Quantification of gastric secretion, mixing and emptying within single breath hold

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Introduction: Quantitative assessment of gastric emptying, secretion and mixing is of major importance for a detailed understanding of how ingested nutrients are processed and emptied in the human gastrointestinal tract. For quantification of gastric secretion and mixing, a noninvasive method was previously reported based on combined T1 and B1 mapping (T1B1) [1]. T1 mapping was based on the dual-flip angle approach. Due to the sensitivity of this scheme to transmit field inhomogeneity, T1 data had to be corrected using a B1 map derived from dual repetition time (dual-TR) measurements. The practical limitation of this method is mainly due to the duration of the B1 mapping acquisition, which gives rise to flow artifacts. More importantly, T1B1 requires three breath hold cycles for imaging the complete stomach volume. The aim of this study was to employ and evaluate the combination of the rapid B1 mapping technique DREAM [3] and slice profile correction for gastrointestinal T1 mapping. The method was optimized and validated for abdominal imaging within one breath hold and compared to the T1B1 mapping reference.

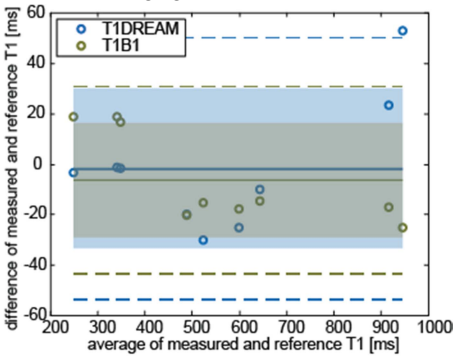

Figure 1: *Bland-Altman plot of in vitro T1 relaxation times of meal samples at different levels of dilution using T1DREAM (blue dots), T1B1 (green dots) with respective lower and upper limit of agreement (dashed lines). Spectroscopic values were used as reference. Bias (solid lines) and standard errors (semi-transparent areas) show that both schemes are in agreement with the reference.*

Methods: Phantom and in vivo experiments were performed using a 1.5T whole-body MRI scanner (1.5 T Achieva, Philips Healthcare, Best, the Netherlands). By substituting the dual-TR with DREAM B1 mapping, the T1DREAM method could be performed in a single breath hold. In order to account for nonrectangular slice profiles caused by standard sinc-gauss RF pulses, an iterative flip angle correction was introduced. First, an initial estimate of T1 was calculated based on the B1 map-corrected flip angles, by assuming uniform B1 through-slice. In a second step, an estimate of the true flip angle was obtained by simulating the theoretical slice profile of the RF pulse applied. The initial T1 value was updated based on the estimated flip angle. This procedure was iterated until convergence was achieved.

Meal: A previously calibrated liquid test meal, containing 10% glucose solution enhanced with contrast agent Gd-DOTA (DOTAREM, Laboratoire Guerbet, France) [2] was prepared.

In vitro: T1 values were acquired with the proposed method using samples of the test meal at different levels of dilution in water and hydrochloric acid. Results were validated with spectroscopic inversion recovery measurements and compared to T1 values from T1B1 mapping.

In vivo: Three healthy volunteers were imagined in right decubitus position. After drinking the test meal, T1DREAM and T1B1 mapping were performed 0, 15 and 30 minutes after meal intake within one and three total breath holds, respectively. Eight transversal slices were acquired to cover the complete stomach volume and a scan pause of 1s was introduced between subsequent DREAM B1 slice acquisitions. T1 mapping sequence parameters: TR/TE=9.0/2.1ms, flip angles=2°/20°, FOV=380x260mm^2, voxel size 2.81x2.81mm^2, slice thickness=15mm, RF pulse time-bandwidth product=8.02, scan duration=2.3s/slice. Dual-TR sequence parameters: TR=20/100ms, TE=2.1ms, flip angle=70°, FOV=380x260mm^2, voxel size 4.00x4.38mm^2, slice thickness=15mm, scan duration=8.4s/slice. DREAM sequence parameters: FID first, TE=1.0/1.5ms, Ts=2.3ms, STEAM flip angle=60°, imaging flip angle=10°, TFE factor=52, slice thickness=15mm, FOV=380x260mm^2, voxel size 3.9x4.1mm^2, scan duration=0.1s/slice.

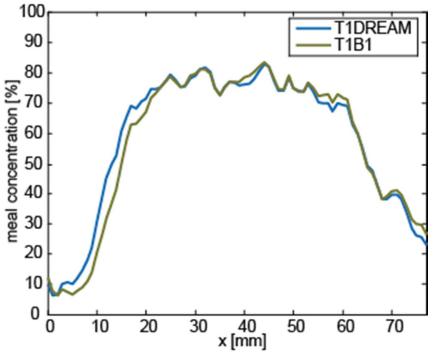

Figure 3: *Comparison of calculated meal concentrations along direction of gravity with T1DREAM (blue line) and T1B1 (green line).Meal concentrations mainly differ at low values, corresponding to high T1 relaxation times.*

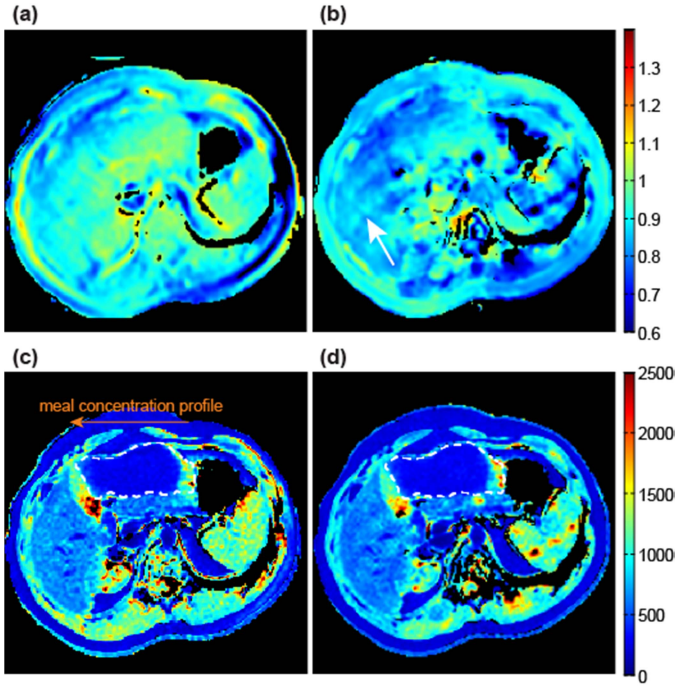

Figure 2: *Representative slice of B1 maps using (a) DREAM and (b) dual-TR. The white arrow indicates flow artifacts, which are not visible in the DREAM B1 maps. Corresponding T1 maps are shown in (c) and (d) with the stomach outlined by the dashed white line. Secretion can be seen as a layer of high T1 values forming on top of the meal. A meal concentration profile gives the distribution of meal along direction of gravity (orange arrow).*

Results: In vitro, both schemes were in good agreement with the spectroscopic reference values (Fig.1). As seen in Fig. 2, flow artifacts occurring in the dual-TR B1 maps due to the prolonged scan duration were not visible in the DREAM B1 maps. Fig.3 shows the profile of meal concentration based on a calibration curve of T1 vs. Gd-DOTA [2] along direction of gravity, where low T1 values correspond to high meal concentrations. Discrepancies between the two schemes were mainly observed for lower meal concentrations, i.e. higher T1 values, which may be due to saturation effects between subsequent DREAM slice acquisitions.

Discussion: Combining dual-flip angle T1 and DREAM B1 mapping allows T1 quantification of gastric content during a single breath hold of 26 sec and improves co-registration of T1 and B1 maps. This enables a more robust quantification of gastric secretion and mixing.

References: [1] Treier R et al. MRM 2007;57:568-76.
[2] Treier R et al. JMRI 2008;28:96-102.
[3] Nehrke K et al. MRM 2012;68:1517-26.