Broadband Decoupled and Single Voxel Localized 2D MR Spectroscopy

H. Chung[1], S. Banakar[2], M. A. Thomas[2]

[1]GE Medical Systems, Waukesha, WI, United States, [2]Radiological Sciences, David Geffen School of Medicine at UCLA, Los Angeles, CA, United States

Introduction: Localized one-dimensional (1D) MR spectra recorded in human brain are complicated by the spectral overlap of several J-coupled metabolites such as NAA, glutamate (Glu), glutamine (Gln), myo-inositol (mI), and GABA. The localized versions of 2D chemical shift correlated and J-resolved MR spectroscopic sequences enable increased spectral resolution, due to the added second spectral dimension [1,2]. However, overlap of several cerebral metabolites was a major concern even in 2D MRS at 1.5T. Dreher et al. recently implemented a 2D MRS sequence, namely CT-PRESS, based on constant time (T_c) chemical shift encoding, which showed improved spectral resolution, on a 4.7T MRI scanner and recorded the 2D spectra in healthy rat brain [3]. Two major goals of this work were 1) to implement a modified version of 2D CT-PRESS with reduced number of refocusing rf pulses on a whole body 1.5T MRI/MRS scanner for spectral acquisition in human brain and 2) to further optimize 2D CT-PRESS through simulated spectra using a GAMMA library [4].

Methods: The modified sequence included three-slice selective (90^0-180^0-180^0) rf pulses for volume localization and the CT chemical shift encoding was achieved as an integral part of volume localization. Two different versions were implemented; in the first version, the constant time was inserted prior to the first spin-echo and in the second version, prior to the second spin-echo. A CHESS sequence was used for global water suppression. A GE 1.5T MRI/MRS scanner (General Electric Medical Systems, Waukesha, WI) operating in the LX 9.0 platform with echo-speed-plus gradients (maximum of 30mT/m) was used. A conventional quadrature body rf coil was used for transmitting the rf pulses and a 3" surface coil for signal reception. The sequence was optimized using phantom solutions of several cerebral metabolites and simulated 2D CT-PRESS spectra of these metabolites. The spectra were simulated using GAMMA that uses a density matrix description of the spin system. The 2D CT-PRESS spectra were recorded in 3x3x3cm^3 voxels of the anterior cingulate and occipital regions of five healthy volunteers. The simulation was performed using identical parameters as the acquisition: spectral width of 2500Hz and 625Hz along the two axes (F_2 and F_1), 1024 complex points along t_2 and 128 points along t_1 dimensions.

Results: Simulated 2D CT-PRESS and CT-COSY spectra are shown in Fig.1(a) and (b). T_c of 125 ms was used. Contour plot of the 2D CT-PRESS spectrum showed the signals only in the diagonal and its vicinity. The simulated 2D CT-PRESS spectrum in Fig. 1(a) shows a considerable increase in SNR as compared to the diagonal spectrum of CT-COSY in Fig.1(b). Shown in Fig.1(c), is the 2D CT-PRESS spectrum of a brain MRS phantom containing NAA, Cr, Ch, mI, Lac and Glu. Fig.1(d), shows a CT-PRESS spectrum recorded in a 28yo healthy human brain .

Discussion: Compared to the basic localized COSY and CT-COSY spectra, a further increase in SNR was obtained by CT-PRESS for coupled resonances since there was no coherence transfer of magnetization between the J-coupled protons leading to disappearance of cross-peaks. A second rf channel is not required to achieve broadband decoupling**.** However, two major drawbacks of the implemented optimized version of 2D CT-PRESS are: 1) The signal amplitude in CT-PRESS depends on T_c. 2) The spectrum has to be acquired in the 2D mode, which requires long acquisition time.

References:

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Figure 1: Simulation : (a) 2D CT-PRESS and (b) 2D CT-COSY spectra of NAA, Cr, Ch, mI, Lac, Glu, Gln and GABA. Experimental: 2D CTPRESS spectra of (c) a brain MRS phantom containing NAA, Cr, Ch, mI, Lac and Glu and (d) a 28yo healthy human brain in the anterior cingulate region.