Improved Characterization of DCE-MRI in Prostate Cancer using MT Derived Relaxivity Correction Maps

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Introduction

It has been hypothesized that the macromolecular protein content in tissues affects the rotational correlation times of water molecules and therefore alters the relaxivity characteristics of standard gadolinium (Gd) based T_1 relaxation agents[1]. It is also known that magnetization transfer effects in biological samples can be shown to reflect macromolecular proton fractions in a quantitative manner [2]. By combining these two processes, previous work has shown that for in-vitro samples, more accurate measures of Gd concentration can be obtained by correcting the relaxivity based on MT derived measures of macromolecular protein content [3]. In addition it has been shown that the macromolecular protein ratios change significantly in pathological tissues as demonstrated by several investigators attempts at using MTr to improve clinical diagnosis of various diseases (4). Since tissue Gd concentration data used in kinetic modeling is determined using relaxivity values it seems prudent to correct DCE-MRI data for these known physiological variations.

To evaluate the importance of this effect we obtained MT ratios of prostate before subsequent measures of DCE-MRI were obtained and then using these MTr maps produced correlated relaxivity maps. The functional form used to correlate measures of MTr to relaxivity was obtained from previous in-vitro measures of egg protein samples. Previous data allowed a linear mapping of MTr to relaxivity for the same clinical contrast agent. To determine the appropriateness of this process we produced a Gadolinium difference (Δ [Gd]) map to see the relative difference and then carried this forward through the DCE-MRI kinetic model to asses relative changes in pharmacokinetic parameters.

Materials and methods

All clinical data was acquired using a Philips 3.0 Tesla scanner (Philips Medical Systems, Best, NL) with a commercial disposable endorectal prostate coil (MedRad BPX-15) tuned up to 127.8 MHz with a home-built tuning/detuning box. MT ratios were obtained using a 3D FFE protocol with and without off resonance MT pulse. DCE-MRI data are obtained with a 3D TFE technique with 6 second temporal resolution. We used a Philips "PRIDE" software tool designed to process DCE-MRI data using a standard General Kinetic pharmacokinetic model with the additional capability of incorporating the MT data for producing in-vivo relaxivity correction maps for subsequent GKM processing.

Results and Discussion

A previously presented calibration function is used for mapping MTr data to relaxivity data. The MT derived relaxivity map is then applied to generate more accurate Gd concentration data. Figure 1 shows a T2 weighted prostate image and corresponding Gadolinium difference (Δ [Gd]) image which shows the change in Gd concentration with and without the relaxivity correction. This process was then applied to one slice of a DCE-MRI data set to demonstrate the difference in GKM pharmacokinetic parameters. Gd concentrations obtained when using this correction scheme. Figure 2 shows one slice of a DCEMRI data set where three regions are selected to show the difference in the calculated K^{trans} value. For these three regions the difference in K^{trans} values are apparent from the values with (w) and without(wo) correction.

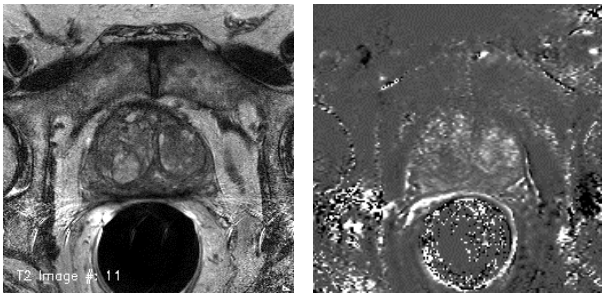
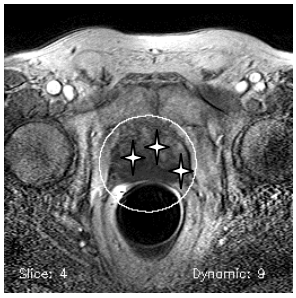


Figure 1. a)T2 weighted prostate image and b) corresponding Δ [Gd] map for same slice data.



K^{trans} Values

ROI 1	ROI 2	ROI 3	
.2142	.05441	.0412	w
.1846	.05190	.0480	wo

Figure 2. DCE-MRI data set with 3 locations of K^{trans} With respective values before and after Relaxivity correction

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