Simultaneous Renal Angiography and Quantitative Perfusion Measurement from a Single Time Resolved MRA Data Set

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Introduction

Time resolved imaging with stochastic trajectories (TWIST) is a method for contrast-enhanced MR angiography that employs a view sharing technique to dramatically reduce the time necessary to obtain dynamic volumetric data sets (1). For renal angiography, it is possible to obtain free-breathing angiograms in less than four seconds per frame. In addition to angiography, however, these data also contain time-resolved enhancement information about the renal parenchyma. Serial T1-weighted weighted images of the kidney are often used to fit perfusion data. Thus the time resolved T1-weighted images obtained with TWIST could conceptually be used for perfusion imaging. Here we provide a proof of concept of this idea, using TWIST angiography data to obtain renal perfusion measurements.

Theory

The expected behavior of MRI signal intensity (SI) in a gradient echo experiment in the presence of various concentrations of contrast agent was modeled by the well accepted relationships derived from the Bloch equations (2). The observed T_1 as a function of concentration was modeled as (2):

$$R_1(C) = 1/T_{1,0} + \alpha_1 C,$$

where C is the concentration, $T_{1,0}$ is the intrinsic T_1 value with no contrast agent obtained from the literature (3), and α_1 obtained experimentally from measurements on gadolinium solutions. A kinetic model of perfusion was introduced as follows:

$$dC_t/dt = K_{trans}\, C_p - k_{ep} C_t$$

where C_p is the plasma concentration of contrast agent, C_t is the tissue gadolinium concentration, K_{trans} the volume transfer constant between blood and the extravascular extracellular space (EES), and k_{ep} the rate constant between the EES and blood plasma. We have followed the nomenclature endorsed by Tofts et al (4). The K_{trans} is related to the tissue perfusion by the following equation:

$$K_{trans} = F(1 - Hct)$$

where F is the perfusion (ml $g^{-1}min^{-1}$).

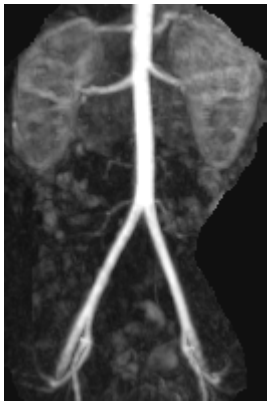

Figure 1: MIP from a renal MRA depicting a single time frame from a TWIST data set.

Materials and Methods

A normal subject (31 yo F), underwent a TWIST dynamic renal MRA examination at 3.0 T (Magnetom Verio, Siemens, Erlangen, Germany). A half-dose (0.05 mMol/kg) of Gadoversetamide (Optimark; Mallinckrodt Inc. St. Louis, MO, USA) was employed and images were acquired using a previously described view-sharing technique and 3D Fast Low Angle Shot readout (FLASH; TR/TE 2.51/0.95 ms, α 21°, BW 1080, FOV 350x284x108mm³, MX 256x208x72, resolution 1.4x1.4x1.5 mm, GRAPPA factor 3, 30 time points, 3.7 s/volume). The obtained time course data were then fit offline using the model described above, using MATLAB (The Matworks, Natick MA). The measured K_{trans} and k_{ep}, were then used to obtain an estimate of the tissue perfusion, F.

Results and Discussion

A maximal intensity projection (MIP) image of a single 3-D volume from the renal angiography TWIST data set is depicted in Figure 1. This confirms the feasibility of free-breathing, 3-D time resolved angiography of the renal arteries with this technique. Figure 2 depicts time course data from the aorta, renal cortex, and renal medulla, and the fitted model results depicting expected signal behavior (5). The measured K_{trans} is 3.42 $Lmin^{-1}$ (cortex) and 0.54 $Lmin^{-1}$ (medulla), respectively, yielding perfusion measurements of 5.38 and 0.85 ml $g^{-1}min^{-1}$.

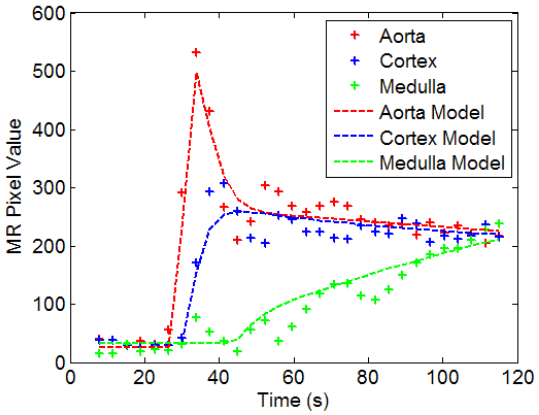

Figure 2: Time course data for ROIs in the aorta, renal cortex, and renal medulla from the time resolved angiogram, with the model fit results

We have demonstrated the feasibility of using time-resolved angiography (TWIST) data to simultaneously obtain perfusion measurements. This analysis could have immediate clinical impact, as it provides a means to assess perfusion deficits created by renal artery stenosis (6). However, combining the perfusion measurement with the time resolved angiography has a striking effect on reducing dose of contrast agent employed. Here, only 0.05 mmol/kg of Gd-DTPA was injected in the present study, six times smaller than versus 0.3 mmol/kg reported previously, when 0.2 mmol/kg were used for the angiography data set, and 0.1 mmol/kg for the perfusion study. In an era of NSF, this is a particularly important improvement. The combination of these two techniques could also help better analyze the effect of small vessel disease in the kidneys. A multi-subject and patient study remains to be done. The data were obtained in a free-breathing fashion, and retrospective respiratory gating can be expected to improve the obtained fits. The renal MRA is lower in resolution than a typical ceMRA (approximately 1.5 mm isotropic resolution with TWIST versus approximately 1 mm isotropic with a traditional ceMRA). The tradeoff between temporal and spatial resolution in TWIST renal angiography, and its effect on the fitted perfusion parameters can be further explored as well.

References

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