Myocardium and blood T_1 measurement using SMART$_1$Map in healthy volunteers at 1.5T

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Target audience: MR scientists and physicians interested in myocardium relaxometry.

Introduction: Spin-lattice relaxation time (T_1) is an intrinsic tissue parameter. Moreover, myocardial extracellular volume, a surrogate for fibrosis extent estimation, can be derived from pre- and post-injection T_1 measurements. This parameter is altered in most, if not all, cardiomyopathies, making it of paramount interest in diagnosis and research for pathophysiology understanding. The most frequently used technique, MOLLI, is based on a Look-Locker (LL) scheme [1] and measures an apparent T_1^*. This apparent T_1^* value is then corrected to obtain an estimated T_1 value. Such a correction may underestimate the true T_1 value [2]. SMART$_1$Map [3] is a single-point method that has been proposed for a true myocardium T_1 measurement. This method also provides insensitivity to heart rhythm variation since it adapts the longitudinal magnetization saturation recovery curve sampling to each subject. In this study, we applied SMART$_1$map on healthy subjects in order to assess the average myocardium normal true T_1 value.

Methods: Our study was carried out in 8 subjects on a 1.5T MR scanner (Signa HDxt, GE Healthcare, WI, USA).
Image acquisition: SMART$_1$Map scans (2D saturation-recovery-prepared balanced-SSFP, TR/TE = ~ 4.1/1.8 ms, cardiac triggered, matrix= 160*128, NEX = 0.5, phase fov = 0.75, slice thickness = 8 mm) were performed 3 times for each subject on one mid-cavity short-axis slice, in end-diastole and in breath-hold. The recovery curve was sampled with 6 or 7 saturation delay times TS depending on the total acquisition time ranging from 205±1ms to 3975±70ms plus an additional point with no saturation pulse, thus corresponding to an infinite saturation delay time.
Image processing: Left ventricle myocardium was divided into 6 segments (***Figure n° 1***), and an additional region of interest (ROI) was drawn in the blood pool. Mean value within each ROI was used to compute T_1 values.
SMART$_1$Map data were fitted using a 3-parameter model and the Levenberg-Marquardt algorithm. Due to the sequence scheme, MR signal follows the theoretical equation $S(t)=M_0-M_0(1-\cos\theta)\exp(-t/T_1)$, usually modeled as $S(t)=A-B*\exp(-t/T_1)$. Mean segmental and blood pool T_1 values per subject were calculated. Results were presented as mean segmental, whole myocardium and blood pool T_1 values over all subjects. In addition, the mean intra-subject variability was assessed using the coefficient of variation (CoV) for segmental, whole myocardium and blood pool T_1 values.

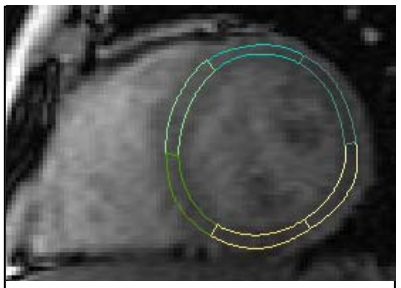

Figure n° 1: Myocardium segmentation drawn on all images.

Results: Mean T_1 values over the whole myocardium extracted from segmental T_1 values and in the blood pool were respectively 1120±109 ms and 1523±59 ms (***Table n° 1***). Mean intra subject variablity over the whole myocardium and the blood pool were respectively 10.8% and 5.3%.

	Mean T1 value over all subjects (n = 8)	Mean (n = 8) intra subject CoV (nb exp = 3)
Segment n°1	1186 ± 94 ms	7.8%
Segment n°2	1163 ± 139 ms	6.8%
Segment n°3	1181 ± 21 ms	8.6%
Segment n°4	1082 ± 104 ms	8.7%
Segment n°5	1023 ± 102 ms	9.0%
Segment n°6	1084 ± 42 ms	8.2%
Whole myocardium	**1120 ± 109 ms**	**10.8%**
Blood pool	**1523 ± 59 ms**	**5.3%**

Table n° 1: Quantitative results.

Conclusions: In this study, we showed that a novel sequence called SMART$_1$Map allowed to obtain T_1 times of the myocardium close to reference values in the literature at 1.5T based on non MOLLI techniques, e.g. 1170±9 ms (SASHA)[4], 1254±191 ms (SASHA)[5], 1160±95ms (SAPPHIRE)[5]. As expected, myocardial T_1 values were slightly higher than published values with the MOLLI technique: 1120±109ms, vs 982±46ms (15 subjects)[6] or 976±46ms (10 subjects)[7], confirming that SMART$_1$Map allows the measurement of the true T_1. T_1 values measured for the blood belonged to previously reported T_1 values range using non MOLLI methods: 1441±120ms[8], 1613±93ms [4]. However, blood T_1 is still challenging to assess accurately since the measurement is performed on a mixture of saturated and unsaturated spins. Future work will focus on applying SMART$_1$map in injected patients.

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