High resolution 3D abdominal T_1 mapping in one breath-hold using the Look-Locker method and non-Cartesian GRAPPA acceleration

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Target Audience This work targets those interested in rapid measurement of relaxation times in abdominal tissues and in applications of non-Cartesian parallel imaging.

Purpose Quantitative knowledge of T_1 relaxation time provides valuable information in a variety of pathological conditions and is also necessary for quantitative perfusion measurements[1]. In practice, measurement of T_1 values can be challenging over large volumes affected by motion, such as the abdomen. Previous studies have used a variable flip angle approach to acquire full volume abdominal T_1 maps in multiple breath-holds[2]. This method is sensitive to B_1 field inhomogeneity and subject to relative motion between breath-holds. The Look-Locker technique is another method for rapid T_1 mapping, but this method combined with a Cartesian readout cannot provide high resolution 3D T_1 maps in short scan times due to the large volume to be covered. In this study, we applied the Look-Locker method with a stack-of-spirals k-space acquisition accelerated using through-time non-Cartesian GRAPPA reconstruction to obtain ultrafast 3D T_1 maps in a single clinically feasible breath-hold. The technique was tested for accuracy in phantoms and is demonstrated in normal volunteers.

Methods MRI experiments were performed on a Siemens 1.5T Espree scanner with 12 receive channels (a six-channel body array coil and 6 channels from the spine array). The inversion-recovery Look-Locker method was combined with a stack-of-spirals trajectory and through-time non-Cartesian GRAPPA to accelerate data acquisition. The scan was divided into four segments (four inversion recovery periods, each of 2.7 sec) with a pause of 3.5 sec between segments. A total of 24 partitions (32 total partitions, partial Fourier 6/8) were divided into four segments and acquired in an interleaved manner. To meet the Nyquist criterion, a total of 48 spiral interleaves in-plane are required. To accelerate the scanning, a reduction factor of four was used in-plane and then reconstructed using 3D through-time non-Cartesian GRAPPA[3]. A GRAPPA kernel of size 2 × 3 was used in the spiral arm × readout direction. To calculate the GRAPPA weights, a reference scan of eight fully sampled 3D volumes (~77 sec) was acquired during free breathing. Overall, eight T_1-weighted 3D volumes were obtained with inversion times from 240 to 2600 ms. Other parameters were: FOV= 40×40 cm; matrix size 208×208 for an effective in-plane resolution of 1.9 mm; TR 4.5 ms; TE 0.6 ms; flip angle 7º; partition thickness 4 mm. Images were reconstructed offline using Matlab and gridding was performed using non-uniform Fourier Transform (NUFFT)[4].

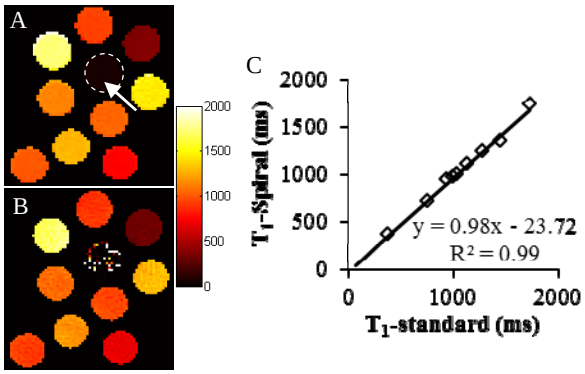

Fig. 1. T_1 maps of multi-compartment phantoms acquired using (A) inversion-recovery single-echo spin echo (TR: 6s) and (B) inversion-recovery stack-of-spirals method. The arrow points to a vial with T_1 of only 70 msec. (C) Comparison of T_1 values from the two sequences.

The accuracy of the T_1 measurement was first validated using a phantom containing several vials with varying concentrations of $GdCl_3$ and agarose. T_1 values measured with inversion-recovery single-echo spin-echo sequence (TR: 6 s; seven inversion times between 23 ms to 3000 ms) were used as the gold standard reference. After phantom validation, five asymptomatic volunteers were scanned. The overall acquisition time for one T_1 map of the whole abdomen with the above spatial resolution was 21 seconds.

Results and Discussion Results from the phantom study suggest that T_1 values acquired with the spiral sequence agree well with the results from an IR spin echo sequence (Fig. 1), with the exception of one vial. The T_1 of this vial was ~70 ms, which is extremely short, and unlikely to be encountered in most practical non-enhanced clinical settings.

Figure 2 shows representative T_1-weighted images along various points on the inversion recovery curve, and a corresponding T_1 map of one slice acquired from a normal subject. Average T_1 values of different tissues from the five subjects are summarized in Table 1, all in excellent agreement with the literature[5].

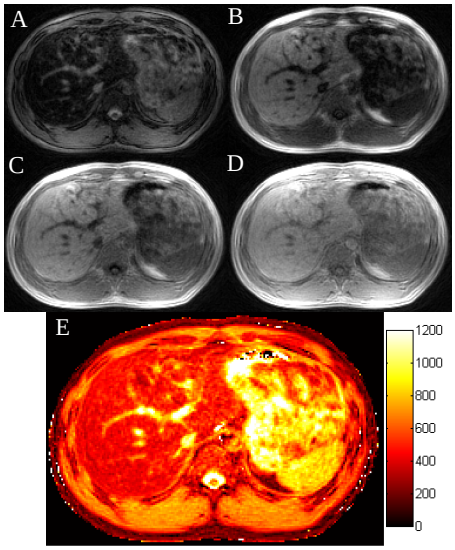

Fig. 2. (A-D) T_1-weighted images of one slice at different inversion times of 243, 587, 931 and 2652 ms. (E) Corresponding T_1 map.

Conclusion In this study, a high resolution 3D abdominal T_1 mapping technique was developed using the Look-Locker method, a stack-of-spirals trajectory and through-time non-Cartesian GRAPPA. This technique allows fast and accurate T_1 mapping of the whole abdomen in one breath-hold without the need for B1 mapping or image registration.

Tab. 1. T_1 relaxation times (ms) for different tissues. Values are means ± standard deviation.

Tissue	T_1 relaxation time (ms)
Liver	545 ± 78
Kidney - Medulla	1384 ± 95
Kidney - Cortex	802 ± 26
Spleen	1001 ± 98
Skeletal muscle	805 ± 50
Fat	256 ± 22

References

1. Tofts PS, et al. Eur Radiol, 2012;22:1320-1330. 2. Kim KA, et al. JMRI, 2012;36:405-410. 3. Seiberlich N, et al. MRM, 2011;66:1682-1688. 4. Fessler JA. JMR, 2007;188:191-195. 5. Bazelaire CM, et al. Radiol, 2004;230:652-659.

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