Quantification of renal DCE-MRI with BLADE: Initial experience

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Introduction

Technical improvements such as higher field strengths, multi-element coils and parallel imaging techniques have made renal DCE-MRI a very important tool for the evaluation of renal kidney diseases over the last decade. Especially, the introduction of compartment model based analyses, such as the two-compartment model, enables a quantitative analysis of renal perfusion and filtration parameters based on the DCE-MRI data. In contrast to standardized laboratory tests, MRI allows a separate functional analysis for each kidney. Kidney malfunction can be easily detected even in the absence of pathological morphology changes [1] and allows better treatment already in early disease stages. However, motion artefacts, primarily due to respiratory motion, remain a major problem in renal imaging. Standard sequences in clinical routine like VIBE or TurboFLASH (TFL) try to improve image quality by respiratory triggering. Hence these sequences are not applicable in patients whose physical conditions do not allow longer breathholds such as pediatric patients or the elderly population. The T_1-weighted BLADE sequence is an approach that allows an intrinsic motion compensation without the need of any respiratory triggering and is furthermore competitive with a standard perfusion sequence like the TFL. The aim of this study was to evaluate whether a T1 weighted BLADE sequence can reliably derive physiological parameters like glomerular filtration rate (GFR) from a pharmacokinetic model while providing an improved motion correction.

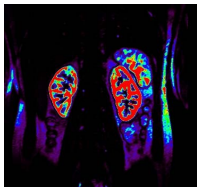

Fig. 1. *Pseudo colour image of a renal DCE examination.*

Materials and Methods

The study was approved by the institutional review board and informed consent was obtained from all subjects prior to the study. A total of 16 healthy male volunteers with a mean age of 27 years and an age range of 20 to 43 years without any known renal diseases were examined on a 3T MR-system (Magnetom Tim Trio, Siemens, Erlangen, Germany). For the chemical assessment of the renal filtration rate blood samples were taken and the CystatinC-level [1] (CysC) was determined preliminary to the 50-minute MR examination. Each exam consisted of a repeated injection of 4 ml Gadobutrol (Gadovist, Bayer-Schering, Berlin, Germany) followed by a saline flush of 30 ml. The two injections were separated by a pause of 30 minutes to minimize any influence of the contrast agent on the second part of the examination. The sequence order was randomized from patient to patient. Each patient was scanned with the BLADE sequence and the TFL as reference. The BLADE sequence was parameterized according to a T_1-weighting [2] and the images were acquired with a spatial resolution of 1,5 x 1,5 x 5 mm^3 and a temporal resolution of 1,6 seconds per image. The TFL had a voxel-size of 2,3 x 2,2 x 7 mm^3 . Figure 2 shows pre- and post-contrast image samples of the two sequences. BLADE recorded one coronal and one transversal slice whereas the TFL-sequence acquired 4 coronal and 1 transversal slices with an overall acquisition time of 0.25 seconds per frame. The total imaging time was 8 minutes each. All examinations were performed without respiratory triggering.

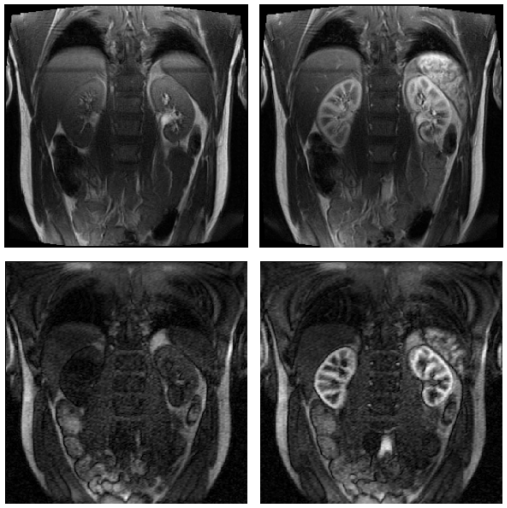

Fig. 2. *Pre- and post-contrast samples of the applied sequences. Top: BLADE. Bottom: TFL.*

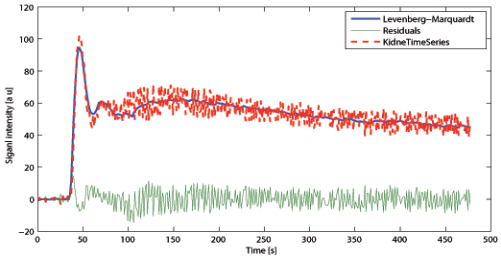

Fig. 3*. Evaluation of DCE-examination (TFL). Data from coronal ROI is plotted in red. Compartment-Fit is plotted in blue. Residuals green.*

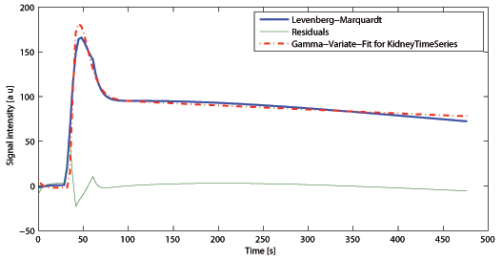

Fig. 4. *Evaluation of fitted DCE-examination (BLADE). Data from coronal ROI is plotted in red. Compartment-Fit is plotted in blue. Residuals green.*

Evaluation/Results

For evaluation of the acquired data in the coronal images, a region of interest (ROI) was drawn in the lower cortex of the kidney and for the assessment of the arterial input function another ROI was drawn in the abdominal aorta in the axial images and the signal intensity was read out. A Two-Compartment-Filtration-Model (2CFM) [3] was applied on these datasets as it is shown in Figure 3. For motion registration, the Akaike Fit Error (AIC-value) [4] was calculated by PMI. The calculations yielded 732±141 for BLADE and 1626±303 for the TFL sequence. The values calculated by the 2CFM were subsequently compared to the values delivered by the blood tests. Hereby we considered the hits in the five different GFR-regions staged by the Kidney Disease Outcome Quality Initiative (KDOQI) [5]. Results showed one match for BLADE and five for TFL. Since all examinations were performed without any respiratory triggering, the datasets had to be smoothed with the Gamma-Variate-Fit [6] for an optimized AIF and tissue function as shown in Figure 4. In this context the GFR-values calculated by BLADE and the TFL each had 10 hits and 6 misfits.

Discussion

The results of the AIC evaluation show that the BLADE data delivers only half the Akaike Fit errors compared to the TFL and can therefore be considered as the better choice concerning motion correction. An appliance of the 2CFM to the unprepared datasets did not reliably produce values that are comparable to the blood tests. It seems that the deviation of the data from an ideal bolus curve due to the respiratory movement has a high impact on the fitting to the compartment model for the BLADE sequence as well as for the TFL and is therefore not robust enough to derive reliable data in free breathing examinations. For this reason we smoothed the data with the mathematical Gamma-Variate approach and found 10 matches of the GFR values computed by the filtration model and the GFR values derived from the CysC concentration in the serum. Hereby we showed that a mathematical fitting of the input data can significantly improve the output of an applied filtration model.

References

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