

EFFECT OF SYSTEMATIC T₁ ERRORS ON LAMBDA CALCULATIONS: COMPARISON OF DIFFERENT T₁ MAPPING TECHNIQUES

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Background Quantitative T₁ mapping is emerging as the technique of choice for imaging of fibrosis found in many cardiomyopathies. Unlike T₁ weighted sequences used to identify focal scarring, myocardial T₁ mapping after gadolinium has been used to characterize diffuse fibrosis¹. Because T₁ values alone are sensitive to many factors such as contrast agent dose, it is common to calculate the blood-tissue partition coefficient (λ) using blood and myocardial T₁ values at baseline and after contrast. The commonly used MOLLI sequence is known to underestimate T₁² and has significant heart rate dependence³, with unknown effects on derived parameters such as λ . In this abstract, the effect of these T₁ inaccuracies on λ calculations will be compared between MOLLI and an alternate SAturation-recovery single-SHot Acquisition (SASHA) T₁ mapping technique, previously validated on phantoms⁴.

Methods Healthy volunteers (n=10, 5 male, 28.8±6.6yrs) were assessed in a single exam using a Siemens Avanto 1.5 T scanner with both MOLLI and SASHA in a mid-ventricular short-axis slice prior to and every 4 minutes following 0.1mmol/kg Magnevist up to 20 minutes. Blood and myocardial T₁s were calculated and λ was derived using the equation $\{\lambda = [R_1(\text{myocardium post}) - R_1(\text{myocardium pre})] / [R_1(\text{blood post}) - R_1(\text{blood pre})]\}$, where $R_1 = 1/T_1$. Typical scanning parameters were: MOLLI: 2 inversion sets of 3 and 5 images, 75% partial Fourier, TImin=110ms with 80ms increment, 35° flip, TE/TR=1.03/2.4ms. SASHA: single-shot SSFP images from 10 consecutive heartbeats with incremented TI spanning the RR interval in the last 9 images (no saturation in the first image), 70° flip, TE/TR=1.3/2.6ms, full k-space.

Results Image quality was excellent in all 10 subjects, who had an average heart rate of 63.4±8.4bpm. Average myocardial T₁, blood T₁ and calculated λ s for both SASHA and MOLLI techniques are displayed in Table 1, for baseline and 20 minutes Post Gd. MOLLI imaging was performed 37.7±5.4s after SASHA measurements at all time points. The pooled individual results for all time points are displayed in Figure 1 for T₁ measurements. The bold black line denotes unity agreement. Myocardial MOLLI T₁ values are linearly and systematically underestimated compared to SASHA, while blood pool T₁ are underestimated to a smaller extent. As a result, MOLLI-derived λ are consistently larger than SASHA-derived values at all times post gadolinium with similar spread (0.45±0.03 vs. 0.36±0.04 respectively, Fig. 2).

	T ₁ Myocardium (ms)		T ₁ Blood (ms)		λ	
	Baseline	20min Post Gd	Baseline	20min Post Gd	20min Post Gd	
SASHA	1175.2 ± 27.6	752.9 ± 48.2	1687.4 ± 85.8	542.6 ± 56.3	0.38 ± 0.03	
MOLLI	935.5 ± 24.9	614.4 ± 33.8	1514.1 ± 107.5	524.9 ± 55.2	0.45 ± 0.02	

Table 1: Average values for 10 healthy subjects.

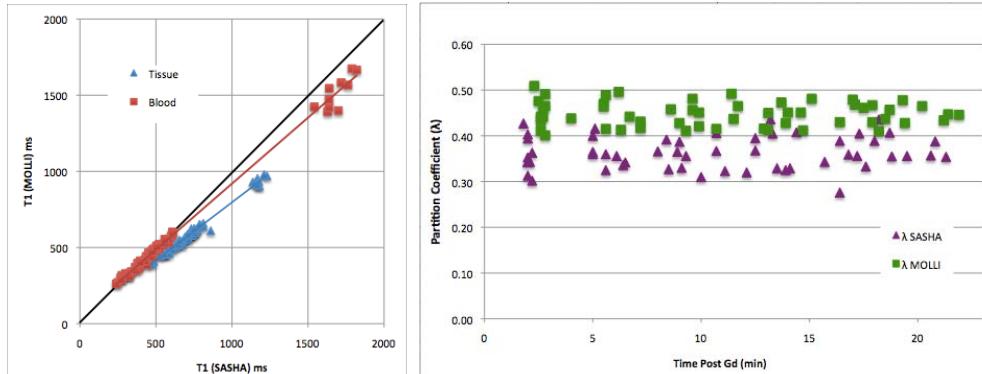


Figure 1: Pooled data for 10 subjects pre and post contrast from MOLLI and SASHA T₁ measurements.

Figure 2: λ displayed as a function of time from contrast injection.

Discussion and Conclusion: The results for each T₁ mapping sequence presented here are in good agreement with literature values. A saturation recovery technique similar to SASHA had average pre-contrast myocardial and blood T₁s of 1219 (±72) ms and 1516 (±21) ms respectively⁵. With a MOLLI sequence using 3 inversion sets (3,3,5 images), pre-contrast myocardial T₁s of 977 ms and 483 ms at 15 minutes post contrast (Gd-DTPA, 0.15 mmol/kg) have been reported². In a small healthy population, similar λ values (0.42 ± 0.02) were calculated using a MOLLI sequence with 3 inversion sets (4,2, and 1 images)⁶. The data presented in this abstract confirm the systematic differences in T₁ values calculated using MOLLI sequences versus saturation-recovery based T₁ mapping techniques. In particular, MOLLI T₁ measurements (regardless of inversion set schemes) are routinely lower than those measured with saturation recovery or SASHA-type sequences, resulting in consistently higher λ values. Additional work is necessary to characterize and correct for errors allowing for comparison between sites and studies.

References: ¹Iles L et al. JACC 2011;57:821–8.

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