

## Pilot Data on Inter-Centre and Inter-Vendor Comparison of MOLLI and ShMOLLI T1 Mapping Variants at 3T

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**Target Audience:** Cardiologists and scientists with interest in myocardial T1 mapping

**Background:** Native T1 mapping methodology has now reached a state of maturity where it may be ready for use in large scale multi-centre, multi-vendor studies, such as the CMR in Hypertrophic Cardiomyopathy (HCMR) Study, which was recently funded by the NIH. However, such an approach will require optimising sequences for maximal comparability. The Modified Look Locker Inversion recovery (MOLLI) [1] method for acquiring T1 maps within a breath-hold has been widely implemented and investigated, both in its original form and in several variants designed to reduce both breath-hold duration and heart-rate sensitivity. We thus compare directly two vendors and three MOLLI T1 mapping variants in preparation for a large multi-centre MR trial, to test compatibility of methods between different vendors.

**Methods:** Five healthy volunteers (3m/2f, age 25-46) underwent scanning on a Philips Achieva 3T TX (Leeds) and a Siemens 3T Trio (Oxford) within 4 days. Two repeat measurements of a single mid-ventricular slice were performed using conventional 3(3)3(3)5 MOLLI [1], 5(1)1(1)1 ShMOLLI [2] and 5(3s)3 MOLLI[3]. The protocols are defined in table 1. Acquisition methods were optimised independently in each centre. Data for each T1 map was acquired within a breath-hold (at end expiration). Pre-scan preparation (including shimming) was performed in a separate breath-hold prior to imaging. T1 maps were generated using published methods, with a conditional fitting algorithm employed for ShMOLLI [1]. Both scanners have inline MOLLI reconstruction, but the ShMOLLI conditional fitting algorithm is not currently implemented in Leeds, therefore offline reconstruction was performed in Oxford for ShMOLLI datasets. Mean mid-wall myocardial T1 for the full circumferential extent was calculated for each study.

	Conventional MOLLI		ShMOLLI		5(3s)3 MOLLI*	
	Number of images (successive RR intervals)	Duration of subsequent recovery period	Number of images (successive RR intervals)	Duration of subsequent recovery period	Number of images (successive RR intervals)	Duration of subsequent recovery period
Inversion 1	3	3 beats	5	1	5	$\geq 3s^{**}$
Inversion 2	3	3 beats	1	1	3	-
Inversion 3	5	-	1	-	-	-

Table 1 - MOLLI variants investigated. \*Leeds/Philips only. \*\*Lowest number of beats required to achieve at least 3 second recovery period

**Results:** Mean myocardial T1 measured across all studies was  $1172 \pm 33$ ms. For the 5 variant/vendor combinations within-subject coefficient of variation ranged from 0.1% to 1.8%. For the variants tested at both centres (conventional MOLLI and ShMOLLI) no significant dependence of T1 on either variant or vendor was demonstrated. Table 2 shows bias (with 95% limits of confidence) for comparisons between sites and variants. Figure 1 shows differences between the two vendors for these variants. In these results higher T1 is observed in females (volunteers 2 & 4, red lines) as observed for this age range in previous work [4].

	Bias (ms)	95% Upper Limit (ms)	95% Lower Limit (ms)
Siemens - Philips	5.1	46.6	-36.3
ShMOLLI - Conv. MOLLI	0.5	37.4	-36.4

Table 2 – Bias and 95% confidence limits for comparisons between vendors and the two variants tested at both centres.

5(3s)3 MOLLI produced the highest myocardial T1 estimates compared to the other variants (bias = 28ms (2.4%),  $P=0.006$  (paired t-test) compared to ShMOLLI and 25 ms (2.2%),  $P=0.03$  compared to conventional MOLLI; only the former is significant following Bonferroni correction for multiple comparisons). Table 3 shows these biases (with 95% limits of confidence) for comparisons on the Philips scanner.

	Bias (ms)	95% Upper Limit (ms)	95% Lower Limit (ms)
5(3s)3 - Conv. MOLLI	24.7	81.8	-32.4
5(3s)3 MOLLI - ShMOLLI	27.6	76.1	-20.9

Table 3 – Bias and 95% confidence limits for 5(3s)3 MOLLI compared to other variants (tested on Philips scanner only).

T1 maps calculated from ShMOLLI data generated on the scanner without the conditional ShMOLLI algorithm produced systematically low T1 (bias = 21% compared to those using the conditional algorithm), as would be expected.

**Discussion and Conclusions:** Accuracy and precision of cardiac T1 mapping methods may depend on a large number of factors which may affect inter-site reproducibility, including selection of T1 mapping method, T1 mapping scheme, and parameter selection. Additionally, system-specific influences and vendor-specific implementation details may potentially affect the T1 estimates, which are beyond the control of the system operator. In our results we found good intra-site agreement between methods in native T1 mapping despite these factors. We found no significant bias between the ShMOLLI and conventional MOLLI variants with the methods and T1 mapping implementations used. Some bias was observed between ShMOLLI and 5(3s)3 MOLLI, which refers only to agreement between the methods and not agreement with ground truth. Testing in a larger sample will establish the robustness of these results. Intra-site intra-subject variation between methods is contained within ~2%. Careful selection of MOLLI techniques allows consistent estimates of myocardial T1, adding support for their use in large multi-centre trials such as HCMR.

[1] Messroghli et al 2007 Modified Look-Locker inversion recovery (MOLLI) for high-resolution T1 mapping of the heart JMRI 26(4) 1081. [2] Piechnik et al 2010 Shortened Modified Look-Locker Inversion recovery (ShMOLLI) for clinical myocardial T1-mapping at 1.5 and 3 T within a 9 heartbeat breathhold JCMR 12(1) 69. [3] Kellman et al 2013 Influence of Off-resonance in myocardial T1-mapping using SSFP based MOLLI method JCMR 15(1) 63. [4] Piechnik et al 2013 Normal variation of magnetic resonance T1 relaxation times in the human population at 1.5T using ShMOLLI JCMR 15(1) 13.

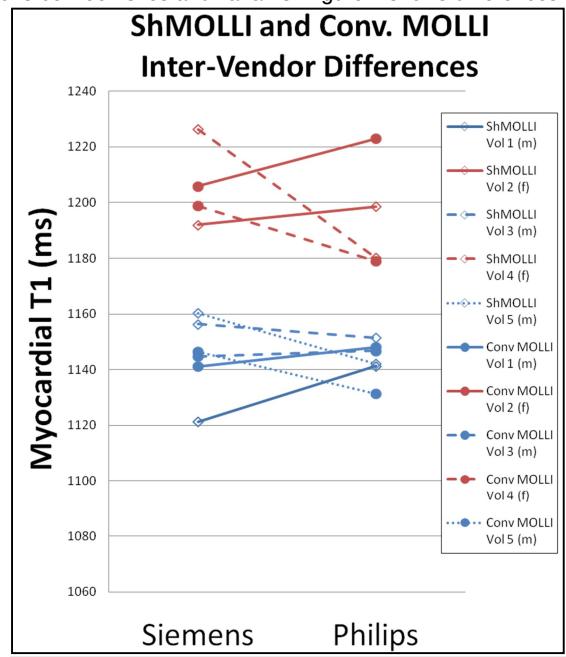


Fig 1 – Differences between mean myocardial T1 values (across two measurements) for each volunteer between vendors. Results are presented for the two variants tested at both sites Clustering of data has arisen due to expected gender specific variation in T1 [4], not variant/vendor dependence.