Introduction

Mapping tCho in breast cancer using MR spectroscopic imaging (MRSI) was reported to improve lesion characterization, thus improving the limited specificity of dynamic contrast enhanced (DCE) MRI [1]. MRSI was also used for treatment monitoring in patients undergoing neoadjuvant chemotherapy to predict outcome [2]. However, a major limitation of conventional chemical shift imaging (CSI) is the long acquisition time due to time consuming phase encoding along the spatial dimensions, which introduces motion sensitivity. Here we demonstrate feasibility of tCho measurement using high-speed Proton-Echo-Planar-Spectroscopic-Imaging (PEPSI) [3]. We used whole slice PEPSI to map total Choline (tCho) in a breast cancer patient and compared with PRESS-CSI and single voxel spectroscopy (SVS) using PRESS. We also measured tCho in a control group of 29 healthy subjects.

Method

Measurements on 1 breast cancer patient (age: 65) and 29 healthy female subjects (mean age: 22±2) were performed with informed consent using 3T MR scanner (Philips Achieva system) equipped with 32-channel body coil. The patient was a 65 year old female diagnosed with locally advanced infiltrating ductal carcinoma, moderately differentiated, ER positive, HER2 negative, and treated with several rounds of chemotherapy. The extent of the cancer was irregular with small satellite lesions noted. The dimensions of the largest mass were approximately 5.8×5.6×6.4 cm. Both PEPSI and CSI scans were performed in the same oblique slice orientation and position. The PEPSI scans performed using long TR to reduce T1-weighting for both the WS and the NWS scans: TE/TR=125/2000ms for WS scan and TE/TR=125/800ms for NWS scan, matrix size = 16×16, TA = 7min. For the healthy control subjects, 2D MRSI data of an entire oblique slice were collected using PEPSI [1]. Water suppressed (WS) metabolite scans were performed with WET water suppression (WET) and FID-MAIA lipid suppression, TE/TR=125/1500ms, matrix size=32×32, voxel size=2×2×2mm³, TA=77 minutes. PRESS SVS data were acquired with the same voxel size using identical TE/TR and acquisition time.

We developed a hybrid quantification method using LCM and a customized basis set with singlet peaks at 3.2ppm for tCho and 3.51ppm for myo in healthy breast tissue. The absolute tCho concentrations measured in the three techniques are comparable for the spatial resolutions being consistent with those from SVS and CSI. PEPSI study advanced in vivo demonstration of conventional CSI studies, similar water line-width, and metabolite SNR, indicating that the eddy current effect accompanying the EPI readout are negligible. The fast acquisition time of PEPSI offers more flexibility in choosing the scan time, for example, to shorten the total acquisition time to reduce the motion artifacts which have limited spectral quality in this study. Spectral quality from the lipid area due to the point spread function (PSF) potentially decreases spectral quality. We are in the process of implementing lipid deconvolution in post-processing to reduce lipid contamination [5].

Further, the low SNR of tCho in the lesion indicates that spatial resolution may be increased in future studies to reduce lipid contamination due to the PSF. The major challenge of breast spectral quantification is the tCho baseline distortion due to the contamination of unsuppressed lipids at 2.3ppm and line broadening because of tissue heterogeneity of the breast. The commonly used polynomial baseline is not sufficient to solve this problem. Therefore a hybrid tCho quantification method was developed to use singlet peaks to compensate for the spurious residual lipid peaks at around 2.3 and 2.8ppms. It allows the fitting over a larger spectral range of 2ppm than the standard LCM fitting, which only works well over a 0.5ppm range around the tCho peak on the WS spectra. In addition, the customized basis set offers more robustness in spectral quantification, which is suitable for automated spectral array data processing.

Results

Fig1a demonstrates the spectral position of the PEPSI and CSI. In a 3×3 neighborhood which is marked by a red square in Fig1a, tCho and water spectral array obtained from the PEPSI and CSI scans are shown in Fig1b and c, respectively. Across the 9 voxels, the tCho concentration measured using PEPSI was 14.6±5.4mmol/kg, vs 12.7±8.0mmol/kg using CSI, and the tCho SNRs were 46.2±31.2 and 41.9±17.2, respectively. In the healthy control group, 10 of 29 subjects demonstrated tCho peaks with signal noise ratio (SNR) larger than 3.0 at 3.22ppm on at least one of the MRS scans, i.e., SVS, PEPSI or CSI. In most of these subjects tCho was detectable with all methods. The extent of tCho was detectable with all methods. The extent of tCho was detectable with all methods. The extent of tCho was detectable with all methods. The extent of tCho was detectable with all methods.

Discussion and Conclusion

Despite the less favorable shimming and lipid suppression conditions compared to SVS, it is feasible to quantitatively map tCho in healthy breast tissue using PEPSI, with the results from PEPSI being consistent with those from SVS and CSI. PEPSI study advanced in vivo demonstrated comparable spectral quality to conventional CSI studies, similar water line-width, and metabolite SNR, indicating that the eddy current effect accompanying the EPI readout are negligible. The fast acquisition time of PEPSI offers more flexibility in choosing the scan time, for example, to shorten the total acquisition time to reduce the motion artifacts which have limited spectral quality in this study. Spectral quality from the lipid area due to the point spread function (PSF) potentially decreases spectral quality. We are in the process of implementing lipid deconvolution in post-processing to reduce lipid contamination [5]. Furthermore, the large SNR of tCho in the lesion indicates that spatial resolution may be increased in future studies to reduce lipid contamination due to the PSF. The major challenge of breast spectral quantification is the tCho baseline distortion due to the contamination of unsuppressed lipids at 2.3ppm and line broadening because of tissue heterogeneity of the breast. The commonly used polynomial baseline is not sufficient to solve this problem. Therefore a hybrid tCho quantification method was developed to use singlet peaks to compensate for the spurious residual lipid peaks at around 2.3 and 2.8ppms. It allows the fitting over a larger spectral range of 2ppm than the standard LCM fitting, which only works well over a 0.5ppm range around the tCho peak on the WS spectra. In addition, the customized basis set offers more robustness in spectral quantification, which is suitable for automated spectral array data processing.

Subject 9 in the healthy group exhibited higher tCho level than documented values which may be due to the higher lipid contamination in this subject. We are currently acquiring data in breast cancer patients using PEPSI on a weekly basis. A comprehensive analysis of these data will be presented.