = 1.002 ms, N = 6. The scan time is 10 sec.

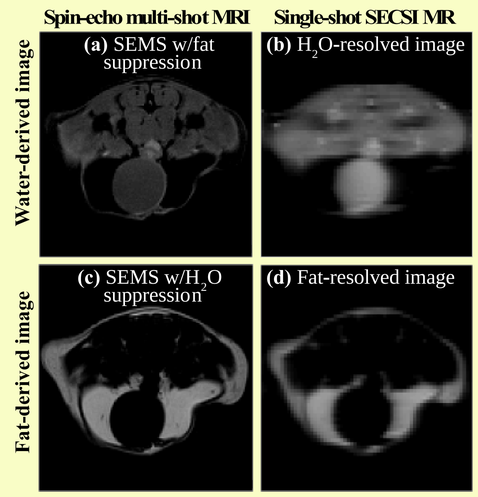

Fig. 4 In vivo fat/water separation capabilities of the SECSI sequence, as applied to abdominal mouse investigations at 7T. (a, c) Multiscan spin echo references involving fat suppression (a) and water suppression (c). (b, d) Water- (b) and fat-tissue (d) images separated by single-scan SECSI acquisition. Common imaging parameters: FOV =32×32 mm^2, TR = 2 sec, TE = 14 ms, slice thickness = 2 mm. The reference image matrix size was 128×128; due to the short T2s the SECSI image size was 64×64, which explains the lower resolution. Total scan time for each spin-echo multi-scan image: 4 min 16 sec. Total SECSI acquisition time (including a reference navigator scan): 4 sec.

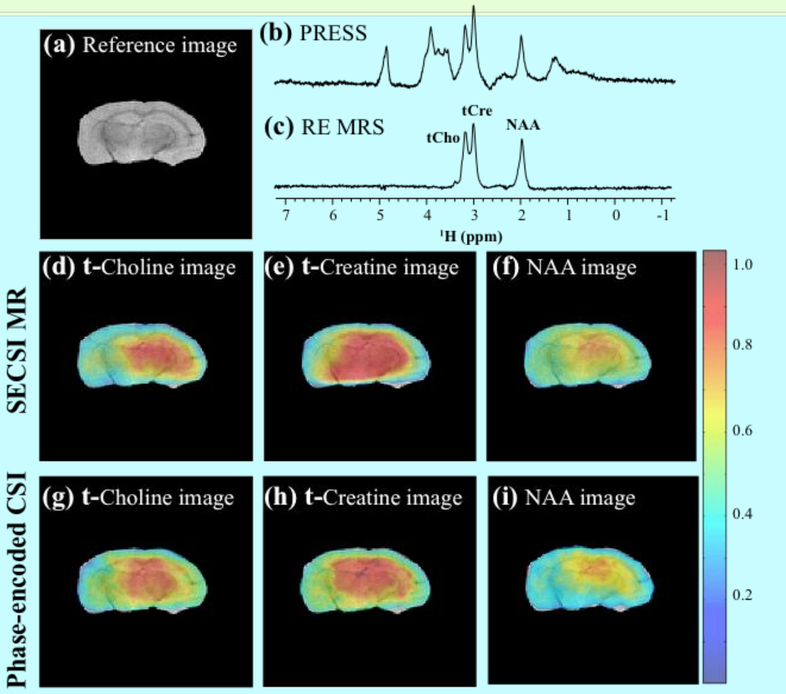

Fig. 3 Comparison of ex-vivo mouse brain results arising from SECSI and from a phase-encoding CSI sequence. (a) Reference SEMS image. (b) Reference PRESS spectrum acquired on a 16×16×4 mm^3 voxel using 32 averages. (c) RE MRS spectrum acquired on the same voxel and scan numbers as (b), using a 40 ms two-band SLR pulse exciting the total Cholines (tCho) and total Creatines (tCre) in one band, and N-Aceytl Aspartate (NAA) in another. (d-f) Cho, Cr, NAA maps (overlaid on anatomical T1-weighted images) arising from the execution of the CPMG-based SECSI sequence in Fig. 1a. (g-i) Idem but for acquisitions based on a phase encoding CSI sequence. Common scan parameters: FOV = 16×16 mm^2, slice thickness = 4 mm, matrix size =32×32, echo time = 50 ms, TR = 2 s. SECSI parameters: τ = 1.524 ms, *N* = 8, averages # = 2048. The number of averages for the RE CSI sequence was 8 per phase-encoding value. The experimental time of the SECSI MRSI experiment was 2 h 16 m (including the reference scans) while the phase-encoded CSI acquisition took 4 h 33 m.

Conclusion: SECSI MRSI provides new possibilities to acquire the MRSI information in a faster, more efficient manner, might find usefulness in hyperpolarized ^{13}C MRSI.

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