Rapid Dynamic 3D T1-Mapping of the Abdomen

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Introduction: Rapid accurate T_1 mapping with large volume coverage is particularly important for abdominal studies of T_1-shortening contrast agent kinetics. The variable flip-angle (VFA) spoiled-GRE method permits rapid T_1 quantification with accuracy similar to that of conventional IR techniques [1, 2]. Provided baseline T_1 information, a dynamic GRE scan can be used for serial T_1 measurements [3]. However, B_1^+ inhomogeneities lead to VFA T_1 measurement errors and both propagate into serial T_1 errors during dynamic measurements. RF profile calibration or *in vivo* B_1^+ mapping can improve the accuracy and precision of VFA measurements [1, 2, 5]. We describe a method for dynamic 3D T_1-mapping across a wide T_1 range (150-2000 ms) for abdominal measurements and demonstrate the accuracy and stability of our method in phantom and animal model studies.

Methods: All experiments were performed using a 1.5T clinical MRI scanner (Siemens Magnetom Sonata) with a single channel coil. Nominal flip angle (FA) slice profiles were generated by numerically solving Bloch equations based upon pulse sequence RF definitions (**Fig. 1**). 3D slice over-sampling was applied to avoid RF side lobe wrapping. Baseline and dynamic T_1 mapping was performed using 3D VFA and 3D single FA GRE acquisitions respectively. Based upon our slice profile calibrations, turbo spin echo (TSE) sequences with double FA measurements were used to provide *in vivo* FA maps [6] which were used to correct both baseline and dynamic T_1 measurements. These calibration steps were performed using nonlinear curve fitting of the integral signal equations over each slice.

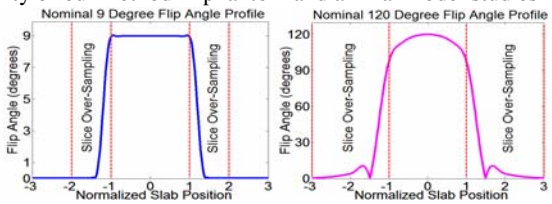

Fig. 1. Nominal FA profiles of GRE FA 9° (left) and TSE FA 120° (right). 3D slice over-sampling avoids side lobe wrapping.

Imaging Parameters Identical for phantom and animal studies. **GRE**: 3D, TR/TE = 6/1.66 ms, 850Hz/pixel BW, 8 slices/slab, 50% slice over-sampling; for baseline T_1: FA = 2°, 9°, 19° [1], 4 averages; for dynamic scan: FA = 9°, 1 average, **1.6s/slab imaging rate**. **TSE:** 3D, TR/TE = 4000/10 ms, 186 Hz/pixel BW, FA = 120°, 60° excitation, 120° refocusing, 2 refocusing pulses, 2 slices/slab, 100% slice over sampling, 2 slabs/scan, 100% spacing, 2 scans interleaved for each excitation FA. **GRE and TSE**: 5mm slice-thickness, 220×124 mm^2 FOV, 128×80 matrix, 1.72×1.72×5.0mm^3, slab-selective RF pulse. IR TSE was used to measure reference T_1 values.

Phantom Studies To evaluate the accuracy of our T_1-mapping methods we initially performed phantom studies using 8 vials containing Gd solutions (T_1 ranging from 75 to 2000 ms) and a Siemens cylindrical phantom with 1.25g $NiSO_4 \cdot 6H_2O$ + 5g NaCl/1kg H_2O.

Animal Studies 6 liver tumors were grown in 4 New Zealand White rabbits. Following abdominal FA mapping and VFA measurements, dynamic T_1 mapping was performed after intra-arterial injection of 3.0mL 2.5% Gd-DTPA. 8 Gd vials were placed next to each rabbit for calibration purposes and to serve as references during dynamic measurements.

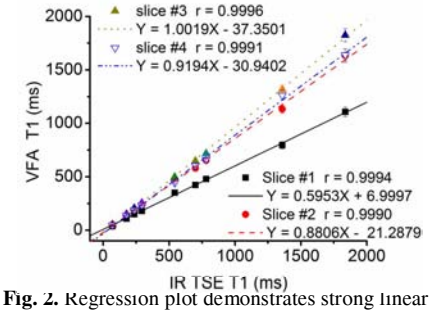

Fig. 2. Regression plot demonstrates strong linear relationships between VFA measurements and reference T_1 values in different slices but also suggests slice dependent systematic errors.

Results: *Phantom Studies* After slice profile and FA calibration, VFA T_1 measurements were highly correlated to reference T_1 values but the measured T_1 values deviated between slices suggesting systematic errors introduced at these different positions. To correct these errors, we performed linear regression between multiple VFA and reference T_1 data points and then back projected alternate VFA T_1 values at the same slice onto the regression curve to interpolate their correct T_1 values. This correction method was validated in the Siemens cylindrical phantom. Corrected VFA T_1 values in the phantom at 4 slices (**Fig. 2**) were 291.8±8.3, 294.9±6.6, 293.0±5.8, 289.6±6.0 ms, all in close agreement with reference IR measurement of 293.2±1.1 ms.

Animal Studies A representative baseline T_1 map and pre and post-contrast dynamic contrast-enhanced T_1 maps are shown in **Fig. 3**. The 8 vials positioned around the rabbit provided accurate calibration regression curves in all studies, all with $r > 0.9985$. In 4 rabbits, the average baseline VX2 liver tumor core T_1 was 1367 ± 153 ms while tumor edge T_1 was 857 ± 102 ms. After Gd injection, T_1 in arterially perfused tumor regions decreased to a minimum of ~250 ms. The dynamic stability of the T_1 measurement across a 150-2000 ms T_1 range over 100s at a 1.6s temporal resolution is shown in **Fig. 4**. Without systematic error calibration, T_1 error was > 10%. With systematic error correction, after spin system equilibrium, the maximum mean T_1 error was <3.6%, and the maximum mean standard deviation was <3.7%.

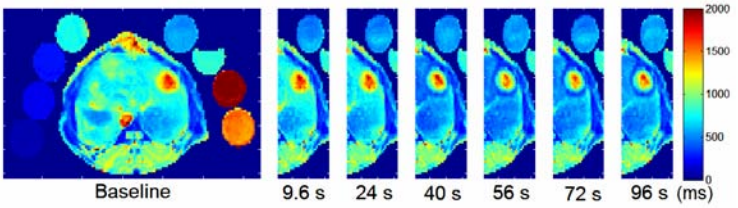

Fig. 3. T_1 maps at different time points during dynamic scan after contrast injection. VX2 liver tumor had higher baseline T_1 value than surrounding tissue. After contrast injection, T_1 at the tumor edge decreased suggesting characteristic peripheral rim contrast uptake but T_1 within tumor core changed much less suggesting necrosis.

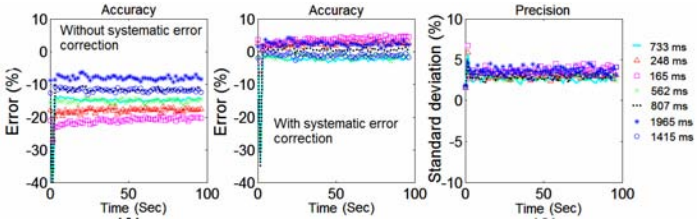

Fig. 4. Dynamic stability of the T_1 measurement across 150-2000 ms T_1 range over 100s at 1.6s temporal resolution. (left) error (%) without systematic error correction: (center) error (%) with systematic error correction (right) Precision: standard deviation (%)

Conclusion: We present a rapid 3D GRE T_1-mapping technique demonstrating high stability, accuracy and precision for 3D baseline and dynamic T_1 measurements. With navigator triggering for FA mapping and breath-holding for T_1 measurements, this technique is readily applicable for abdominal imaging in humans particularly because the volume coverage provided by our multi-slab FA mapping strategy can be scaled with only minimal acquisition time penalties. With rigorous calibration of slice profiles, B_1^+ nonuniformity, and slice dependent systematic errors, we can achieve accurate dynamic 3D T_1-mapping with large volume coverage for adnominal imaging applications.

References: [1] Cheng MRM 2006 55:566-574 [2] Wang JMR 2006 182:283-292 [3] Zheng JMRI 1999 10:576-581 [4] Cernicanu AcadRad 2006 13:686–693 [5] Parker MRM 2001 45:838–845 [6] Wang MRM 2005 53:408-417