A New Method for Obtaining Quantitative ASL Perfusion Maps: A Comparison with the FAIR Method

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Introduction
Flow-sensitive alternating inversion recovery (FAIR (1,2)) has been used to obtain quantitative perfusion maps in humans and animal models. Two methods of calculating these maps have been employed: one introduced with FAIR and known as the FAIR method (2), and another known as the T1 method (3). The first requires the calculation of a T1 map from a series of control images and a perfusion image from the subtraction of the tag and control images. The second requires two T1 maps, one calculated from tag images and one from control images. Both methods have limited clinical applicability because several images are required to measure relaxation times accurately. We have previously presented another method for obtaining quantitative ASL images (4) using a perfusion sequence with a different tagging scheme (EST (5)). This method is based upon the mole fraction of exchangeable water that flows into the imaging plane during a given time. By imaging at the null point of blood, we can determine the magnetization of blood, which is subsequently used to calculate the perfusion rate. Our method requires fewer measurements and calculations, bringing it closer to clinical applicability. We have compared the results of our method to the results of the other two methods in measuring renal perfusion in healthy volunteers.

Methods
Six healthy volunteers were imaged on a Siemens 1.5 T system using a body phased-array coil. Anterior coil elements were turned off to reduce motion artifacts and a 3-D shim was performed. Tagging pulses for each sequence were followed by HASTE with the following parameters: TE 36 ms, FOV 350 mm, matrix size 256x256, slice thickness 10 mm, 1 acquisition. A transverse slice through both kidneys was imaged, avoiding the renal arteries. Receiver gains were set using the FAIR sequence with the shortest inversion time and kept constant for the rest of the images. FAIR and EST images were obtained at TI values of 300, 400, 600, 800, 1200, and 1600 ms. EST inversion and saturation tag images were also obtained at the null point of blood (assumed to be 900 ms). Fat saturation pulses were used with all sequences. The data was analyzed using the three methods described in the introduction. For the mole fraction (x) analysis, \( \frac{x(M_c - M_t)}{M_c - M_a} \), which is approximately equal to \( \frac{T1}{\lambda} \), where \( M_c \), \( M_t \), and \( M_a \) are the magnetization of the control image, the tag image, and the incoming blood.

Results
Typical renal perfusion rates are 330-400 ml/100g/min (6). The results obtained with the T1 method ranged from -1000 ml/100g/min to 600 ml/100g/min due to error in the T1 map. The difference expected between the nonselective and selective T1's is about 5%. To obtain T1 measurements with this accuracy, it is necessary to use more time points and/or signal averaging. With the FAIR method, the inaccuracy in the T1 map contributes only a few percent error, and we obtained reasonable perfusion rates. The numbers obtained at short inversion times are higher, probably due to incomplete inversion of the imaging slice, but soon become stable (Figure 1). We obtained similar results with the mole fraction method. The value obtained at 1200 ms was often much higher than the others, due to division by low numbers where \( M_t \) is approximately equal to \( M_c \) (Figure 2). At 800 ms, a time that avoids both slice profile effects and division by zero, both methods give good results. The values for each of our six volunteers are plotted in Figure 3. The average value for all volunteers for FAIR is 387±53.5 ml/100g/min, and for the mole fraction method it is 385 ± 53.9.

Discussion
A major drawback of quantitative ASL has been the relatively large number of images required to obtain accurate perfusion rates. We were unable to consistently fit a T1 curve to a series of less than five inversion times, and we actually acquired six images so that the pixel with the lowest signal could be discarded. Using a FAIR sequence that acquires tag and control images within a single breathhold, it took six breathholds to obtain the perfusion maps. With the mole fraction method and a similar EST sequence, we can obtain perfusion maps in as few as three breathholds: one for an inversion tag and control image at the null point, one for a saturation tag image at the null point, and one for a control and tag image at 800 ms. This effectively halves the time required for data acquisition or doubles the number of averages one can obtain in a given study.