Radial R2* distribution : a new method to analyze BOLD MRI of kidneys

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Purpose : To evaluate a new post-processing method for renal BOLD-MRI (Blood Oxygenation Level-Dependent MRI), based on the radial distribution of R2* (a parameter that is inversely correlated with oxygenation), and to measure the response to an intravenous injection of furosemide in controls and renal disease patients.

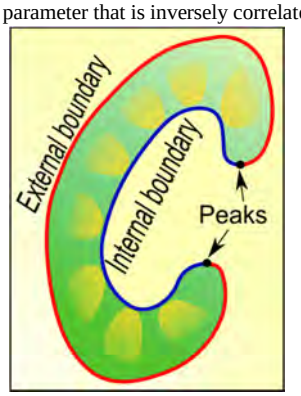


Figure 1

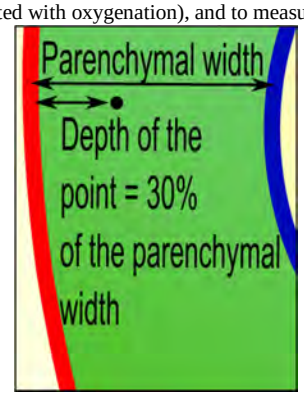


Figure 2

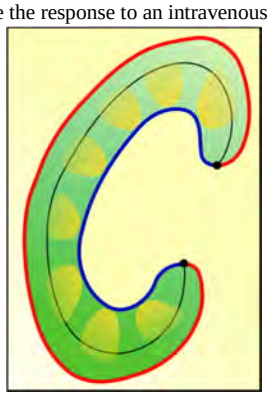


Figure 3

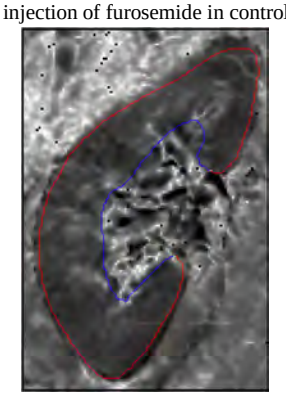


Figure 4

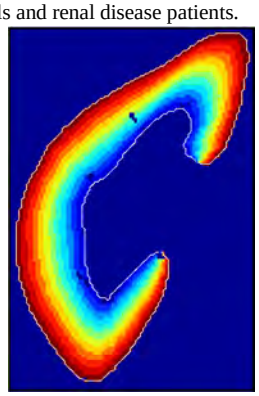


Figure 5

Image analysis and definitions : A coronal slice of a kidney with segmentation of the renal parenchyma, excluding the pelvis and calices is drawn. We obtain a kind of croissant containing the medulla surrounded by a cortical layer (Fig 1 displays the cortex in green and the medulla in yellow). The two extremes (peaks) of the croissant divide the boundary in two parts. The **external boundary** represents the boundary of the cortical side, and the **internal boundary** the medullary side (Fig.1). Every point inside the croissant is at a certain depth inside the renal parenchyma. We can express this depth as a percent of the total parenchymal width. We define the points of the external boundary to have a depth of 0% and the points on the internal boundary to have a depth of 100%. Fig 2 shows graphically an example of a point at 30% depth. Consider now a curve that starts at one peak, travels within the croissant and joins the other peak of the croissant with every point of this curve at a constant depth, for example 30% of the width. This curve willo be called the **longitudinal curve** of depth 30% (Fig.3). We can design a collection of such curves at equally spaced depths, for example 0%, 10%, 20%, …, 100%. Let's now consider the areas between each two neighboring curves. These areas fill the entire parenchyma in a concentric manner and we will call them the **concentric objects (CO)**. We assign the depth of 0% to the more external CO, the depth of 10% to the next, and so on. The R2* value in a concentric object is then representative for the corresponding depth. We call the function which gives the mean R2* value as a function of depth **radial R2* distribution**. The method we propose here relies on the evaluation of this function. The simplest method to evaluate this function is to measure the mean R2* values in CO's of equally spaced depths. Doing so, we obtain several CO's that contain pure cortex and others that contain a mix of medulla and cortex. This is why the measured radial R2* distribution accounts for the kidney anatomy. Fig.4. shows the BOLD-MRI of a kidney with its manual segmentation and Fig.5 shows the corresponding numerical computation of 12 CO's of equally spaced depth.

Figure 6 Radial R2* distributions

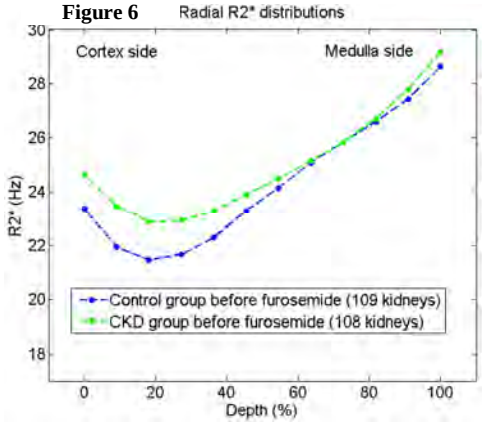
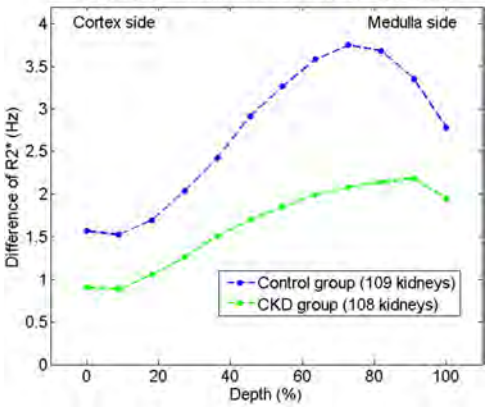


Figure 7
Response to furosemide of the radial R2* distributions



Methods : MR images were acquired using four coronal slices on a 3T-whole-body MR system (Magnetom Prisma, Siemens Medical Systems, Erlangen, Germany). Twelve T_2*-weighted images were recorded for each coronal slice within a single breath-hold of 16.6 seconds (in expiration) with a modified Multi Echo Data Image Combination sequence (MEDIC) for BOLD analysis with the following parameters: repetition time (TR) 65 ms, echo time (TE) 6-52.2 ms (equidistant echo time spacing of 4.2 ms), radiofrequency excitation angle 30°, field of view (FOV) 400 x 400 mm^2, voxel size 0.8 x 0.8 x 5 mm^3, slice thickness 5 mm, slice distance 5.5 mm, bandwidth 331 Hz/pixel, matrix 256x256 (interpolated to 512x512). MR imaging was performed before and 15 min after a furosemide injection (which blocks oxygen-consuming active transport of sodium in the loop of Henle) in 58 chronic kidney disease (CKD) patients (mean eGFR 43±24 ml/min/1.73m²) and 56 healthy volunteers (eGFR 101±28 ml/min1.73m²). R2* values were fitted for each pixel by a linear-least-square-of-log algorithm and values smaller than 10 Hz and bigger than 50 Hz were excluded. Cysts and tumors were excluded by a manual segmentation. The parenchyma of each kidney was segmented manually on the first of the twelve T2* weighted images. For this purpose, we followed the boundary inside of the kidney rather than outside to avoid boundary artifacts. The pelvis and calyxes where excluded of the selection. We computed the radial R2* distribution by choosing 13 numerically computed longitudinal curves at equally spaced depths from 0% to 100%. Then, we computed the response to furosemide of the radial R2* distribution at each depth as follows: group-mean before furosemide minus the group-mean after furosemide injection.

Results : Fig.6 displays the graphs of the radial R2* distributions for the control group (blue line) and CKD group (green line) before the IV injection of 20 mg furosemide and fig 7 shows the response to furosemide. Each graph contains 12 measurements. Each graph shows a minimum reached between 16% and 33% of the parenchyma on the cortex side and a maximum reached on the internal boundary (medulla side). Note the higher R2* at baseline in CKD patients essentially in the cortical layers but not in the medulla suggesting a reduced cortical oxygenation in CKD patients. In contrast, upon administration of furosemide, the change in R2* occurs in part in the cortex (depth 0-40%) but mainly in the medullary regions (depth 40-100%) which is in accordance with the site of action of furosemide with marked differences between controls and CKD patients

Conclusion: Analysis of renal BOLD-MRI images using the newly developed radial R2* distribution appears to be a reliable method which provides more useful information than regions of interest as it enables to assess the distribution of R2* throughout the entire kidney as a continuous variable. The analysis of clinical data obtained in controls and CKD patients clearly show the improved ability to analyze data using the profile of the curves.