IMPROVEMENT OF RENAL DIFFUSION-WEIGHTED MR IMAGING WITH READOUT-SEGMENTED ECHO-PLANAR IMAGING AT 3T

Iris Friedli[1], Lindsey A Crowe[1], Magalie Viallon[1], Sophie de Seigneux[2], and Jean-Paul Vallée[1]
[1]*Radiology, Geneva University Hospital, Geneva, Switzerland,* [2]*Nephrology, Geneva University Hospital, Geneva, Switzerland*

Introduction

The results of diffusion-weighted renal imaging are prone to artifacts limiting their use in clinical practice, especially at 3T. There is an important need to optimize the acquisition protocol of the EPI based diffusion MR sequences in order to have consistent high-quality images and thus ensure more robust quantification measurements. A 'readout segmentation of long variable echo-trains' (RESOLVE) strategy (1) was compared to a reference single-shot SE-EPI protocol (2) and a single-shot SE-EPI protocol with an increased matrix, bandwidth and acceleration factor.

Methods

21 healthy volunteers were scanned at 3T on a MR Siemens Magnetom Trio Tim system with a 45mT/m maximum gradient capability with 3 diffusion-weighted sequences synchronized to the patient respiration using a respiratory belt. Six coronal-oblique slices of 5mm covered the kidney. The diffusion gradients were applied in 3 orthogonal directions with b-factor of 0, 300, 500 and 900 seconds/mm^2. The MR parameters for the reference single-shot SE-EPI were as follow: a TR of 2500ms, a TE of 71ms, a 400×400mm field of view, a 128×128 matrix size, parallel imaging (GRAPPA) with acceleration factor 2 and a bandwidth of 1500Hz/pixel. A second single-shot SE-EPI with higher bandwidth and acceleration factor (called thereafter modified EPI) was acquired with parameters TR of 2600ms, TE of 68ms, a 336×400mm field of view, a 200×168 matrix size, acceleration factor 3 and a bandwidth of 2272Hz/pixel. Parameters for RESOLVE were TR of 2600ms, TE of 68ms, a 342×397mm field of view, a 196×167 matrix size, acceleration factor 3, a bandwidth of 981Hz/pixel and 5 number of readout segments. Quantitative ADC maps were calculated on a voxel-by-voxel basis with OsiriX ADC map plugin (3). Furthermore, sharpness of RESOLVE and modified EPI were evaluated. On the gradient images associated to the b_0 images, a 'Canny' filter was applied to assess the quality of the edges. The filter returned binary images and the sharpness was calculated from the number of white pixels. SNR and distortions were measured with a phantom (width of 18.7cm) acquired with the same imaging parameters as in vivo experiments. For quantitative evaluation of distortion, image fusion between diffusion images and MOLLI T1 images as reference was performed. Distortions were measured as the maximum distance in the phase-encoding direction between the phantom edges on the diffusion image and the MOLLI image.

Results

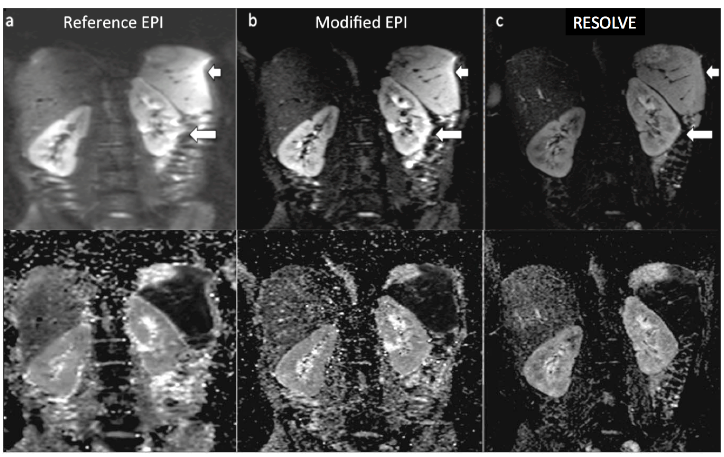

Figure 1 *Coronal MR Images of the kidneys in 26-year-old female. Comparison of sequences in vivo. Upper row (a, b, c): b_0 images of reference EPI (a) modified EPI (b) and RESOLVE (c). White arrows point to areas of distortion and high signal intensity artifact at the interface of bowel. Stronger distortions and blurring are clearly visible on both single-shot SE-EPI images compared to RESOLVE images. Furthermore, the difference between the cortex and medulla is clearly more delineated and sharper on the RESOLVE images. Lower row shows the respective ADC maps.*

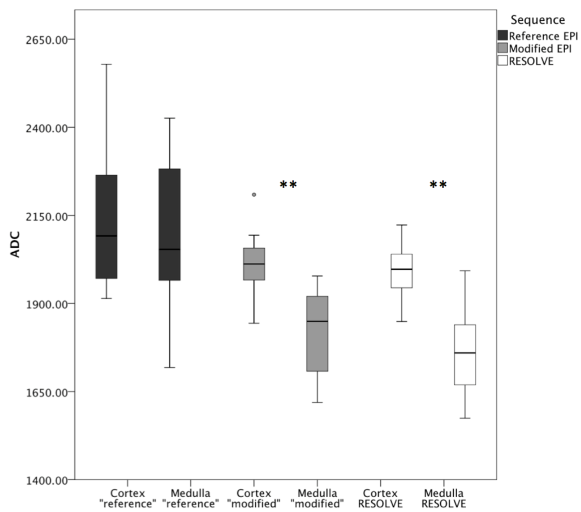

Figure 2 *Box plot illustrating the difference in mean ADC (10^{-6} mm^2/s) between the cortex and medulla with the 3 sequences: reference EPI, modified EPI and RESOLVE. Data were obtained in both kidneys in 16 volunteers, with $P < 0.001$ (**). A highly significant difference is revealed between the cortex and medulla of RESOLVE and modified EPI.*

As shown in Figure 1, by comparison to single-shot EPI, RESOLVE clearly reduced distortions at sites of susceptibility artifacts resulting in a better parenchyma delineated. Furthermore, the deviation from linearity measured at the corner of a straight phantom is reduced (1.34cm for reference EPI, 0.95cm for modified EPI and 0.47cm for RESOLVE). The sharpness as measured by the 'Canny' filter was significantly improved on the RESOLVE images by comparison to the modified EPI ($p = 0.0196$). The difference of contrast between the cortex and medulla on the b_0 images was also more visible with RESOLVE ($p=0.0024$) despite a drop in SNR. The SNR ratios between RESOLVE and modified EPI and between RESOLVE and reference EPI were 0.32 and 0.14 respectively. A potential limitation of RESOLVE is that the overall acquisition time is 5 times longer compared to single-shot SE-EPI. RESOLVE and modified EPI allow measurement of a significant difference in ADC ($p < 0.001$) between the cortex and medulla, as shown in Figure 2.

Discussion and Conclusions

There is a real advantage in using RESOLVE instead of single-shot SE-EPI to improve the quality of renal diffusion-weighted images. An important factor gained by the use of RESOLVE is the distinction between the cortex and medulla, despite using the same spatial resolution for both the improved sequences, modified EPI and RESOLVE. RESOLVE is less sensitive to susceptibility artifacts, and yielded a higher sharpness making RESOLVE an exciting sequence to detect renal abnormality in clinical application.

References

1. Porter et al. Magnetic Resonance in Medicine 62:468-475 (2009).
2. Thoeny et al. Radiology 259(1):25-38 (2011).
3. ADC map Calculation version 1.6 available on https://www.stanford.edu/group/bmr/cgi-bin/mediawiki/index.php/Software