A Total Choline Quantification Method for Water- and Lipid-Suppressed Breast Spectra at 3T

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INTRODUCTION Quantification of total Choline compounds (tCho) in breast spectra is challenging due to the contamination of unsuppressed lipids at 2.3 and 2.8ppm and line broadening because of tissue heterogeneity of the breast [1]. This abstract presents a tCho quantification method and demonstrates its application to mapping tCho concentration in breast spectra acquired using Proton-Echo-Planar-Spectroscopic-Imaging (PEPSI) [2]. This quantification method uses a simulated basis set with singlet peaks at 3.2, 2.8±0.1ppm and 2.3±0.1ppm for tCho and lipids, respectively. The breast spectra are then fitted over the range of 4.0 to 2.0ppm using a Linear Combination algorithm (performed using LCModel). In the fitted spectra, the baseline in the vicinity of tCho was identified, and the tCho area was computed by integrating the area enclosed between the tCho peak and baseline. The feasibility of this tCho quantification method was evaluated on 2D spectroscopic imaging data acquired using PEPSI both in vitro and in vivo.

METHOD In vitro and in vivo experiments were performed on ACRIN 6657 phantom [3] and 3 healthy females, respectively, on a Siemens 3T system using the PEPSI sequence. Written informed consents were obtained before participation. Acquisition parameters for in vitro/in vivo scans were: matrix size = 32×32, TR=2s, TE = 125ms, voxel size=1×1×1cm^3/2×2×2 cm^3, number of averages=8/16, axial/coronal slice orientation, multichannel head/breast coils used. WET and MEGA were used for water and lipid suppression (WS), respectively, whereas reference scans without water/lipid suppression (NWS) were performed by switching off the suppression modules and acquiring a single average. For NWS spectra, the water area was calculated by integrating the ranges of [5.0ppm, 4.0ppm]. In the basis set formulation, tCho was simulated as a singlet at 3.2ppm, and residual lipids were simulated as six singlet peaks at 2.3±0.1ppm and 2.8±0.1ppm, to compensate the peak shift and the broad line-widths which are usual for unsuppressed residual lipids. This fitting of WS spectra was performed using LCModel (Version 6.20). The outputs of LCModel, including the original and fitted spectra were sent to a Matlab program (Mathworks 2008a) to calculate tCho:water area ratio, tCho concentration and residual noise level. On the fitted WS spectra, the tCho peak was identified by finding the local maximum at 3.2ppm. Then, two samples with local minimum values in the fitted spectra to the right and left side of the tCho peak within the range of 3.2±0.15ppm were identified. The tCho baseline was generated by linear interpolation using these two samples. The tCho areas were computed by integrating the area enclosed between the tCho peak and baseline. With the tCho/water area ratio available, the molal concentration of tCho (millimoles per kilogram of solute, mmol/kg) was calculated using eq.9 in [1]. tCho SNR's were calculated based on tCho peak amplitudes and standard deviation of residual noise.

RESULTS Fig.1a shows the PEPSI slice position over the ACRIN 6657 phantom. Fig.1b shows the 2×2 spectral array, showing the vicinity of the Choline peak between 2 and 4 ppm, obtained from red square shown in Fig.1a. Cho peaks are clearly seen in the spectra from the center 2×2 voxels with only minor lipid partial volume contributions. In these four voxels, the Cho to water area ratios are $(1.2\pm0.3)^{-4}$. Assuming $T_{2,water}$= 250ms, $T_{2,Cho}$= 500ms and the same T1 for water and tCho, the absolute tCho concentration measured in the four tCho voxels is 1.1±0.29mmol/kg, which is comparable with the actual concentration of 1mmol/kg. In addition, the line-width of the non-suppressed water peak is 3.7±0.4Hz and the Cho SNR is 4.5±0.7. Fig.2 shows the spectroscopic data obtained in one female subject (subject 2 in Table 1). Fig.2a shows the PEPSI slice position. Fig.2b shows an example spectrum that illustrates the quantification of the tCho concentration. This plot shows the raw spectrum (white), fitted spectrum over the 4-2ppm range (blue), residual noise (top) and the x3 magnified tCho peak (shown in between residual noise and the spectrum). Fig.2c demonstrates the consistency of tCho quantification in a 2D WS spectra array within the breast, which is overlaid onto a high resolution breast MRI. In this subject, a total of 13 spectra within the breast area were analyzed and 11 voxels (85%) showed Cho signals with SNR greater than 3. For these 11 voxels, the average SNR is 4.9±1.1 and the tCho/water area ratio is $(3.1\pm0.78)^{-4}$. Using the relaxation values documented in the literature: $T_{1,water}$=870 ms, $T_{2,water}$=60 ms, $T_{2,cho}$= 399ms, and assuming $T_{1,cho}$ to be the same as $T_{1,water}$, the Cho concentration measured in this subject is 0.65±0.16mmol/kg. In Table.1, the quantification results for all three subjects are summarized, including tCho level, tCho/water area ratio, water and lipid line-width.

DISCUSSION AND CONCLUSION The distorted and slightly shifted residual lipid peaks make the tCho baseline detection and thereby tCho quantification very difficult. In this work, a basis set with singlet peaks for tCho and 2 adjacent lipid resonances was simulated. By simulating 3 singlet resonances with 0.1ppm gaps for each lipid resonance, the broad lipid line-width and peak shifts are accounted for. tCho quantification in breast spectra obtained from in vivo and in vitro PEPSI experiments demonstrated that this basis-set can provide appropriate spectral fitting using a Linear Combination algorithm with homogeneous residual noise. In the phantom experiment, the estimated concentration was slightly above the actual value, yet within acceptable range. In vivo, the tCho concentration obtained from subject 2 was consistent with other reports in healthy control at comparable age [4]. The tCho level from subject 1 was higher than the typical range for normal fibroglandular tissue. In subject 3, overwhelming lipid content was detected and no tCho signal was observed. As listed in Table 2, water peaks from subject 3 exhibited a larger average line-width than that of the other two subjects, which may suggest that large lipid content is associated with increased B0 inhomogeneity. In general, these in vitro and in vivo SI results demonstrate the feasibility of the proposed quantification method for measuring tCho in healthy breast spectra. This method does not require manual adjustment and is suitable for automatic tCho quantification in breast SI data in clinical studies.

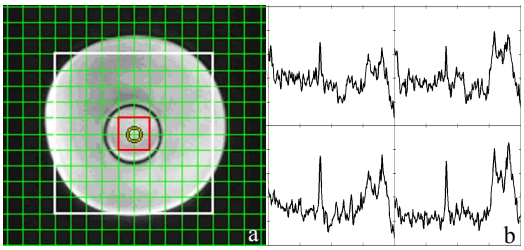


Fig.1 Phantom PEPSI experiments. (a) Slice position on the ACRIN phantom. (b) 2×2 spectral array of the tCho voxels, marked by a red square in (a).

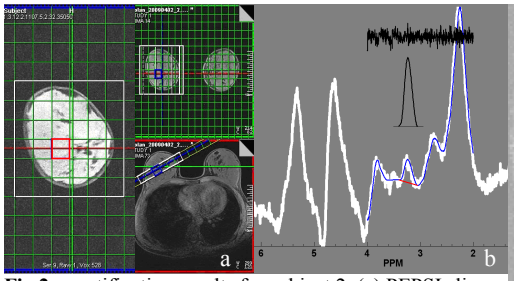
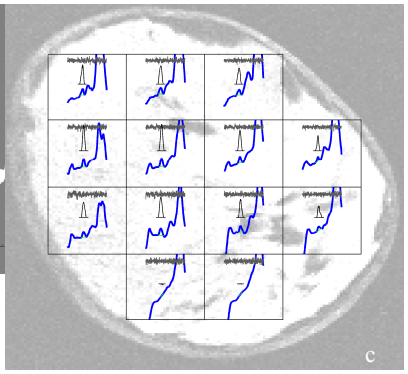


Fig.2 quantification results for subject 2. (a) PEPSI slice position. (b) An example showing the spectral quantification. (c) Spectral array within the breast area.



	Age	Voxel size (cm^3)	Water FWHM(Hz)	Lipid FWHM (Hz)	tCho/Water Area Ratio	[tCho] mmol/kg
Subject 1	21	2×2×2	25.9±9.9	27.9±7.3	$(8.0\pm2.5)\times10^{-4}$	1.68±0.53
Subject 2	20	2×2×2	24.8±7.1	51.3±13.0	$(3.1\pm0.78)\times10^{-4}$	0.65±0.16
Subject 3	35	1.5×1.5×1.5	>30Hz♣	33.9+6.6	0♦	0♦

Table 1 Summary of the quantification results for the three subject. ♣ Only a few voxels are evaluated due to low water content across voxels. ♦ tCho not detectable.

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