Intra-Renal BOLD MRI at 3.0T: Evaluation of Voxel Size Dependence and Utility of ASSET

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INTRODUCTION

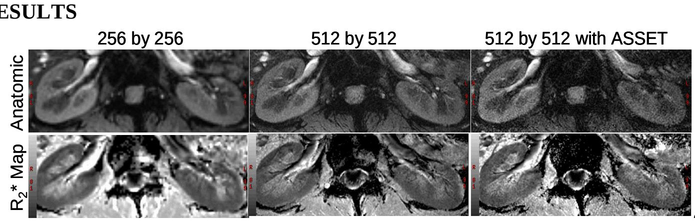
We had previously demonstrated that R_2* in the renal medulla and ΔR_2* (pre – post R_2*) following administration of furosemide at 3.0 T were significantly higher than those at 1.5T [Proc. ISMRM'02: 170; Proc. RSNA'03]. Higher-field strength also offers the unique opportunity to increase spatial resolution, thereby minimizing partial volume effects and improving the accuracy of quantitative intra-renal R_2* measurements. However, the long breath-hold times may render such acquisitions impractical. Parallel imaging such as array spatial sensitivity estimation technique (ASSET) could reduce scan time. In addition to signal to noise ratio, the magnitude of BOLD effect varies with voxel size [MRM 1993; 29: 139]. In this study, we performed preliminary evaluation of varying spatial resolutions and use of ASSET on measured R_2* and ΔR_2* in the kidney. We also evaluated the feasibility of obtaining whole kidney data in a single breath-hold interval using ASSET.

METHODS

Six healthy young volunteers (Five male and one female; average age: 32±7.2 years) participated in this study. Each volunteer gave informed consent to a protocol approved by our Institutional Review Board. The subjects came to the study after abstaining from food and water for about 12 hours. After obtaining baseline BOLD MRI data, 20 mg of furosemide was administered intravenously. Post-furosemide images were acquired starting about 5 minutes following administration to measure the BOLD response. The experiments were conducted on a GE Signa Vh*i* 3.0T whole body scanner (GE Medical Systems, Milwaukee, WI) using a multiple gradient echo (mGRE) sequence with selective water excitation pulse to acquire 16 T_2* weighted images within a single breath-hold. A standard four-coil torso array was used for signal reception. R_2* maps were constructed using FUNCTOOL by fitting a single exponential function to the signal intensity ***vs.*** echo time data. Regions of interest (ROI) covering at least 10 pixels were drawn on the anatomic template from each of the slices acquired and on both kidneys. The data were combined to obtain a single representative mean value of R_2* per subject per time point. The statistical significance was assessed using the two-tailed paired Student's t-test.

Since varying the matrix size has a direct effect on the TE and TR values, we obtained data with 2 different TR/TE settings. (a) For voxel size comparison, TR/TE/Flip angle/BW=82.3/7.7-72.8ms/30/62.5 kHz were used. Data with different matrix sizes, 512x512, 256x256, 128x128 with 5 mm slice thickness and 256x256 with 3 mm slice thickness were obtained. The inter-echo spacing was kept constant. (b) For higher spatial coverage protocol, TR/TE/Flip angle/BW=60/6.4-40.8ms/30/62.5 kHz was used. Data with 128x128 with and without ASSET and 256x256 matrix sizes were obtained with 5 mm slice thickness.

RESULTS



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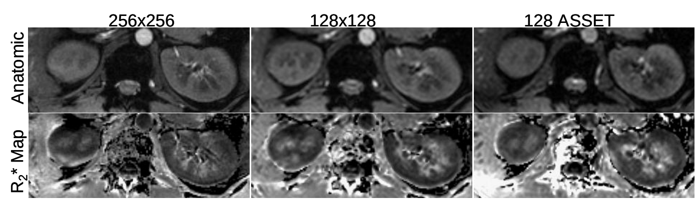

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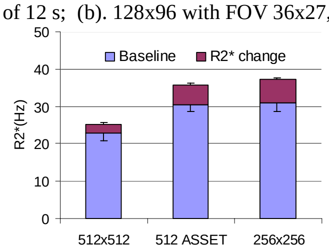
<u>Figure 1:</u> <u>Higher spatial resolution.</u> Representative anatomic images and corresponding R_2* maps with higher spatial resolution and with ASSET. (a). 256x192 with 36x27 FOV in 16 s breath hold; (b). 512x384 with 36x27 FOV in 32 s breath hold; (c). 512x512 with 36x36 FOV and ASSET in 22 s breath hold.

<u>Figure 2: Higher spatial coverage.</u> Representative anatomic image and corresponding R_2* maps obtained with (a). 256x192 with FOV of 36x27, one slice in breath-hold of 12 s; (b). 128x96 with FOV 36x27, one slice in breath-hold of 8 s, (c). 128x128 with ASSET, 7 slices covering the entire kidney in breath-hold of 28 s.



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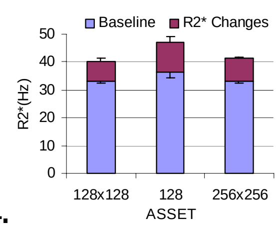

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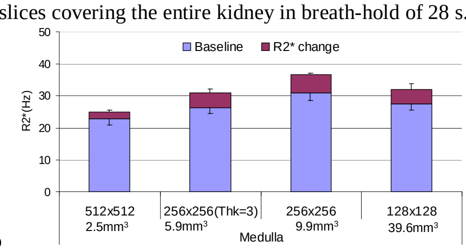

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<u>Figure 3: The summary of high resolution study</u>. The average baseline R_2* values and ΔR_2* (pre – post R_2* value) following administration of furosemide from 6 volunteers. BOLD MRI images were acquired along 3 axial planes placed in the middle of the kidney. Shown are data in medulla. Note that the baseline R_2* was significantly reduced in the high-resolution data. The surprising result is that even with high resolution, when using ASSET both R_2* as well as the ΔR_2* were comparable to those at 256x256.

<u>Figure 4:</u> <u>The summary of high spatial coverage</u>. Average baseline R_2* and ΔR_2* following administration of furosemide from 6 volunteers in renal medulla obtained with 128x128 and 256x256 matrix size. BOLD MRI images were acquired along 7 axial planes covering the entire kidney. The R_2* as well as ΔR_2* in medulla did ***<u>not</u>*** show significant difference among three protocols.

<u>Figure 5: Voxel size dependence</u>. Averaged baseline R_2* values and ΔR_2* following administration of furosemide from 6 volunteers in renal medulla for different matrix size and slice thickness (and hence different voxel size). BOLD MRI images were acquired along 3 axial planes placed in the middle of the kidney. Note that the both R_2* and ΔR_2* for 256x256 matrix size with 5 mm had the highest values compared with other matrix size scanning. Coincidentally that was the values we have used in our previous studies. Partial volume averaging may explain why 128x128 show smaller R_2* and ΔR_2* compared to 256x256.

DISCUSSION AND CONCLUSION

In addition to the obvious signal to noise advantage of 3.0 T, inherent sensitivity to BOLD effects is significantly increased. While the higher SNR can be traded to achieve higher spatial resolution, this also affects the BOLD sensitivity. With smaller voxel size, there is less "effective inhomogeneity" and so less signal loss on BOLD acquisitions. For the same reasons, a change in blood oxygenation should lead to a greater fractional change in R_2*. Based on our results, it is clear that 512x512 matrix size has significantly smaller medullary R_2* values and ΔR_2* compared to 256x256. On the other hand, 128x128 provided comparable R_2* and ΔR_2* values. With use of ASSET, 128x128 acquisitions allow for significantly improved spatial coverage within a single breath-hold. Surprisingly, with ASSET, 512x512 acquisitions actually resulted in R_2* and ΔR_2* values comparable to those at 256x256. We are currently investigating the probable explanation for this observation.

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