Renal-ASL using a Multiple-Inversion Time, Free Breathing, STAR-HASTE Technique at 3T

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Introduction

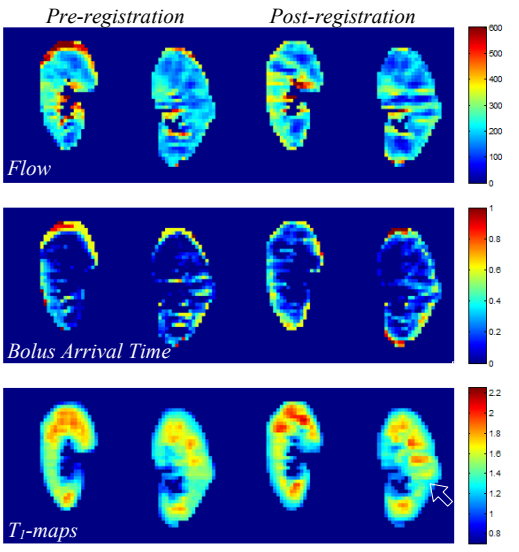
Arterial spin labelling (ASL) is a non-invasive MR technique used for measuring tissue perfusion in which the endogenous blood water is magnetically labelled and acts as a tracer. ASL has been applied extensively in the brain, but there has been increasing interest in applying ASL to the kidneys (1), particularly as a result of concerns over the link between gadolinium-bearing contrast agents and NSF. Currently, most human renal-ASL has been performed using a *single inversion time*, and applying a simple model for quantification; this means that effects of bolus arrival time and tissue dynamics cannot be accounted for. Using a multiple inversion time (TI) acquisition allows us to treat the labelled blood as a bolus, and avoids the above error by fitting (with a suitable model) for the bolus arrival time, as well as perfusion. Multiple time point acquisitions also yield more information on bolus dynamics, allowing the application of more complex models. The increased SNR at high field strength, coupled with the extended T_1 of blood at 3T, gives a theoretical SNR advantage over lower field strengths. However, the disadvantage of this is the potential for increased artefacts due to air-tissue susceptibility differences and RF inhomogeneity. Additionally, there are problems of motion artefacts to overcome (2). Thus, in this abstract we aim to demonstrate the feasibility of applying the Buxton model (3), at 3T, using a STAR based labelling technique (4) and a free breathing approach. Here, we demonstrate the practicality of fitting for arrival time, producing high quality parametric output.

Methods

Four healthy volunteers (3 male, informed written consent was given) were imaged using a 3T Philips Achieva scanner and a torso phased-array coil. A 40 mm thick STAR label was applied to the aorta in a sagittal oblique plane (shown in Figure 1). To avoid effects of unwanted tagging of renal tissue, to reduce subtraction error of background signal, and to remove any residually labelled blood, we used pre and post labelling saturation pulses (4). TIs of 300, 600, 900, 1200, 1500, 1800, 2100 and 2700 ms were acquired with 21 control-label pairs at each TI. A single slice half-Fourier acquisition TSE readout (HASTE) (factor 0.6, 180° refocusing), TR/TE/α = 6000 ms/4.9 ms/90°, FOV of 400×400×8 mm and matrix of 128×128 was used with a low-high slice ordering giving an effective TE of 4.9 ms. This gave an ASL acquisition time of ~34 min. We aimed to acquire the slice along the long the axes of the both kidneys, in a coronal oblique plane, and posterior to the renal pelvis to avoid large blood vessels. To correct for motion artefacts we used weighted 2D ridged body registration (5) with the assumption that most motion was along the long-axes of the kidneys. A saturation recovery fit was applied to the control images to fit for T_1 and M_0, which was possible because of the pre and post labelling saturation pulses. The Buxton model (3) was fitted on a voxel-by-voxel basis with parameters: T_1-blood = 1.66 s (6), inversion efficiency = 0.63 (measured in a phantom), partition coefficient = 0.9 (2), time to label end = 3 s, T_1-tissue and M_0 were values taken from the saturation recovery fit (using M_0 in this way has the advantage of normalising any inhomogeneities in the imaging field). The cortex and medulla were segmented using the T_1 maps (tissues above 1000 ms was deemed to be kidney tissue, then a cortex-medulla threshold of 1350 ms was set from literature values (6), and then adjusted to give an even cortex-medulla distribution (2)). The mean arrival time and flow was then calculated for each volunteer.

Results

The mean flow values over the volunteers over both kidneys were 216 (range 150 – 300) ml /(min 100 ml) for the cortex and 133 (range 93 – 190) ml /(min 100 ml) for the medulla. The mean bolus arrival time was 142 (range 80 – 262) ms for the cortex and 70 (range 6 – 153) ms for the medulla.



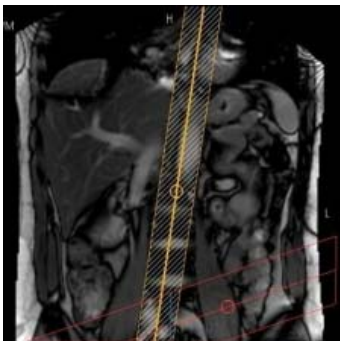


Figure 1. *(right) A balanced SSFP image showing the planning of the labelling pulse*

Figure 2. *(left) Maps of flow (ml blood min^{-1}100 ml), bolus arrival time(s), and T_1-tissue (s) for a volunteer. Pre-registered images are shown on the left and post registration on the right*

Figure 3. *(bottom) Examples of ASL difference curves (normalised to M_0) from pixels in the left kidney in the registered example shown (highlighted by the white arrow shown on the T_1-map of Figure 1). Error bars are the standard error on the mean.*

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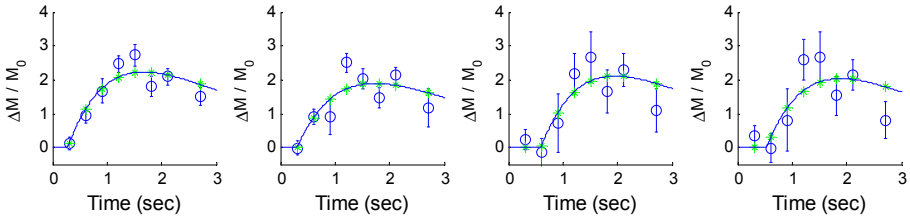

Discussion

The difference in magnetisation plot in Figure 3 shows the bolus arriving in the voxel, before decaying via T1 and outflow and also good ASL SNR. This figure illustrates the quality of the fits. The registration reduced motion artefacts and made flow maps more defined, as illustrated in Figure 2. The technique found the arrival time increased toward the outside of the kidneys, as expected. With further optimisation it should be possible to reduce the imaging time via reductions in the number of averages and TIs. In this work we have demonstrated that renal-ASL using a bolus tracking, free breathing, STAR-HASTE technique at 3T can be applied to the kidneys. However, while we have been able to take account of arrival time, we found systematic deviations from the Buxton model; data acquired using this method allows extensions of the model to be investigated.

Acknowledgements: AstraZeneca and EPSRC for funding. Dr David Higgins for scanner and pulse programming support.

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