Original article

Absolute renal blood flow quantification by dynamic MRI and Gd-DTPA

J.-P. Vallée, F. Lazeyras, H. G. Khan, F. Terrier

Division de radiodiagnostic et radiologie interventionnelle, Département de Radiologie, Hôpitaux Universitaires de Genève, 24 rue Micheli-du-Crest, CH-1211 Geneva, Switzerland

Received: 9 September 1999; Revised: 31 January 2000; Accepted: 16 March 2000

Abstract. The aim of this study was to demonstrate the feasibility of the absolute renal blood flow quantification using MRI and injection of contrast media. Using a T1-weighted fast gradient sequence following an intravenous bolus injection of Gd-DTPA, dynamic images of the kidney were obtained in patients with well-functioning native kidneys (n = 7) or transplant (n = 9), with significant renal artery stenosis (n = 4) and with renal failure (n = 7). After signal intensity calibration, the absolute renal perfusion was equal to the wash-in slope of the renal transit curve divided by the contrast medium concentration at the peak of the bolus in the aorta. The cortical blood flow was 2.54 ± 1.16 ml/min per gram in well-functioning kidneys decreasing to 1.09 ± 0.75 ml/min per gram in case of renal artery stenosis (p = 0.04) and to 0.51 ± 0.34 ml/min per gram in case of renal failure (p < 0.001). These measurements were in agreement with previous results obtained by other methods. A standard MRI imaging sequence and a simple model can provide realistic quantitative data on renal perfusion. This work justifies further studies to compare this model with a gold standard for renal blood flow measurements.

Key words: Gadolinium – Genitourinary system – MR imaging – Kidney – Renal circulation

Introduction

Renal perfusion is an important parameter in the evaluation of the renal function that remains difficult to measure non-invasively [1]. Quantitative information obtained by nuclear medicine technique are limited by the low spatial resolution. Higher resolution as well as functional information can be obtained by MRI. Different methods have been developed to quantify renal perfusion. Phase-contrast MR sequences measure the blood flow in the renal arteries and have been successfully applied to native and transplant kidney [2]. However, this method is well suited for the detection of proximal renal stenosis, but it does not assess the perfusion inside the kidney. Renal perfusion can be assessed by diffusion-weighted MRI [3] or by MRI with arterial spin tagging [4]. However, these methods are technically challenging and are characterized by a low signal-to-noise ratio and a reduced spatial resolution. Much higher contrast-to-noise ratio can be obtained by injection of a contrast medium such as Gd-DTPA. Furthermore, by performing dynamic MRI during the injection, the transit of the contrast medium through the kidney can be followed. Qualitative assessment of the renal function by this method has shown differences in the curves pattern between well-functioning kidneys and pathologic kidneys. Differences from the normal response profile have been observed in ischemic kidney [5–8], renal failure [9], and after renal transplantation [10, 11]; however, the analysis was qualitative or semi-quantitative using parameters such as the maximum of the renal peak or the slope of the wash-in.

Recently, the relationship between the MR signal intensity of fast gradient-echo sequences and the relative gadolinium concentration in the tissues has been established [12]. Using an optimized sequence, saturation of the signal intensity at the peak of the bolus in the aorta could be avoided to accurately determine the arterial input function and the myocardium response. Because assessment of the arterial input function by MRI has been proven to be possible, new methods of analysis can be applied to the processing of renal transit curves.

In this study we apply a simple model for absolute quantification of the renal perfusion by dynamic MRI-coupled Gd-DTPA injection to patients with well-functioning and diseased kidneys.

Correspondence to: J.-P. Vallée
Methods

Patients

Twenty-seven patients referred for an MR exam of the kidneys were included in the study. Patients were divided in three groups: normal renal function (n = 16); renal failure (n = 7); and renal artery stenosis (n = 4). The first group (54 years, SD ± 15 years) with normal renal function as attested by a normal blood creatinine level included 7 patients with native kidneys (63 years, SD ± 16 years) and 9 patients with kidney transplant (48 years, SD ± 10 years). In the second group (n = 4, 63 years, SD ± 8 years), 2 patients had a unilateral renal artery stenosis (95 and 75% on MRA). 1 patient had a unilateral renal artery stenosis in a single kidney (status post nephrectomy; 64% stenosis on MRA), and 1 patient had a bilateral renal artery stenosis (70 and 50% stenosis on digital subtraction angiogram). In the third group (50 years, SD ± 19 years), all 7 patients were in renal failure at the time of the MRI exam (blood creatinine level = 316 ± 148 μM with normal values ranging from 56 to 115 μM). The etiology of the renal failure was an HIV nephropathy (n = 1), nephroangiosclerosis (n = 1), IgA glomerulonephritis (n = 1), graft rejection (n = 1), and unknown etiology (n = 3). All patients were on a normal diet without special water restriction or overload.

MR imaging

In each patient a single 10-mm-thick slice oriented in the transverse plane was obtained through the kidneys using a Picker Edge 1.5-T MR system and the fast low-angle shot (FAST) sequence [13] with a symmetric phase-encoding order preceded by an arrhythmia-insensitive magnetization preparation pulse. The magnetization preparation consisted of a non-selective 90° radio-frequency (RF) pulse followed by a spoiler gradient and a 180° RF pulse followed by a second spoiler gradient [14]. The delay between the two RF pulses (Ti1) was 50 ms and the delay between the 180° RF pulse and the beginning of the FAST sequence (Ti2) was 100 ms. The imaging parameters were as follows: body coil; TR 6.8 ms; TE 2.3 ms; flip angle 90°; field of view (FOV) 46 × 46 to 23 cm (according to the abdomen size), matrix size 256 × 192 with a symmetric phase-encoding order, one average per slice, photoplethysmograph (PPG) triggered. As a contrast medium, a bolus of Gd-DTPA (Magnevist, Schering, Berlin, Germany) at a dose of 0.025 mmol/kg body weight was injected manually in a brachial vein followed a 10 ml of isotonic NaCl solution. A series of 90–120 images were recorded in each patient.

In 11 patients, three external references containing a solution of Gd-DTPA with various T1 (76, 138, and 838 ms) were included in the FOV.

Signal intensity calibration

For the conversion of the signal intensity into gadolinium concentration, an in vitro calibration curve was constructed from a phantom of 49 tubes filled with Gd-DTPA solutions at various concentrations (from 0 to 5 mM) [15]. The signal intensity of the tubes measured by the FAST sequence used for the perfusion study were plotted as a function of the tubes 1/T1 (which is linear to the Gd-DTPA concentration) [15]. Figure 1 shows the in vitro calibration curve with the polynomial fit. The signal intensity time curves were then converted in 1/T1 time curves using the following polynomial equation derived from the fit of the calibration curve:

\[
1/T1 = k \cdot (2.72 \times 10^{-4} + 3.07 \times 10^{-5} \cdot SI + 1.21 \times 10^{-6} \cdot SI^2 - 1.28 \times 10^{-8} \cdot SI^3 + 5.59 \times 10^{-11} \cdot SI^4),
\]

where SI is the signal intensity and k is a scaling constant.

The scaling constant k was used to correct for differences in signal reception and was determined from the known T1 and SI of the external references in 11 patients. For the patients without external references, the subcutaneous fat was used as an internal reference with a constant T1 value assumed to be 366 ms. This value was determined from the calibrated images of the 11 patients with external references (fat T1 = 366 ± 61 ms).

A linear relationship between 1/T1 and Gd-DTPA concentration was assumed as previously discussed [12] yielding:

\[
[Gd_{\text{tissue}}] = \frac{\Delta(1/T1)_{\text{tissue}}}{k} \]

(1)