Improved T_1 Mapping and DCE-MRI Quantification for Prostate at 3T by Incorporating B_1 Inhomogeneity Correction

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Introduction and Purpose

Dynamic Contrast Enhanced (DCE) MRI is used for the assessment of tumor vascular properties with application to prostate cancer detection, characterization, and treatment monitoring [1]. MR signal intensity changes versus time during the uptake of Gd-DTPA are measured and used in conjunction with pharmacokinetic (PK) models to provide a number of tumor vascular properties. An initial step in the PK analysis requires conversion of signal intensity vs. time into contrast-agent concentration (C(t)) vs. time. Since signal intensity changes are non-linearly related to contrast agent concentration, this requires knowledge of pre-contrast tissue T_1 values. Variable Flip Angle (VFA) imaging is a preferred T_1 mapping method since it provides T_1 maps using the same 3D SPGR sequences that are used for DCE acquisition, so that identical spatial resolution and coverage can be obtained in reasonable acquisition times. VFA analysis fits the imaging equation as a function of flip angle α to obtain pixel-wise T_1 values. However, VFA suffers from large errors at higher field strengths due to B_1 field inhomogeneity and applied flip angles ($\alpha_{applied}$) differing from the actual flip angles (α_{actual}) seen by the tissue with $K = \alpha_{actual} / \alpha_{applied}$ varying spatially within the imaged volume. In this work, we demonstrate the application of the Bloch-Siegert-based B1 estimation method [2], a validated method for measuring α_{actual}, to correct the VFA curves and the DCE curves, thus obtaining improved T1 maps and PK values. Such a corrected method has promise in improving DCE-MRI analysis and providing consistent results allowing improved cancer detection and characterization.

Methods

26 subjects were scanned on a GE (Waukesha, WI) 3.0T Twinspeed HDx system after obtaining informed consent under IRB approved protocol.
Acquisition: (A) **VFA protocol**: 3D FSPGR, SPECIAL fat-suppression, TR 15ms or TR 9.1ms, TE 3.1ms. FA 21/18/15/12/9/6 degrees. 14-16 slices. Slice thickness 6mm. Matrix 128x256. FOV 26x26 cm^2, BW ±15.6Khz. (B) **Bloch-Siegert (BS) protocol**: 2D SE, TR/TE/Flip 950ms/22ms/90 degrees, 2 Khz off resonance Bloch-Siegert B1 pulse [2], Matrix 128x128, FOV 30x30cm^2, BW ±31.3Khz, Slice thickness 6mm. Acquisition time 4 min/16 slices. (C) **DCE protocol**: 3D FSPGR, SPECIAL fat-suppression, TR/TE/FA 4.0/1.4ms/15 degrees. 14-16 slices, 160x256. FOV 26x26cm^2, BW ±64Khz, Slice Thickness 6mm, imaged every 5 sec for 6 minutes after administration of 0.1 mmol/kg GD-DPTA i.v. at 0.3 cc/sec.
Analysis: (A) **B_1 mapping**: B_1 spatial re-sampling was performed to match the DCE and T_1 images. B_1 maps in units of μT were divided by the nominal applied B_1 of 5000 μT to yield maps of K, which were truncated to retain only values of $0.5 < K < 1.5$ to exclude holes created by brachytherapy needles or prior biopsies. (B) **T_1 mapping**: The SPGR equation $SI(\alpha) = M0 * \sin\alpha * (1 - \exp(-TR/T_1)) / (1 - \cos\alpha * \exp(-TR/T_1))$ was fitted to the signal versus α curve. B_1 correction was incorporated by correcting the flip angles using $\alpha_{actual} = \alpha_{applied} * K$ on a pixel-wise basis.
(C) **DCE Signal Correction** : The ratio of signal intensity at time t, SI(t), to signal intensity at baseline SI_{pre} is $SI_{pre}/SI(t) = [1-\exp(-TR/T1_{pre})]/[1-\cos\alpha \exp(-TR/T1_{pre})] * [1-\cos\alpha \exp(-TR/T_1(t)]/[1-\exp(-TR/T_1(t)]$, where we utilized the corrected α_{actual}. The resulting $T_1(t)$ was then used to compute C(t), which was then fed into PK modeling, using the Generalized Kinetic Model [3].

Results and Discussion

T_1 results before and after B_1 correction (Table 1) were computed over an ROI in the prostate for 26 subjects using the TR 9.1 (N=15) and 15ms (N=13; 2 subjects had data for both short and long TR) VFA sequences. The longer TR yielded improved T_1 quantification, which compared well with literature values. Fig. 1 shows T_1 maps before and after B_1 correction, as well as the B_1 map (in μT) for one subject. We then compared PK results computed using four approaches: (i) Using uniform prostate tissue T_1 of 1597ms; (ii) Using VFA T_1 mapping without B_1 correction; (iii) Using T_1 mapping performed with B_1 correction, but DCE signal conversion to C(t) for PK analysis performed without B_1 correction; and (iv) Using T_1 mapping and PK analysis both performed with the B_1 correction. The K^{trans} maps obtained from methods (i)-(iv) were clinically evaluated (Fig. 2) in a yellow-highlighted ROI placed on a tumor based on a T_2-weighted image (A) and the ADC map (B), which was later confirmed to be malignant by direct in-bore MR-guided biopsy. In Fig.2 (i), without T_1 mapping, the tumor is not visible on the K^{trans} map. Both tumor and normal tissue regions are highlighted after using T_1 mapping in (ii). Incorporating B_1 mapping improved discrimination between tumor and normal tissue in (iii), and the K^{trans} value in the tumor further increased in (iv), which shows that B_1 correction increased the sensitivity to tumor detection.

	TR=15ms (13 cases)		TR=9.1ms (15 cases)	
T_1 (ms)	W/o correction	B_1 Correction	W/o correction	B_1 Correction
mean	977.87	1261.89	594.56	803.98
std/mean	0.12	0.15	0.17	0.22

Table.1: Prostate T_1 mean/std of all cases for long/short TR at 3T.

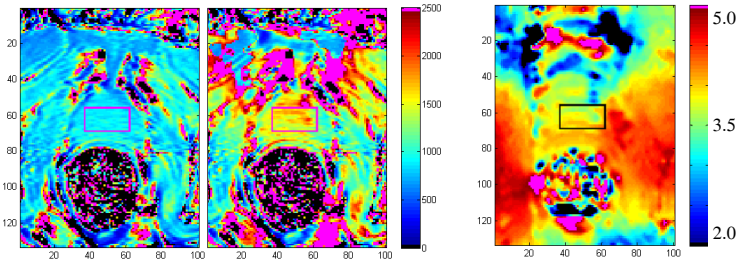


Fig.1: T_1 map (ms) before (left) and after (middle) B_1 correction, and corresponding B_1 map (μT) (right). Average ROI $T_{1before}$ = 895.80 ms, T_{1after} = 1540.59 ms.

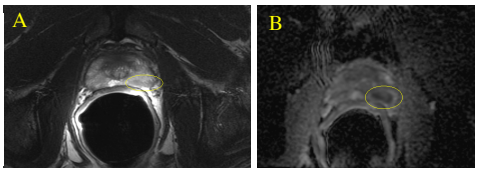
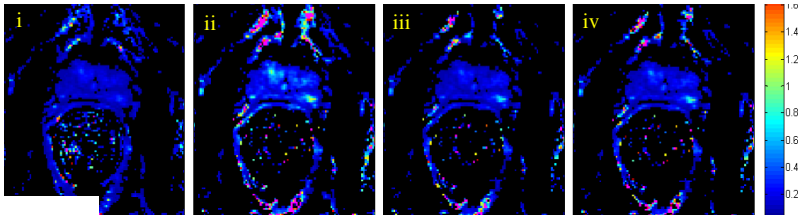


Fig.2: T_2w image (A); ADC map (B); K^{trans} maps for 4 methods (i)-(iv). Yellow highlighted region denotes confirmed tumor.



Conclusion

The Bloch-Siegert method of correcting for B_1 inhomogeneity improves T_1 mapping of prostate at 3T. We validated the method on 26 subjects and demonstrated good T_1 quantification using long TR VFA sequences combined with B_1 correction. We also showed better PK maps by incorporating B_1 correction into DCEMRI quantification.

References

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