An iterative convolution approach for the non-invasive assessment of cortical perfusion in renal transplant using DSC MRI

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Introduction: Perfusion MRI using contrast-enhanced techniques with conventional Gd agents is challenging in the renal setting due to rapid filtration of contrast agent from the blood pool through the nephrons. In kidneys with normal perfusion, first pass is readily identified and modeled with a conventional gamma-variate function, but for reduced perfusion in disease, temporal mixing of first pass and slowed filtration through the nephrons contributes to error in the perfusion estimate. We proposed to determine if an iterative convolution approach for estimation of the tissue impulse response function, H(t), would allow more quantitative and reproducible results in cases of reduced perfusion observed in disease. We compared renal perfusion calculated using the proposed iterative technique to conventional gamma-variate fitting combined with direct Fourier transform (FT) deconvolution in the renal transplant population. The results were analyzed for the ability to differentiate between disease groups.

Methods: MR perfusion imaging (1.5T GE) was performed on 17 subjects with recent renal transplants within 48 hours of biopsy, using an echo planar, T2*-weighted perfusion sequence during contrast injection of 0.1 mmol/kg gadodiamide. Five (5) subjects had clinically normal function, 8 had acute rejection and 4 had ATN on clinically indicated biopsy. During the acquisition, the subjects held their breath for 30 seconds, followed by 150 seconds of free breathing. Parameters: TR/TE/flip = 1000ms/30ms/ °, FOV = 340 x 340 mm^2, matrix = 128 x 128, 3 slices at thickness = 10 mm. Temporal resolution = 1.0 second.

Fig 1:

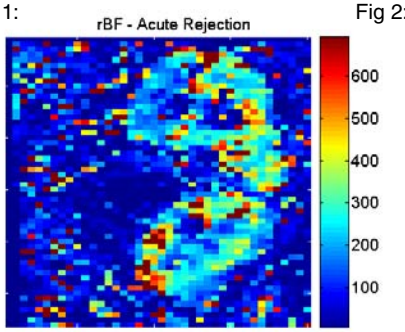
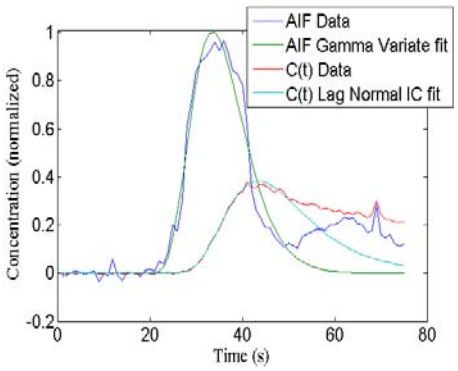


Fig 2:



In all cases the regional renal blood flow (rRBF) was calculated using indicator dilution methods. The rRBF was calculated from the regional renal blood volume (rRBV) and the mean transit time (MTT) according to rRBF = rRBV/MTT. The rRBV was calculated from the area under the tissue concentration time curve, C(t), divided by peak of the arterial input function (AIF). MTT was calculated from the tissue H(t). The two approaches differed with respect to the modeling of C(t) and H(t). In the iterative convolution method, H(t) is achieved through an initial guess assuming an exponential decay model based on a 5 parameter lag normal distribution [1],

$$H_i(t) = \frac{2C}{\sigma\sqrt{\pi}} \int_0^{t-t_{lag}} e^{-(\theta - t_c)^2/\sigma^2} e^{-(t-t_{lag}-\theta)/\gamma} d\theta \quad (1)$$

where σ, γ, t_c, t_{lag}, C are free variables. Iterative convolution (IC) with the AIF yields a new estimate $C_i(t)$ for the ith iteration,

$$[C_i(t)] = \{[H_i(t)] \otimes [AIF]\}. \quad (2)$$

Iteration continues until χ^2 of the fit between the estimate and the measured C(t) is minimized. The more conventional method fits a gamma variate model to the measured C(t), also using χ^2 minimization. H(t) was then calculated from the direct FT *deconvolution* of the AIF from C(t). For both approaches the rRBF for each subject was calculated as the mean over 4-6 regions of interest placed within the cortex over the three slices encompassing the transplant kidney. Statistical analyses of the mean cortical rRBF values for each group was performed using the two-sample t-test including comparisons between normal and ATN, normal and rejection, and ATN and rejection.

Fig. 3

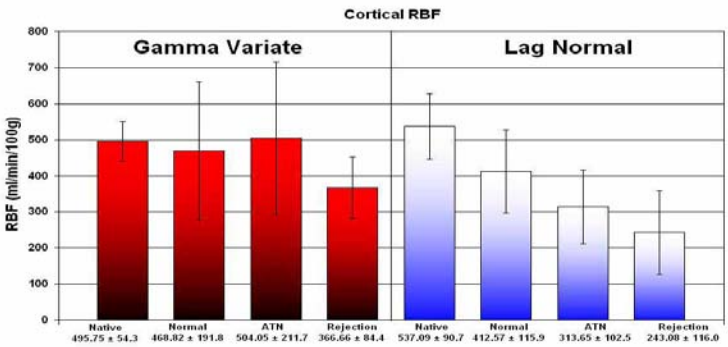


Table 1: p-values for group comparisons

Two-Tailed t-test	Gamma -Variate	Lag Normal
Normal vs. ATN	0.813	0.711
Normal vs. Rejection	0.373	0.031
ATN vs. Rejection	0.289	0.381

Results: Cortical and medullary structures were well differentiated in both analyses (Fig. 1). The perfusion values calculated using the gamma-variate method tended to over-estimate rRBV and consequently rRBF compared to the IC method (Fig. 2). This resulted in greater variability within disease groups for the gamma-variate method compared to the IC method (Fig. 3). For the IC method, measured perfusion values were **412.57 ± 115.92** for normal function, **376.77 ± 151.47** for ATN and **243.08 ± 116.02** for acute rejection (perfusion units: **ml/min/100g**). The student's t-test resulted in a significant p-value between the normal transplant group and the acute rejection group using the IC method (p value = 0.031) only. No significant differences were observed using the gamma-variate method.

Conclusion: Recent studies suggest that MRI can evaluate renal cortical perfusion [2] but quantification remains challenging. In the present work, both the range and consistency of the calculated perfusion values within disease groups is improved using the proposed IC technique relative to a more conventional gamma-variate method. Mean values for the new technique fall within expected physiological ranges [3], and the reduced variability in the measured perfusion within the patient groups studied suggests the technique may be more sensitive for distinguishing disease in the transplant setting. Future work will extend these techniques to evaluate patients undergoing chronic rejection, as well as a larger group of patients with acute rejection.

References: 1. Bassingthwaite et al. Circulation Research, vol. XVIII, April 1966; 238-415. 2. Lipscomb et al. RSNA proceedings 2005; 248. 3. Renal ischemia: a new perspective. Kidney International 1984; 26:375-383.