Comparison of free-breathing versus navigator-controlled diffusion-weighted MR imaging of the kidneys: effects on ADC statistics.

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Introduction

There is not yet consensus regarding the optimum method of obtaining diffusion-weighted images of the abdomen [1], particularly for diffusion images that often require long acquisitions due to multiple b-values; movement arising from the patient's respiration can complicate analysis or degrade image quality. Methods aiming to remove or minimize respiratory movement involve acquiring shorter scans during breath-hold, or using a navigator-guided sequence to track the movement and selectively acquire data during specific parts of the cycle. These methods have their own complications; many patients are unable to breath-hold for consistently long periods, thus limiting suitability of some protocols as well as limiting individual scan time, and navigator-driven sequences are time-inefficient, highly dependent on repeatability of the respiratory cycle, promising only a reduction in movement to within a given tolerance at a fixed location. Commonly, global statistics form the basis of clinical decisions [2], thus any potential subtlety afforded by more complex acquisition strategies can be lost; while free-breathing acquisitions necessarily contain averaging of abdominal motion, they have the advantage of patient comfort and time-efficiency. We demonstrate that diffusion parameters derived from multiple free-breathing (FB) scans are similar to those obtained from navigator-controlled (NC) acquisitions, in both renal cortex and pyramid. Further, we demonstrate that the distributions of signal intensities for individual voxels at different b-values for the two methods are statistically indistinguishable.

Experimental

Diffusion scans were performed with two consented volunteers on a 1.5T Siemens Avanto scanner, using standard body array and spine coils centred on the kidneys. Scan parameters were matched between FB and NC acquisitions where possible, and acquired as single acquisitions, in succession with no averaging, making the same total scan time of 10 minutes. Acquisition parameters were: 2D EPI sequence, coronal acquisition, TE 75 ms, voxel size 1.5 mm^2 in-plane, slice thickness 5 mm, 128x128 matrix interpolated to 256x256. Ten b-values were acquired (0, 20, 40, 60, 80, 100, 250, 500, 750, 1000 s/mm^2) with orthogonal directions. TR for free-breathing was 1700 ms (total scan 53 seconds), whereas for navigator TR was a (nominal) 4100 ms. For navigator-controlled acquisition, the navigator was placed over the upper boundary of the liver. ROIs were drawn over sections of renal cortex, renal pyramid, and whole kidney. Fitting of the ADC diffusion model was performed using b-values ≥ 250 s/mm^2, using a Levenberg-Marquardt algorithm in proprietary software (ADEPT, Institute of Cancer Research, UK).

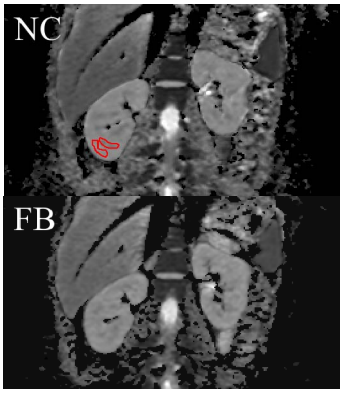

Figure 1: ADC maps from NC and FB, showing ROIs chosen for renal cortex and pyramid. There is little evidence of significant difference in amount of motion blurring.

Results

Figure 1 shows ADC maps for each protocol, together with the chosen ROIs; each ROI was matched to landmarks to ensure consistent placement between modalities. Visual inspection of these maps shows little, if any, extra blurring in the FB ADC map, even at the boundaries of the kidney. Descriptive statistics for each ROI are given in **Table 1**, and show close agreement in the two acquisition regimes. Distributions of the ADC for each ROI in volunteer 1 are given in **Figure 2**, and show that the distributions share gross features, with the global distribution averaging local variances reflected in the smaller ROIs. Extracting the signal values for each voxel in the smaller ROIs and normalising them to the fitted mean S_0, it can be seen that the distribution of signal at each b-value matches very well between the two breathing regimes (**Figure 3**); a similar pattern is observed for both cortex and pyramid in both volunteers. The datasets formed from the signal intensities from each diffusion b-value, direction and average for an individual voxel (chosen at random) are shown in **Figure 4**; an unpaired t-test at each b-value failed to produce any p-value less than 0.2; the same was true for cortex and pyramid in both volunteers.

Table 1: ADC (10^{-5} mm^2s^{-1}) values (mean ± s.d., median) calculated from navigator-controlled and free-breathing diffusion studies in 2 volunteers. Cortex and pyramid ROIs were ~70 voxels.

		whole kidney		renal cortex		renal pyramid	
		NC	FB	NC	FB	NC	FB
1	mean	172.1 ± 30.6	164.4 ± 42.9	187.2 ± 5.5	186.3 ± 5.4	171.5 ± 8.2	171.3 ± 9.0
	median	179.7	177.0	187.8	186.4	170.9	171.7
2	mean	158.1 ± 33.9	167.5 ± 21.8	163.1 ± 4.9	179.6 ± 9.6	147.1 ± 7.5	161.1 ± 6.5
	median	157.5	167.5	163.3	177.7	147.7	161.8

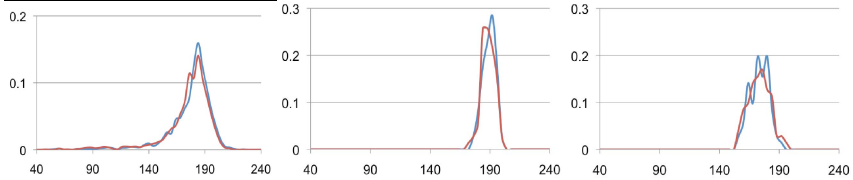

Figure 2: ADC distributions from NC (blue) and FB (red) for whole kidney, renal cortex, and renal pyramid ROIs.

Discussion

The utility of a scanning protocol is defined by the question it seeks to answer, and we demonstrate in this detailed small volunteer study that global descriptive statistics of the kidney appear insensitive to any differences between navigator-controlled and free-breathing acquisitions. Further, smaller specific ROIs share this indifference, and show that the degree of movement anticipated in free-breathing scans does not adversely affect the resultant perfusion-insensitive ADC values. In the 10 minutes set for acquisition in each modality, the NC ran 4 complete averages versus the 10 acquired under FB, and this greater time-efficiency translates to increased SNR. Examining the individual signal values normally averaged at the point of acquisition suggests that, at this level, the two modalities yield distributions that are indistinguishable.

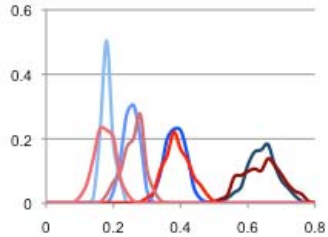

Figure 3: Distributions of relative signal intensity in renal cortex ROI, volunteer 1. NC blue, FB red, b=250 (dark) to 1000 (light).

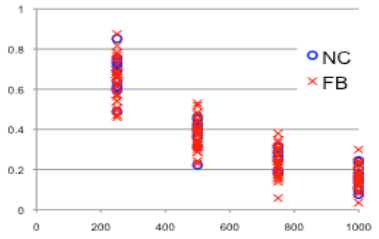

Figure 4: Individual data points for each direction and average show that NC and FB distributions are not significantly different.

Conclusion

Data acquisition using free-breathing is desirable since it avoids the discomfort of breath-hold studies, and the limitations of navigator-controlled scans. We show here for the kidney that distributions of perfusion-insensitive ADCs drawn from free-breathing and navigator-controlled studies do not appear substantially different at the level of a global statistic, most likely to be used for clinical decisions, at an ROI distribution, or even at the level of individual voxels. A larger cohort is needed to further qualify these observations, including perfusion parameters and with other tissues also considered. It appears that in this renal study, the gain in signal averaging from performing diffusion studies in free-breathing is not mitigated by compromised resultant parameters.

References & Acknowledgements [1] D-M Koh, D J Collins, *AJR* 2007, 188:1622-35 [2] HC Thoeny, F De Keyzer, *Radiology* 2011, 259:25-38

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