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Reproducibility of free-breathing multi-slice native myocardial T_1 mapping using the slice-interleaved T_1 (STONE) sequence

Jihye Jang[1,2*], Sébastien Roujol[1], Sebastian Weingärtner[1], Tamer A Basha[1], Sophie Berg[1], Warren J Manning[1,3], Reza Nezafat[1]

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Background

Quantitative myocardial T_1 mapping is a promising technique for assessment of interstitial diffuse fibrosis. Recently, a novel T_1 mapping sequence for free-breathing, multi-slice, myocardial T_1 mapping using the slice-interleaved T_1 (STONE) has been developed [1], which was shown to provide superior accuracy compared to MOLLI [2]. However, in-vivo reproducibility and precision of this sequence was not studied. In this study, we sought to investigate the reproducibility and precision of the STONE sequence for in-vivo native myocardial T_1 measurement.

Methods

Nine healthy adult subjects (37±22y, 4 m) were scanned on a 1.5 T Philips scanner using the STONE T_1 mapping sequence. The STONE sequence enables sampling of the undisturbed T_1 recovery curve by selectively exciting each slice once after a single nonselective inversion pulse. The STONE sequence was implemented using a b-SSFP

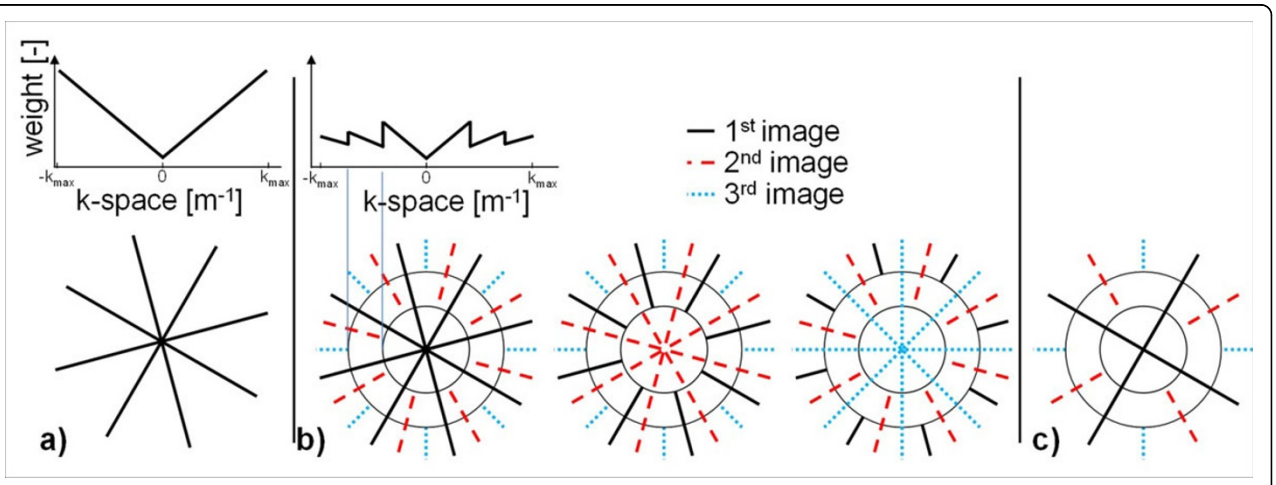

Figure 1 Example of in-vivo T_1 maps of five repeated scans with the STONE and MOLLI sequences in one subject. The three mid-ventricular slices are displayed for the STONE sequence. The quality of T_1 maps appears homogeneous and reproducible over five repetitions.

[1]Department of Medicine, Beth Israel Deaconess Medical Center and Harvard Medical School, Boston, MA, USA
Full list of author information is available at the end of the article

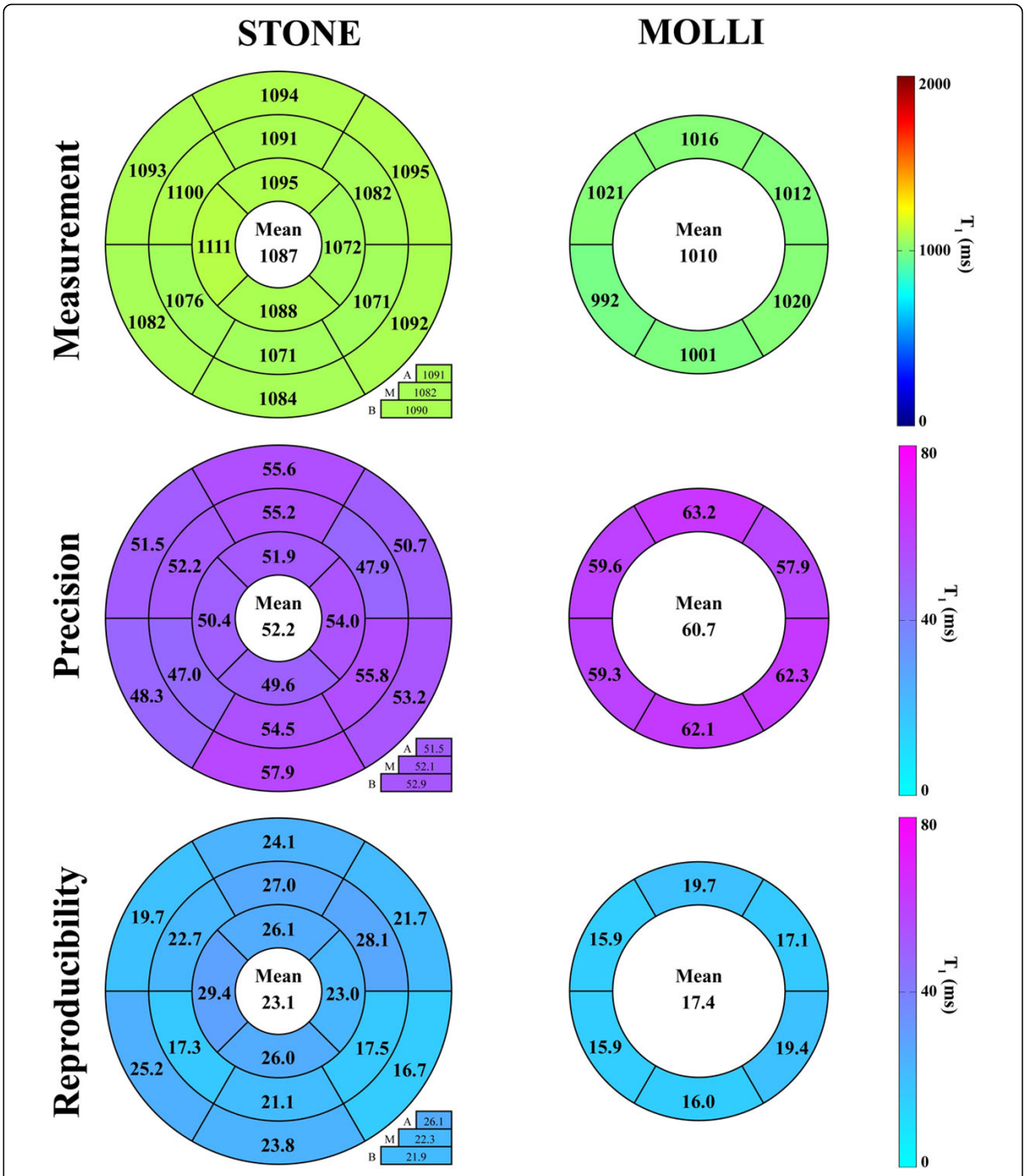

Figure 2 In-vivo characterization of native T_1 times obtained with the STONE sequence and the MOLLI sequence in terms of measurement, precision and reproducibility. A 16-segment model based analysis was performed using the three mid-ventricular slices of the STONE sequence, and is compared with a 6-segment model based analysis of the MOLLI sequence using a single slice which corresponds to the middle slice of the STONE sequence. The STONE sequence yields higher accuracy ($p<0.001$), higher precision ($p=0.001$), and similar reproducibility ($p=0.18$) compared to MOLLI.

imaging readout and the following parameters: TR/TE=2.8/1.41ms, flip angle=70°, FOV=280×272 mm^2, voxel size=2×2 mm^2, slice thickness=8 mm, 5 slices, slice gap=8mm, number of phase-encoding lines=43, linear ordering, 10 linear ramp-up pulses, SENSE factor=2.5, half Fourier=0.75. To compensate for respiratory motion, prospective slice tracking was combined with retrospective in-plane image registration [3]. The STONE sequence was compared to a single slice breath-hold MOLLI sequence which was acquired with a 5-(3)-3 scheme and similar imaging parameters. The single slice of the MOLLI corresponded to the middle slice of the STONE, which represented the mid left ventricle. Both sequences were acquired 5 times repeatedly for each subject. In-vivo measurement, precision (i.e. spatial variability) and reproducibility of T_1 values were evaluated based on a 16 myocardial segment model for STONE and a 6 myocardial segment model for MOLLI. Precision was defined as the standard deviation of T_1 values over each segment. Reproducibility was defined as the standard deviation of the T_1 values over the 5 repeated scans within each segment. A paired t-test was performed on the measures of the mid left ventricle slice of STONE and MOLLI to assess for statistical significant differences between the two sequences.

Results

Figure 1 shows an example of T_1 maps obtained in one subject. Homogenous T_1 signals were obtained over all myocardial segments, slices, and repetitions. The STONE sequence showed higher T_1 values (1087±35ms vs. 1010±36ms, $p<0.001$), higher precision (52±11ms vs. 61±16ms, $p=0.001$), and similar reproducibility (23±13ms vs. 17±11ms, $p=0.18$) than MOLLI (Figure 2).

Conclusions

The STONE sequence yields higher T_1 times, higher precision and similar reproducibility than MOLLI for in-vivo native T_1 mapping.

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Authors' details
[1]Department of Medicine, Beth Israel Deaconess Medical Center and Harvard Medical School, Boston, MA, USA. [2]Computer Aided Medical Procedures, Technische Universität München, Munich, Germany. [3]Department of Radiology, Beth Israel Deaconess Medical Center and Harvard Medical School, Boston, MA, USA.

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