

Fast MRSI of Human Breast using Spiral Sel-MQC

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Introduction. Magnetic Resonance Spectroscopic Imaging (MRSI) has emerged as a new tool to improve cancer diagnostic specificity as demonstrated in the clinical MRSI trials of brain, prostate, and breast cancer [1]. MR spectroscopy in breast cancer requires efficient methods for lipid and water suppression. We have developed a family of Selective Multiple Quantum Techniques (Sel-MQC) to detect metabolites such as lactate, choline and Polyunsaturated Fatty Acids (PUFAs) in tissues containing high concentration of fat[3,4]. However, the low tissue concentrations of these metabolites impose a severe limit on spatial and temporal resolution in MRSI applications. To address the issue, we present here a spiral approach for the Sel-MQC editing (spiral-SelMQC) with excellent lipid and water suppression in a single scan. Spiral data acquisition has been demonstrated as an efficient data acquisition method in cardiac MRI and Time-resolved MR Angiography[2]. Spiral has also been combined with spin-echo based MRSI methods to improve SNR and temporal resolution [5]. In this study, the Spiral-SelMQC sequence was successfully applied to map PUFAs in human breast tissue. The data acquisition along t axis was no longer necessary; discrete kx and ky phase-encodings in the previous Sel-MQC CSI methods [3] were replaced with the fast readout along spiral trajectories.

Methods. The Spiral-SelMQC sequence starts with a Selective Multiple-Quantum-Coherence Transfer (Sel-MQC) pulse train, which is followed by the spiral acquisition. This spin editing technique was first used to edit two J -coupled protons in lactate at 4.2 ppm and 1.3ppm respectively, with simultaneous suppression of water and lipid signals [3]. Recently, we applied SelMQC to detect PUFAs changes in breast cancer, which was used here as a demonstration system for Spiral-MRSI (Fig.1). Basically, the first two Sel-MQC 90° pulses excited olefinic methylene protons ($-\text{CH}=\text{CH}-$) of the PUFA at 5.3 ppm and the allylic methylene protons ($-\text{CH}_2-\text{CH}=\text{CH}_2$) of unsaturated acyl chain at 2.8 ppm, and prepared these coupled protons into MQ states. In contrast, magnetizations from water and other lipid protons stay in the SQ mode, which was dephased by the MQ-gradients. The inter-leaved spiral data acquisition started at the center of the PUFAs coherence transfer echo following the Sel-MQC editing RF pulses. To produce a Spiral-SelMQC image, 2 spiral inter-leaves were used in 2 TRs on a GE Signa 3T clinical scanner. The RF transmitter frequency was set at 1.3ppm on the sharpest peak of lipid. All 4 pulses were offset to 5.3ppm or 2.8ppm relative to the transmitter frequency. Spiral length was 2.9ms. FOV was 12cm, matrix size was 20^*20 , and 724 data points per leaf were acquired at receiver bandwidth of 125kHz. The data from 2 interleaves was gridded onto a 256^*256 matrix. NEX = 16, TR = 2s, and total scanning time = 64 seconds.

Results and Discussions. The Spiral-SelMQC sequence was demonstrated in phantoms and in normal healthy human volunteer studies. A four compartment phantom was constructed using olive oil and corn oil to image the different PUFAs levels. (Corn oil contains about four times higher level of PUFAs than olive oil.) Three 1cm test tubes in diameter were filled with olive oil, corn oil, and a 1:1 mixture of both. All three tubes were placed in a large spherical container of corn oil. A coronal image of 1cm slice thickness was acquired by Spiral-SelMQC sequence (Fig.2a), with a standard spin-echo image acquired as a reference (Fig.2b). The spin-echo MRI results showed no difference of PUFAs levels in different compartments. However, the Spiral-MRSI image gave distinctive UFAs contrast in three inner tubes. The tube filled with corn oil showed the same PUFAs signal intensity as in the outer container. Yet, the tube filled with olive oil showed lowest PUFAs level, whereas the tube filled with 1:1 oil mixture presented an intermediate PUFAs level. In the human subject study, the Spiral-SelMQC was applied to acquire PUFAs images in two different 1 cm sagittal slices from the right breast of a 50 year old healthy volunteer (Fig. 3). Spin echo images (Fig. 3a&3c) were also acquired to obtain breast anatomical structures (Fig. 3b&3d). The resolution of the spin-echo and spiral-SelMQC images were 128^*256 and 20^*20 , respectively. FOV = 12cm. It appears that the fat content in the breast tissue correlated with the PUFAs level in this volunteer scan. More uniform PUFAs level was observed in the slice with uniform fat content (Fig. 3a&3b). In another slice of the breast tissue areas with more glandular tissue and less fat contents, less PUFAs was found in the corresponding spiral MRSI imaging area (Fig 3c&d).

The low imaging resolution in spiral-MRSI can be advantageous to reduce the number of spiral interleaves. When the single shot spiral was first implemented for fast Sel-MQC MRSI, we set the sequence to obtain a sub-centimeter resolution that required a spiral trajectory longer than 8ms. Due to the fast T_2^* decay, low PUFAs signal at the tail of the long spiral trajectory caused severe under-sampling artifacts. When 2-shot spiral-SelMQC was implemented, the length of a spiral interleaf was reduced to 2.9ms, which was comparable to the length of the PUFA echo. As a result, improved image quality was observed.

Conclusion. The feasibility of *in vivo* spiral-SelMQC imaging was demonstrated to map PUFAs and metabolite distributions in human. The Spiral-SelMQC produces a image in 64sec, which would require 10min x 8 scan using the original Sel-MQC CSI techniques. In principle, the SEE-SelMQC technique achieves higher temporal and spatial resolution, and can be easily added to the clinical MRI scans of human breast cancer in a few more minutes of scan.

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