

# EFFECT OF SYSTEMATIC T<sub>1</sub> ERRORS ON LAMBDA CALCULATIONS: COMPARISON OF DIFFERENT T<sub>1</sub> MAPPING TECHNIQUES

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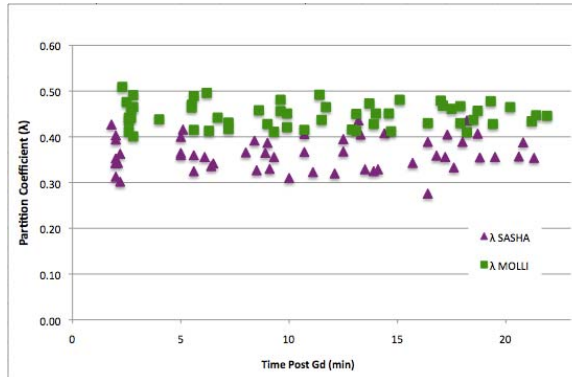
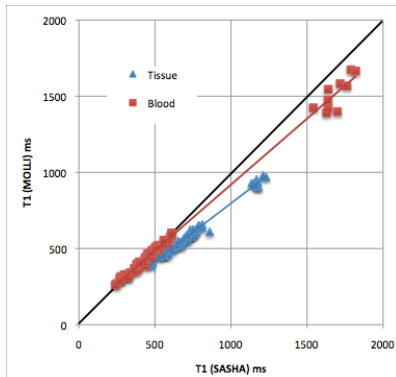
**Background** Quantitative T<sub>1</sub> mapping is emerging as the technique of choice for imaging of fibrosis found in many cardiomyopathies. Unlike T<sub>1</sub> weighted sequences used to identify focal scarring, myocardial T<sub>1</sub> mapping after gadolinium has been used to characterize diffuse fibrosis<sup>1</sup>. Because T<sub>1</sub> values alone are sensitive to many factors such as contrast agent dose, it is common to calculate the blood-tissue partition coefficient ( $\lambda$ ) using blood and myocardial T<sub>1</sub> values at baseline and after contrast. The commonly used MOdified Look-Locker Inversion-recovery (MOLLI) sequence is known to underestimate T<sub>1</sub><sup>2</sup> and has significant heart rate dependence<sup>3</sup>, with unknown effects on derived parameters such as  $\lambda$ . In this abstract, the effect of these T<sub>1</sub> inaccuracies on  $\lambda$  calculations will be compared between MOLLI and an alternate SATuration-recovery single-SHOT Acquisition (SASHA) T<sub>1</sub> mapping technique, previously validated on phantoms<sup>4</sup>.

**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 T<sub>1</sub>s were calculated and  $\lambda$  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, T<sub>min</sub>=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 T<sub>1</sub>, blood T<sub>1</sub> and calculated  $\lambda$ 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 T<sub>1</sub> measurements. The bold black line denotes unity agreement. Myocardial MOLLI T<sub>1</sub> values are linearly and systematically underestimated compared to SASHA, while blood pool T<sub>1</sub> are underestimated to a smaller extent. As a result, MOLLI-derived  $\lambda$  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 <sub>1</sub> Myocardium (ms)		T <sub>1</sub> Blood (ms)		$\lambda$
	Baseline	20min Post Gd	Baseline	20min Post Gd	20min Post Gd
<b>SASHA</b>	1175.2 ± 27.6	752.9 ± 48.2	1687.4 ± 85.8	542.6 ± 56.3	0.38 ± 0.03
<b>MOLLI</b>	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 T<sub>1</sub> measurements.

**Figure 2:**  $\lambda$  displayed as a function of time from contrast injection.

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

**References:** <sup>1</sup>Iles L *et al.* JACC 2011;57:821–8.

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<sup>4</sup>Chow *et al.* Proc ISMRM 2011;19:1373

<sup>5</sup>Wacker CM *et al.* MRM 1999;41:686–695

<sup>6</sup>Schelbert *et al.* JCMR 2011;13:16