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Technical note

# Combined renal MRA and perfusion with a single dose of contrast

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**Abstract**

Both anatomical and functional scans are often performed when diagnosing renovascular diseases, which in many cases require two separate contrast injections. With nephrogenic systemic fibrosis being associated with gadolinium, minimizing contrast injection dosage is desirable. In this study, a technique which performs time-resolved renal magnetic resonance angiography (MRA) and perfusion with a single scan and single dose of contrast has been evaluated in six healthy volunteers. A previously developed three-dimensional MRA technique called Contrast-enhanced Angiography with Multi-Echo and Radial *k*-space (CAMERA) has been used to acquire images, and perfusion analysis was performed using deconvolution methods. Time-resolved MRA, as well as renal blood flow, renal volume of distribution and mean transit time maps, were acquired.


*Keywords:* Renal MRA; Perfusion; Time-resolved; Single-dose

## 1. Introduction

Comprehensive assessment and diagnosis of patients with renovascular disease requires both anatomical and functional imaging. The use of gadolinium-DTPA in time-resolved magnetic resonance angiography (MRA) is a promising tool for assessment of normal and compromised kidneys. Time-resolved renal MRA [1–3] and renal perfusion [4–10] are by themselves active areas of research, and often they are performed back to back during a renal exam.

In particular, there have been successful attempts to quantify renal perfusion using dynamic contrast-enhanced (DCE) methods which have been shown to be feasible [4–10]. However, previous studies acquired only a single slice of the kidney or several thick slices in order to have sufficient temporal resolution for perfusion analysis. In addition, an angiogram of the renal arteries required a separate scan with an additional injection of contrast agent. With nephrogenic systemic fibrosis being correlated with Gd-based contrast agents in patients with renal failure, it is critical that injection doses be kept to a minimum.

In this study, we demonstrate the feasibility of using a previously developed three-dimensional (3D) MRA technique called Contrast-enhanced Angiography with Multi-Echo and Radial *k*-space (CAMERA) [11] to obtain angiographic information in the renal vessels as well as perfusion information in the renal parenchyma with only one dose of contrast agent. The CAMERA sequence achieves this by utilizing sliding window reconstruction [12,13], which not only allows subsecond image updates for dynamic bolus depiction and perfusion analysis but also reduces sensitivity to respiratory motion and contrast bolus modulation.

## 2. Methods

### 2.1. Deconvolution analysis

To a degree, some information about renal perfusion can be obtained by graphically observing the maximum signal enhancement and/or the rate of signal enhancement of the renal parenchyma. However, this technique does not take into account the shape of the arterial input function (AIF), which depends on the amount of contrast, injection rate, cardiac function, dispersion and recirculation. As a result, the perfusion values are only semiquantitative, although this

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information may be useful in quickly assessing unilateral renal diseases [8].

To measure perfusion independent of injection rate, cardiac function, dispersion and recirculation, the kinetics of a physiological tracer can be modeled using the following system

$$C = \mathrm{AIF} \otimes \mathrm{IRF}, \tag{1}$$

where $C$ is the concentration of the tracer in a region of interest (ROI) of the tissue over time and IRF is the impulse response of that tissue. Since AIF and $C$ are measured, IRF can be obtained by deconvolving $C$ with AIF. The IRF that is obtained describes the perfusion characteristics of the tissue of interest independent of the magnitude and shape of the AIF.

There are several different ways to deconvolve Eq. (1). The easiest and the most intuitive approach uses inverse Fourier transforms; however, Fourier techniques are sensitive to noise [14]. Another general approach is the linear algebraic method. For discrete signals, Eq. (1) can be expressed in the following matrix form [15]:

$$\begin{pmatrix} C(t_1) \\ C(t_2) \\ \dots \\ C(t_N) \end{pmatrix} = \Delta t \cdot \begin{pmatrix} AIF(t_1) & 0 & \dots & 0 \\ AIF(t_2) & AIF(t_1) & \dots & 0 \\ \dots & \dots & \dots & \dots \\ AIF(t_N) & AIF(t_{N-1}) & \dots & AIF(t_1) \end{pmatrix} \cdot \begin{pmatrix} IRF(t_1) \\ IRF(t_2) \\ \dots \\ IRF(t_N) \end{pmatrix}. \tag{2}$$

The IRF vector can be obtained by linear algebraic methods such as regularization and singular value decomposition (SVD). Investigators have found that the SVD approach is relatively less sensitive to noise and results in accurate calculations [15]. A more detailed discussion on the accuracy of deconvolution methods can be found through other sources [14–17].

After the IRF is obtained, the perfusion parameters renal blood flow (RBF), renal volume of distribution (RVD) and mean transit time (MTT) are calculated as the following [7]:

$$\begin{aligned} \mathrm{RBF} &\equiv \frac{1}{k_v} max(\mathrm{IRF}) \\ \mathrm{RVD} &\equiv \frac{1}{k_v} \int_0^\infty \mathrm{IRF}(t)dt \\ \mathrm{MTT} &\equiv \frac{\mathrm{RVD}}{\mathrm{RBF}}, \end{aligned} \tag{3}$$

where $1/k_v$ is a correction applied at the vascular inlet and used to adjust for filtration, water resorption and secretion with $k_v$ set to 1.3616. The units of RBF, RVD and MTT are ml/100 g/min (ml of blood per 100 g of tissue per min), ml/100 g and seconds. For RBF and RVD values, a tissue density of 1.04 g/ml was used [5]. The RVD and RBF values were also multiplied by a constant, $k_h$=0.73, which is commonly used to adjust for differences in arterial and capillary hematocrit [16].

### 2.2. MR acquisition

In this feasibility study, the CAMERA sequence was evaluated for renal MRA and perfusion in a small number of healthy volunteers. With institutional review board approval, six healthy volunteers were scanned with the protocol. A single dose (0.1 mmol/kg) of Magnevist (Berlex, Wayne, NJ, USA) was injected for each study. All images were acquired on a Siemens Trio 3-T scanner (Siemens AG, Erlangen, Germany) using a phased array body coil.

The CAMERA sequence, a radial 3D spoiled gradient echo with multiecho in the partition direction and sliding mask subtraction, was used to acquire the data in the coronal plane. The following imaging parameters were used: echo train length=4, number of projection ($N_P$)=192, readout points ($N_{RO}$=192, 75% fractional echo), field of view=240 mm×240 mm, slices=32, slice thickness=3.0 mm, flip angle=30°, repetition time (TR)=6.02 ms and echo times (TEs)=1.45, 2.48, 3.51 and 4.54 ms. During image reconstruction, magnitude subtraction images are generated by subtracting each measured volume by the volume acquired prior to it. In a static mask subtraction, the subtracted volume is the initial acquisition. The sliding mask technique, which has been previously described in Cashen et al. [12], is a method for improving the separation of arterial and venous phases by subtracting each acquired volume by the volume acquired a fixed amount of time prior. This process approximates the time derivation of the signal–time curve at each pixel and, as such, is better suited than static subtraction for imaging that may involve subject movement.

The scans were performed with a two-part breath hold technique. The subject held his/her breath for the first repetition (~9.5 s), which served as the first precontrast subtraction mask. Following a short break (15 s), the remaining four consecutive repetitions were acquired with the subject holding his or her breath for as long as possible (~36–40 s). The subjects were observed during the course of the imaging to ensure compliance with the breath hold protocol. This breath hold protocol was successfully used in the evaluation of patients with pulmonary arterial hypertension [18]. A single dose of contrast agent was injected at 4 ml/s followed by 20 ml of saline at 4 ml/s at the beginning of the second breath hold.

### 2.3. Image reconstruction

The images were reconstructed online on the scanner with a sliding window factor of 16, resulting in frame rates of approximately 558 ms/frame or 1.7 frames/s. There were a total of five repetitions producing 81 time points, with the first 16 time points corresponding to the mask measurement and final 65 time points corresponding to the dynamic measurements. Full 3D volumes of 32 slices were obtained for each