Comparison of two strategies to improve quality of in vivo 1H MR spectra in the presence of motion

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Introduction

In vivo hydrogen (^{1}H) MR spectroscopy has proved valuable for evaluating tumours in the brain, prostate, breast, liver, and uterine cervix [1]. However, the acquisition of ^{1}H spectra in the abdomen (and in particular the liver) is complicated by respiratory motion. Studies of abdominal motion show the diaphragm typically moves 15–20 mm during free breathing, with abdominal lesions moving from 5mm to 23mm [2]. Motion of this magnitude degrades the spectral quality by three main processes, phase and frequency distortions and modification of the point spread function (PSF). In this study we compared two distinct approaches to combat motion in liver spectroscopy, as assessed by the signal-to-noise ratio (SNR) and linewidth of the trimethylammonium (TMA) peak at 3.2 ppm. The first method utilises a post-processing approach to correct phase and frequency distortions as employed by Helms and Pringer [3], the second method employs Siemens 2D PACE methodology to prospectively gate the spectral acquisition with the respiratory movement of the abdomen.

Methods and Materials

Data from eight volunteers were acquired with and without prospective gating on a 1.5 Tesla Siemens Avanto scanner. In each case a water suppressed and un-suppressed (8 acquisitions) dataset were acquired from a 30x30x30mm voxel in the superior section of the liver. A combination of body array and spine coils was used to maximise the SNR. All data were collected with a TE of 135ms. Free-breathing acquisitions, for the post-processing approach, were acquired with weak water suppression and a TR of 1500ms (total acquisition time 5 minutes). When acquiring metabolite data using the PACE sequence, full water suppression was used and the number of acquisitions (50) was calculated to closely match the total acquisition time for the corresponding non-gated protocol.

Post-processing correction of the phase and frequency distortions was carried out in Matlab using a similar method to that employed by Helms and Pringer in the brain [3]. First the phase of the initial data point was used to correct for zero order phase differences between each FID, then the maximum amplitude (of the residual water) in the frequency domain was used to correct for frequency offsets. After summation of the individual FIDs (per coil element) the un-suppressed water signal was used to scale the contribution from each coil element.

Signal-to-noise ratio and linewidth measurements were performed in JMRUI for the PACE data and Matlab for the post-processing methodology. The trimethylammonium (TMA) SNR was defined as the peak of the TMA signal at 3.2 ppm divided by the standard deviation of the noise in a metabolite free region between 7 and 10 ppm. The TMA linewidth was calculated as the FWHM of the signal at 3.2 ppm.

Results

A peak at 3.2 ppm was detected in 6 out of 8 volunteers scanned. We were unable to resolve the constituent metabolites contributing to the 3.2 ppm peak (see figure 1), instead we chose to classify the whole peak as trimethylammonium (TMA) resulting from betaine and choline-containing compounds. In all cases the post-processing method resulted in a reduction in the TMA linewidth (median reduction 25.8%) and an increase in the SNR (median increase 70%), see figure 2. The PACE acquisition protocol led to an overall reduction in the linewidth (median reduction 18.8%) and a 16% median increase in SNR. Acquisitions acquired using the PACE protocol appeared to have less lipid signal than either the raw free-breathing data or the post-processed version.

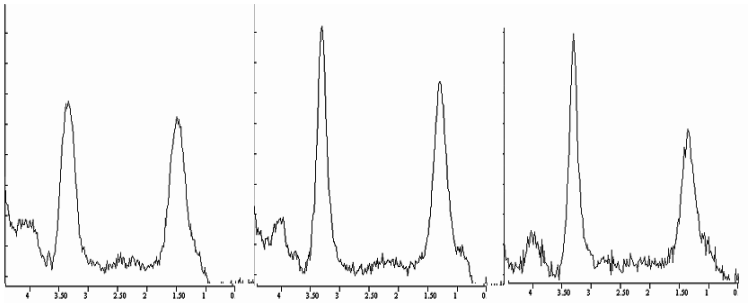

Figure 1.Example liver spectra acquired in free-breathing (left), corrected for phase and frequency distortions (centre), prospectively gated (right).

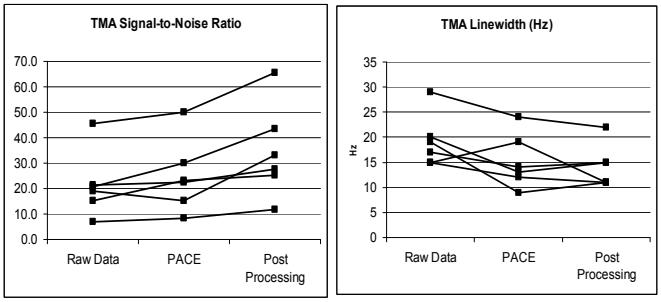

Figure 2. Trimethylammonium (TMA) SNR and linewidth (Hz) for 6 volunteer ^{1}H liver acquisitions, acquired in free-breathing (raw and post-processing) and with prospective respiratory gating (PACE).

Discussion and Conclusions

Both of the techniques examined appear to offer an improvement over a standard free-breathing protocol, both in terms of linewidth and SNR. However, the long TR required for the prospectively gated acquisitions, and the resultant reduction in signal averages, appears to penalise the PACE methodology in terms of SNR. However the PACE method should significantly reduce the signal acquired from outside the target volume, making the measurement more representative of the target VOI. This is supported by the reduced lipid content in the PACE datasets. Spins contributing signal in the non-PACE data from outside the target VOI will also only be excited in some acquisitions, experience reduced partial saturation effects, and therefore contribute relatively more contamination to the total signal detected than their volume alone would predict. Further tests have to show whether phase and frequency correction of the PACE data or acquisitions with some residual water can further improve the SNR in the PACE acquisitions.

References

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