A voxel-by-voxel benchmark comparison between two in vivo prostate MRSI techniques

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INTRODUCTION:

In a recent review article, Casciani *et al* point out the key trade-off in prostate MRSI related to sizing and placement of the excitation region of interest (ROI). In an attempt to maximize coverage, expanding the ROI to include the entire prostate gland results in unwanted contamination artifacts from periprostatic lipid [1]. Shrinking the ROI reduces this artifact but excludes tissue in the peripheral zone of the prostate where 80% of cancers are detected. To facilitate optimal coverage of the prostate, we previously presented a suppression technique, called conformal voxel MRS (CV-MRS) [2], which automatically optimizes the placement of spatial saturation planes , thereby adapting the excitation to the shape of the prostate and reducing spectral contamination[2]. Previous initial results showed very effective lipid suppression over all subjects[3]. By reducing the contaminating lipid the overall baseline of the spectra improved, resulting in better fitting of the key metabolites (i.e. Citrate, Choline, Creatine, and Polyamines) used in assessing normal and malignant prostate tissue. In our current work we present a voxel-by-voxel comparison of prostate spectra obtained with the standard MRSI technique and obtained with the conformal MRS approach.

METHODS;

All subjects were recruited in accordance with the dictates of the research ethics board. Subjects were scanned on a General Electric 1.5T Signa MR scanner equipped with Echospeed gradients. A standard endorectal coil (Medrad Inc.) in combination with a torso phased-array coil was used. The PRESS pulse sequence was modified to include the optimized CV-MRS technique. Using an offline program, the CV-MRS algorithm uses the acquired prostate MR images to calculate the offsets and rotations of the spatial saturation planes. In addition, the program performs two further optimizations: (1) modification of the flip angle of each spatial saturation pulse to account for T1 regrowth, and (2) temporal re-ordering of the spatial saturation planes to minimize the impact of overlapping planes. In vivo prostate spectra were obtained using this optimized technique. The *in vivo* data were then processed using a modified version of LCModel (LCModel version 6.1, © Stephen Provencher, Ph.D.) with simulated prostate metabolite peaks (i.e. Citrate, Choline, etc.) in addition to its superior lipid fitting routine.

RESULTS:

Eighteen subjects were scanned using both the standard PRESS and the modified CV-MRS technique. The first acquisition utilized manual placement of the spatial saturation planes, which were followed by the standard PRESS excitation with TE/TR =130/1100ms. The second acquisition employed the optimized CV-MRS technique followed by the standard PRESS excitation with TE/TR =130/1100ms. Each 3D MRSI acquisition used a 16x8x8 phase encode matrix, with a voxel size of 0.42 cm^3. Only voxels that fell within the excitation region were analyzed, and metabolites that fell within the spectral range of 0.6-3.85 ppm were fitted using LCModel. For each metabolite that LCModel fits, it gives the relative concentration of that metabolite as well as an estimate of the goodness-of-the-fit quantified by the Cramer-Rao lower bound and quoted as a standard deviation. LCModel rejects spectra with poor baselines caused by contaminating artifacts or incomplete water suppression. In addition, we reject all spectra with standard deviations exceeding 40% to isolate poor fits. Figure 1b, and 1c illustrate spectra and LCModel fits obtained from the same voxel from both acquisitions. Applying our rejection criteria to voxels acquired using both techniques, we observed over all eighteen subjects a 40±16% increase in the number of analyzable spectra when using the conformal voxel MRS technique.

DISCUSSION AND CONCLUSION:

Our earlier *in vivo* work [3] showed consistently improved lipid suppression, with an observed reduction as high as ~98% over regions of the prostate. Currently over 18 subjects, we are observing an average lipid reduction of 60±0.1%. This significant improvement has led to an improved baseline and easily visualized spectra throughout the prostate. Jung et al [4] and Kreis [5] both report metrics to assess spectra. Jung's criteria, which specifically look at prostate spectra, address the need to remove spectra that have been affected by lipid-induced baseline distortions. Kreis's work,which investigated quality of spectra rejects all spectra that exceed a standard deviation greater than 50%. Based on this prior work, we implemented the following rejection criteria: 1) Poor baseline (using LCModel's implmentation) and 2) standard deviation of peak fits of 40% or higher (slightly stricter than Kreis's recommendation). We then compared the number of spectra that were not rejected for the two MRSI acquisition techniques. We observed that when using the CV-MRS technique there is a dramatic increase of 40±16% in the number of acceptable spectra with a range 13-75%. Signal bleeding from peripheral voxels containing high amounts of periprostatic lipids can be clearly a problem as illustrated in Figure 1b. Voxels as far as ~15mm within the prostate suffer from severe lipid contamination. The effect of optimally suppressing peripheral lipid results in superior fitting and identification of metabolite peaks as seen in Figure 1c. In summary, by comparing each technique against a standardized benchmark test we have demonstrated that using the CV-MRS method significantly improves the diagnostic quality of spectra throughout the prostate.

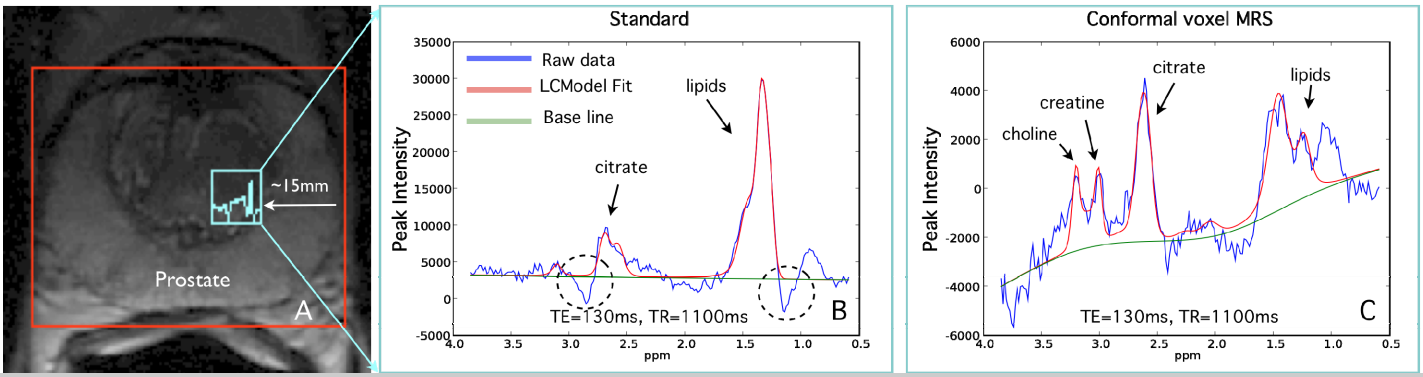

Figure 1: In (A), if the ROI of is taken over the entire prostate (solid red line) including some peripheral tissue, the resulting spectrum will contain unwanted contaminating lipid, as seen in (B). In (C), we present spectra from the same voxel location, but employing the optimized CV-MRS technique. In this voxel metabolites are clearly visualized and fitted indicating that suppression of peripheral lipids (~15mm away) using the conformal voxel technique has an immediate effect. Please note that in (B) the scale is up to five times larger. The large dips, highlighted by the black dashed circles, are problematic and can cause massive deviations in the baseline. Further resulting in incorrect fitting.

Reference:

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4. Jung, J.A., et al., Radiology, 2004.
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