Quantification of renal perfusion on a voxel-by-voxel basis: first patient results.

M. I. Dujardin[1], S. Sourbron[1], R. Luypaert[1], P. Van Schuerbeek[1], S. Makkat[1], J. Sennesael[2], D. Verbeelen[2], T. Stadnik[1]

[1]Radiology/BEFY, Vrije Universiteit Brussel, Brussels, Belgium, [2]Nefrology, Vrije Universiteit Brussel, Brussels, Belgium

Purpose: Dynamic Contrast Enhanced MRI is a promising non-invasive method for imaging renal perfusion and function [1-5]. The feasibility of voxel-by-voxel perfusion mapping based on deconvolved T1-DCE renal data has already been shown by our group [5]. In spite of the extreme sensitivity of the deconvolution procedure to noise, this technique was found to lead to images of sufficient anatomical quality for region-of-interest (ROI) analysis. This study presents our first results with an optimized version of this technique, in a normal subject group as well as in the pathological case of a kidney transplant with known cortical infarction zones.

Methods:

In vivo perfusion measurements were performed on 14 human patients without known or suspected renal disease and one transplant patient in the supine position using a 1.5 T scanner (Philips, Intera, The Netherlands). All experiments were approved by the local ethical board. The first pass of 0.1 mmol/kg Gd-DTPA, injected by power injector at 2cc/s, was acquired using single slice axial Turbo flash (180° preparatory pulse, FA 50 °, TI 172 ms, TR 4.4 ms, TE 2.2 ms, slice thickness of 4 mm, matrix size of 128*256, temporal resolution 0.3s/slice). Post-processing was performed offline on a personal computer using software written in-house in IDL for Linux (Research Systems, Boulder, CO). Signals were calibrated by using a test tube of 2mM Gadolinium in saline solution placed in the FOV during the measurement. Conversion to tracer concentrations was made on the basis of the theoretical expression from reference [6] and by assuming a linear relation between Δ (1/T1) and the Gd-DTPA concentration. An arterial input function (AIF) was selected manually in the aorta and the tissue time courses were deconvolved using standard-form Tikhonov regularization and the L-curve criterion for selection of the regularisation parameter [7]. Parametric maps of relative renal blood flow (rRBF), relative renal distribution volume (rRDV) and relative mean transit time (rMTT) were calculated as the maximum of the IRF, the time integral of the IRF and the ratio rRDV/ rRBF.

rRBF, rRDV and rMTT were calculated of whole left and right cortex and medullar ROIs, drawn on the rRBF images. They were compared to literature values for normal renal cortical and medullar perfusion. Relative quantification was tested in the transplant by determining global rRBF for the entire transplant cortex as well as by voxel-by-voxel rRBF value determination along the curved line drawn across center and edges of the cortical pathological zones, respectively (figure 2). The quantitative values of perfusion for the pathological transplant case were situated in our normal population by determining the corresponding percentiles (figure 3).

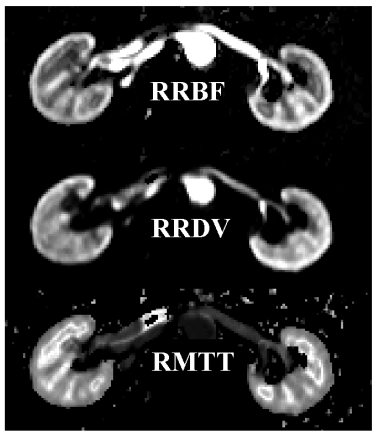

Figure 1: Parametric maps of rRBF (scale 0-2.4 ml/ml/min), rRDV (scale 0-0.5 ml/ml) and rMTT (scale 0-50 sec) in a normal male exhibiting an average case. The data are masked by removing all voxels with a maximum signal intensity below 12% of the overall maximum.

Results: Figure 1 illustrates a typical result for the quantitative parametric maps of rRBF, rRDV and rMTT. For the normal patient group average rRBF was 1.6 ml/min/ml with SD 0.8 ml/min/ml. Mean cortex to medulla rRBF ratio was 3. Average rRDV and rMTT were 0.4 ml/ml SD 0.1 ml/ml and 17s SD 6s. Mean rRBF value for the transplant cortex was 1.0 SD 0.2 ml/ml/min. A gradual symmetric increase from 0 to 1.2 ml/ml/min for the cortical defect on the right (figure 2 middle) and from 0.5 to 1.2 ml/ml/min (figure 2 bottom) for the anterior cortical infarction zone is found.

Conclusion: Although the ratio of cortical/medullar RBF of 3 is near the literature value of 4 [8], rRBF values are lower than those found in the literature [2,3,8]. This is presumably due to dispersion and/or inflow effects on the AIF estimate: an important flow related enhancement during systole causes an overestimation of the arterial input function and therefore an underestimation of the perfusion values [9]. The application of a preliminary inflow correction method leads to an average rRBF of 2.5 ml/ml/min in our normal patient group. Although the absolute quantification still needs a more robust inflow correction, quantitative T1 perfusion images show sufficient sensitivity to detect internal rRBF abnormality in pathological zones (figure 2).

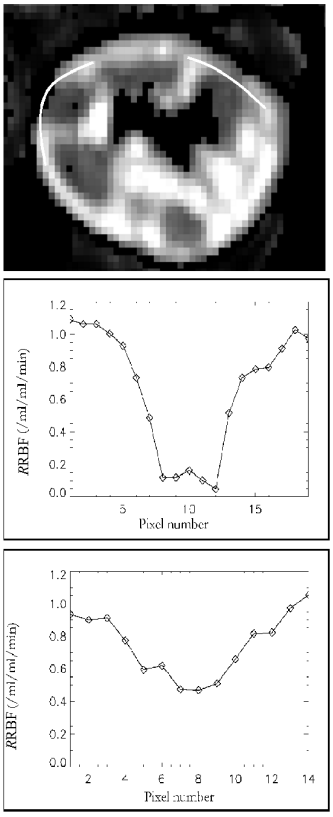

Figure 2 : rRBF image (top) of the kidney transplant in a patient with known severe atherosclerotic disease (colour scale ranges from 0 (black) to 1.2 ml/ml/min (white)). Cortical rRBF values in ml/ml/min are measured and plotted clockwise for each pixel along a curved line through the right cortical defect (middle) and the anterior cortical infarction zone (bottom).

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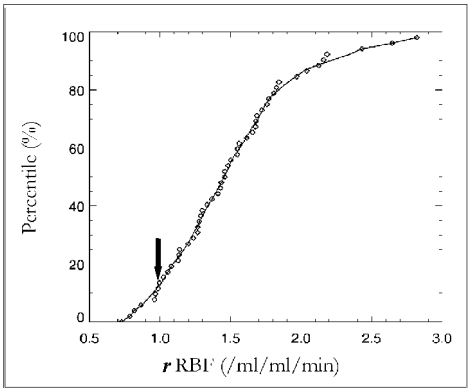

Figure 3: Cumulative distribution of the rRBF values measured in the population of normally perfused kidneys. Plotted are the measurement (diamonds) and the fit used for measurement. The arrow indicates the position of the transplant result on this distribution.