DCE-MRI of the kidney using BLADE – A feasibility study

F. Lietzmann[1], F. G. Zöllner[1], H. J. Michaely[2], S. Haneder[2], U. Attenberger[2], and L. R. Schad[1]
[1]Department of Computer Assisted Clinical Medicine, Heidelberg University, Mannheim, Germany, [2]Institute of Clinical Radiology and Nuclear Medicine, University Medical Center Mannheim, Mannheim, Germany

Introduction

Since the number of end-stage renal diseases (ESRD) is still growing with up to 800 reported cases per million across the European Union and about 1500 cases in the United States [1] alternative diagnostic modalities that allow to detect even slight morphological and functional renal changes within early disease stages gain further importance, especially with regard to the patient's outcome. In this context the dynamic contrast enhanced MRI (DCE-MRI) provides a promising non-invasive technique for the assessment of physiological parameters like renal blood flow or glomerular filtration rate without the need of ionizing radiation.
One of the major advantages of DCE MRI lies in the separable assessment of perfusion and filtration parameters for each kidney while blood tests just deliver global data. On the other hand severe problems in abdominal imaging are image artefacts due to motion. Primarily the respiratory movement of the patient induces massive distortions that affect the evaluation of recorded images. Conventional sequences like VIBE try to solve this problem with breath-hold-techniques. However, patients whose physical constitution does not allow breath holds like elderly people or children cannot be examined without severe motion artefacts.
Therefore the self-navigating BLADE-sequence with a certain robustness to motion artefacts in combination with an injection of a contrast agent offers an approach for a motion corrected DCE-examination without the need of respiratory triggering. The purpose of the this study was to compare a T_1-weighted, contrast-enhanced dynamic BLADE sequence to a TurboFLASH sequence, considered so far as the gold standard for renal DCE MRI.

Materials and Methods

The study was approved by the institutional review board and informed consent was obtained from each volunteer. A total of 16 male volunteers (mean age 27; age range 20-43) without any known renal diseases were examined on a 3T Magnetom Tim Trio System (Siemens, Erlangen, Germany).
Each volunteer underwent a 50-minute MR examination with a repeated injection of 4 ml Gadovist (Schering, Germany) followed by a saline flush of 30 ml. A 30-minute pause was inserted between the injections to diminish the influence of the contrast agent-prestressed patient on the second part of the examination. Additionally the sequence order was cycled from patient to patient. The BLADE sequence was parameterized according to a T1-weighting and images were recorded with a 256 x 256 matrix and a subsequent resolution of 1.5 x 1.5 x 5 mm^3 [2]. The blade width was changed, whereas 8 patients were examined with a Blade-width of 32 lines, the other 8 patients with a width of 64 lines. Every patient was examined with the gold standard TFL-sequence [5] as a reference with a 384 x 348 matrix and a voxel-size of 2.3 x 2.2 x 7 mm^3. Figure 1 shows pre- and post-contrast samples of the recorded BLADE/TFL-series of the same patient. BLADE recorded one coronal and one transversal slice with an acquisition time of 1.6 seconds per image whereas the TFL-sequence recorded 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.

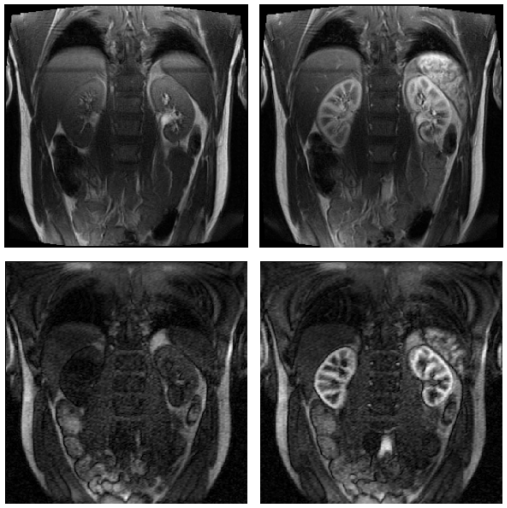

Figure 1. Pre- and post-contrast images. Upper row: BLADE; lower row: TFL

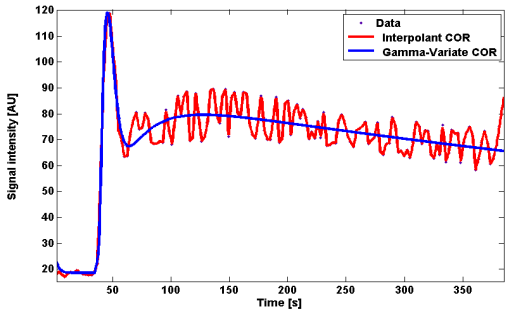

Figure 2. Signal intensity-time data of the ROI-readout. Raw data is plotted in red. Gamma-Variate-fit is plotted in blue.

Results

A ROI was drawn into the cortex of the right kidney in every recorded coronal image and signal intensity data was read out. For a better comparability only 150 time-equal data points of the BLADE- and TFL-series were taken into account. Afterwards, a Gamma-Variate-Fit [3] was applied to the signal intensity data, describing mathematically the arrival of the contrast agent. In Figure 2 the Gamma-Variate-Fit is plotted in blue and the signal intensity data in red. The deviation of the SI-data from the ideal bolus curve describes the quality of the technique concerning motion correction whereas smaller SSE values (sum of squared errors) depict a better stability towards motion. SSE data was calculated from each of the 32 series by this means and is plotted in Figure 3. The height of each box plot refers to the mean SSE value of the corresponding parameterization and the thickness of each box demonstrates a 5% confidence interval. The error bars correspond to the standard deviation. The green plot represents the BLADE-measurement with a Blade-width of 32 lines and constitutes the smallest SSE-value (6065). The red plot represents the measurement with a width of 64 lines (13849) and the blue plot the TFL-data (11884).

Discussion

Though successful motion correction by a BLADE k-space sampling technique was proven for CE T_1w brain imaging [4], there is no data illustrating the benefits of this k-space technique for abdominal imaging, mainly restricted due to low spatial and temporal resolution. The results of our study demonstrated the success of a T_1-weighted renal DCE-MRI using the BLADE k-space sampling technique for motion correction. Besides, the parameterization of the BLADE-sequences matched the spatial and temporal restrictions for renal imaging demanded by [5].
The results have been obtained without any further processing of the recorded images and show robustness towards motion artefacts. Despite the relatively long acquisition time compared to the gold standard TFL, future work is directed to imaging time and postprocessing of the data. We envision that using BLADE in DCE-MRI of the kidneys will also improve the accuracy of physiological parameters derived by pharmacokinetic models [6].

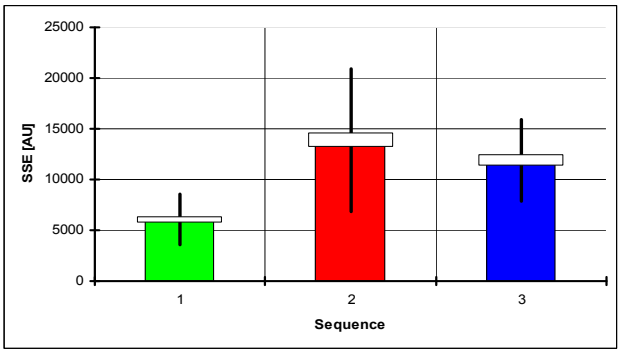

Figure 3. Boxplots of SSE data derived from the entire 32 signal intensity-time series. Sequence 1: BLADE (32 lines). Sequence 2: BLADE (64 lines). Sequence 3: TFL.

References

[1] RS Barsoum, *N Engl J Med* 2006; 354: 997 –999.
[2] F. Lietzmann, Proc ISMRM 2009; 4137.
[3] H. J. Michaely, Invest Radiol. 2006 Feb; 238:586-596.
[4] U.I. Attenberger, Invest Radiol 2009
[5] H.J. Michaely, Invest Radiol. 2008 Feb; 43(2):120-8.
[6] S.P. Sourbron, Invest Radiol. 2008 Jan; 43(1):40-8.