

A Siemens Single-Shot T1 Mapping Sequence as an Alternative to MOLLI

Une séquence Siemens de cartographie T1 en acquisition single-shot comme alternative à MOLLI

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ABSTRACT

Background: Native T1 mapping has become an essential tool for quantitative myocardial tissue characterization in cardiac magnetic resonance (CMR). However, widely used techniques such as Modified Look-Locker Inversion Recovery (MOLLI) remain limited by their proprietary nature and limited accessibility, particularly in resource-constrained settings.

Aim: This study aimed to develop and validate a more accessible Single-Shot T1 mapping technique as a practical alternative to MOLLI, and to assess its agreement and diagnostic performance against a reference standard (Circle Cardiovascular Imaging, CVI⁴²).

Methods: A retrospective study was conducted on 40 subjects (25 healthy controls and 15 patients with cardiac pathologies) who underwent 3T CMR imaging. Native T1 values were acquired using a modified Single-Shot inversion recovery scheme (3(3)3(3)5). Quantitative analysis was performed using custom MATLAB-based post-processing and compared with reference measurements obtained using CVI⁴² software. Agreement was assessed using Bland-Altman analysis, while group differences were evaluated using independent t-tests.

Results: Pathological subjects demonstrated significantly elevated native T1 values compared to healthy controls (1566 ± 65 ms vs. 1079 ± 80 ms, $p < 0.001$). The proposed method showed strong agreement with the reference standard, with a mean difference of 5.7 ms and no statistically significant bias. Additionally, the Single-Shot approach exhibited significantly reduced inter-subject variability compared to CVI⁴²-based measurements.

Conclusion: The proposed Single-Shot T1 mapping technique provides a reliable, reproducible, and accessible alternative to MOLLI, with comparable accuracy and improved numerical stability. This approach may expand access to advanced myocardial tissue characterization, particularly in low-resource settings.

Keywords: Cardiac Magnetic Resonance, T1 mapping, Single-Shot, MOLLI alternative, myocardial tissue characterization

RÉSUMÉ

Contexte : La cartographie T1 native constitue aujourd'hui un outil essentiel pour la caractérisation quantitative du tissu myocardique en imagerie par résonance magnétique cardiaque (IRM cardiaque). Toutefois, les techniques de référence telles que la séquence Modified Look-Locker Inversion Recovery (MOLLI) restent limitées par leur nature propriétaire et leur accessibilité restreinte, en particulier dans les contextes à ressources limitées.

Objectif : Cette étude vise à développer et valider une technique de cartographie T1 en acquisition single-shot, plus accessible, comme alternative pratique à MOLLI, et à évaluer ses performances diagnostiques ainsi que son degré d'accord avec une méthode de référence.

Méthodes : Une étude rétrospective a été menée sur 40 sujets (25 volontaires sains et 15 patients présentant des pathologies cardiaques) ayant bénéficié d'une IRM cardiaque à 3T. Les valeurs de T1 natif ont été acquises à l'aide d'un schéma d'inversion Single-Shot modifié (3(3)3(3)5). L'analyse quantitative a été réalisée via un traitement dédié sous MATLAB et comparée aux mesures issues du logiciel de référence CVI⁴². L'accord entre les méthodes a été évalué par analyse de Bland-Altman, et les comparaisons intergroupes par test t de Student.

Résultats : Les patients atteints de pathologies cardiaques présentaient des valeurs de T1 significativement plus élevées que les sujets sains (1566 ± 65 ms vs. 1079 ± 80 ms, $p < 0,001$). La méthode proposée a montré un excellent accord avec la référence, avec une différence moyenne de 5,7 ms sans biais statistiquement significatif. Par ailleurs, l'approche Single-Shot a présenté une variabilité interindividuelle réduite par rapport aux mesures issues de CVI⁴².

Conclusion : La technique de cartographie T1 Single-Shot proposée constitue une alternative fiable, reproductible et accessible à la séquence MOLLI, avec une précision comparable et une meilleure stabilité numérique. Cette approche pourrait élargir l'accès à la caractérisation tissulaire myocardique avancée, notamment dans les environnements à ressources limitées.

Mots-clés : IRM cardiaque, cartographie T1, Single-Shot, alternative à MOLLI, caractérisation myocardique

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INTRODUCTION

Cardiovascular diseases (CVDs) remain the leading cause of mortality worldwide, placing a substantial burden on healthcare systems and highlighting the importance of early and accurate diagnosis. Although imaging modalities such as echocardiography and computed tomography (CT) are widely used, they provide limited capability for detailed myocardial tissue characterization [1].

Cardiac Magnetic Resonance (CMR) imaging has emerged as the reference standard for comprehensive cardiac evaluation, offering accurate assessment of cardiac anatomy, function, and tissue composition. It plays a key role in the diagnosis of myocardial diseases, including myocarditis and fibrosis. To standardize CMR-based diagnosis of myocarditis, the Lake Louise Criteria (LLC) were introduced in 2009, requiring the presence of at least two of the following features: myocardial oedema (T2-weighted imaging), hyperemia (early T1-weighted enhancement), and fibrosis or necrosis (Late Gadolinium Enhancement, LGE). However, these conventional techniques rely primarily on qualitative or semi-quantitative assessment, which may limit sensitivity to diffuse myocardial abnormalities and introduce inter-observer variability. In addition, contrast agent use may be contraindicated in certain patients, and image quality can be degraded by motion artifacts or metallic implants [2,3]. To address these limitations, T1 mapping has emerged as a robust quantitative technique for myocardial tissue characterization. Measuring native T1 relaxation time provides direct insight into tissue properties such as water content, fibrosis, and inflammation. The generation of pixel-wise parametric maps enables objective and reproducible detection of myocardial abnormalities [4]. Its clinical utility was further reinforced in the 2018 revision of the La, which incorporated T1 mapping as a key component for the non-invasive diagnosis of myocarditis [5].

The accuracy of T1 mapping is highly dependent on the acquisition sequence. The Modified Look-Locker Inversion Recovery (MOLLI) sequence is the most widely validated and clinically adopted approach, providing reliable T1 estimation through multiple inversion recovery measurements. Several sampling schemes have been proposed to optimize the balance between acquisition time, heart rate dependence, and accuracy, including the commonly used 3(3)3(3)5 protocol and its shortened variants [6–10]. More recent adaptations incorporating saturation pulses and recovery intervals have further improved robustness under varying physiological conditions [11–13].

Despite these advances, T1 mapping remains dependent on specialized CMR sequences, dedicated post-processing tools, and technical expertise, which limits its accessibility in resource-constrained settings. To address this limitation, we propose a Single-Shot acquisition strategy as a more accessible alternative for T1 mapping. Traditionally used for rapid imaging, Single-Shot sequences offer shorter acquisition times and reduced sensitivity to patient motion. The proposed approach aims to approximate the diagnostic performance of

MOLLI while simplifying acquisition requirements and improving clinical feasibility.

METHODS

Population Characteristics and Study Design

This single-center retrospective study included patients who underwent CMR imaging between February 2021 and January 2023 for suspected inflammatory myocardial disease (e.g., myocarditis), differential diagnosis of inflammatory conditions (e.g., sarcoidosis), or post-myocarditis follow-up. All examinations were performed within routine clinical practice.

Exclusion criteria comprised standard contraindications to CMR or gadolinium-based contrast agents, including the presence of pacemakers or implantable cardioverter-defibrillators, severe claustrophobia, pregnancy, and significant renal impairment.

A total of 40 subjects were included, comprising 25 healthy controls (mean age: 46 ± 16 years) and 15 patients with confirmed cardiac pathology. Healthy controls were required to meet strict inclusion criteria, including absence of cardiovascular symptoms, no history of malignancy, normal cine-derived cardiac function, body temperature $\leq 37.5^\circ\text{C}$, blood pressure $\leq 140/90$ mmHg, normal troponin T levels, and a normal 12-lead electrocardiogram. No matching strategy was applied between the control and patient groups.

CMR Imaging and Adapted Single-Shot Sequence

CMR examinations were performed on a 3T Avanto system (Siemens Healthineers) using a 32-channel phased-array receiver coil. Cine imaging was acquired in standard long- and short-axis views under electrocardiographic (ECG) gating.

For myocardial tissue characterization, LGE and Single-Shot acquisitions were performed to ensure full left ventricular coverage from base to apex, including both four-chamber and short-axis orientations. LGE images were acquired 10–15 minutes following intravenous administration of a gadolinium-based contrast agent at a dose of 0.1–0.2 mmol/kg.

In the absence of a dedicated T1 mapping sequence, a Single-Shot inversion recovery acquisition was adapted to emulate T1 mapping. This approach followed a MOLLI-like 3(3)3(3)5 sampling scheme, enabling the acquisition of 11 images at different inversion times (TIs) within a single breath-hold. Imaging parameters were as follows: repetition time/echo time (TR/TE) = 7.0/1.04 ms, flip angle = 35° , and field of view (FOV) = 256×100 mm (see Figure 1).

Mapping Reconstruction and Post-Processing

The acquired images were first sorted according to their respective inversion times (TIs). Regions of interest (ROIs) were manually delineated on the myocardium and ventricular cavities on the initial frame and subsequently propagated across all images to ensure spatial consistency.

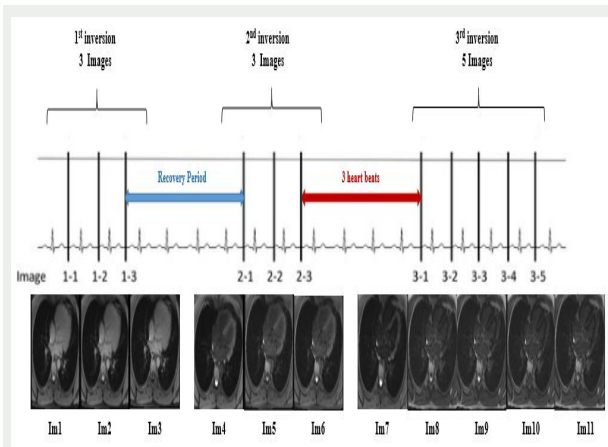


Figure 1. Schematic representation of the adapted Single-Shot acquisition strategy for cardiac T1 mapping.

Post-processing was performed using MATLAB (MathWorks, Natick, MA, USA). Several curve-fitting strategies, including least-squares optimization, were evaluated to determine the most appropriate signal model. Signal intensity was modeled using a three-parameter inversion recovery equation:

$$S(TI) = A - B \cdot \exp\left(-\frac{TI}{T1^*}\right)$$

where A represents the equilibrium magnetization (signal scaling factor), B accounts for inversion efficiency, and $T1^*$ denotes the apparent relaxation time. Pixel-wise T1 values were subsequently estimated using the standard correction:

$$T1 = T1^* \cdot \left(\frac{B}{A} - 1\right)$$

Global myocardial T1 values were obtained by averaging all pixel-wise T1 estimates within the defined myocardial ROI. For completeness, the conventional inversion recovery signal model is given by:

$$S(TI) = A \cdot \left(1 - e^{-\frac{TI}{T1}}\right)$$

Finally, quantitative T1 maps were generated by projecting pixel-wise T1 values onto a color scale ranging from blue (low T1) to red (high T1) (Figure 2).

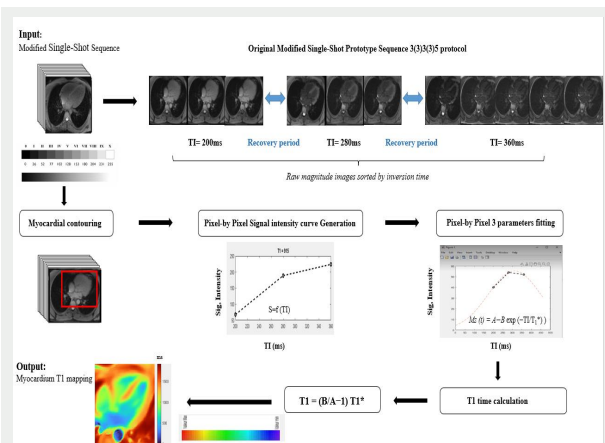


Figure 2. Schematic diagram of the offline T1 mapping reconstruction workflow using the Single-Shot sequence prototype strategies.

Statistical Analysis

Statistical analyses were performed using IBM SPSS Statistics (version 16.0; IBM Corp., Armonk, NY, USA). Continuous variables are reported as mean $\pm$ standard deviation, while categorical variables are expressed as frequencies and percentages.

Normality of continuous variables was assessed prior to parametric testing. Differences between healthy and pathological groups were evaluated using independent samples t-tests. Agreement between the proposed method and the reference standard (CVI⁴²) was assessed using Bland–Altman analysis. Pearson correlation analysis was performed to evaluate the linear relationship between T1 values obtained using the proposed method and those derived from CVI⁴².

To further assess robustness, comparative analyses were conducted between healthy and pathological subjects using both the proposed method and CVI⁴². The study cohort included 25 healthy subjects and 15 patients with cardiac pathology. Statistical significance was defined as $p < 0.05$.

For validation purposes, four measurement sets were defined: X1 (proposed method in healthy subjects), X2 (CVI⁴² in healthy subjects), X3 (proposed method in pathological subjects), and X4 (CVI⁴² in pathological subjects). Each healthy group (X1, X2) included 25 observations, while each pathological group (X3, X4) included 15 observations.

RESULTS

Measurements Population Characteristics and T1 Measurements

A total of 40 subjects were retrospectively included, comprising 25 healthy controls and 15 patients with cardiac pathology. Baseline demographic and functional characteristics are summarized in Table 1 and are expressed as mean $\pm$ standard deviation.

Table 1. Baseline characteristics of the study population

Patients	Healthy subjects (n=25)	Patients with cardiac diseases (n=15)
Age (years)	46 $\pm$ 16	37 $\pm$ 22
Sex (male/female)	14/11	8/6
LVEF (%)	49 $\pm$ 2	41 $\pm$ 4
EDV (ml)	80 $\pm$ 11	39 $\pm$ 65
ESV (ml)	45 $\pm$ 36	16 $\pm$ 22

EDV: End-diastolic volume; ESV: End-systolic volume; LVEF: left ventricular ejection fraction.

The mean native T1 value in healthy subjects was 1041 $\pm$ 56 ms. Representative T1 maps in healthy volunteers demonstrated homogeneous myocardial signal intensity without focal abnormalities, consistent with normal myocardial tissue characteristics (Figure 3).

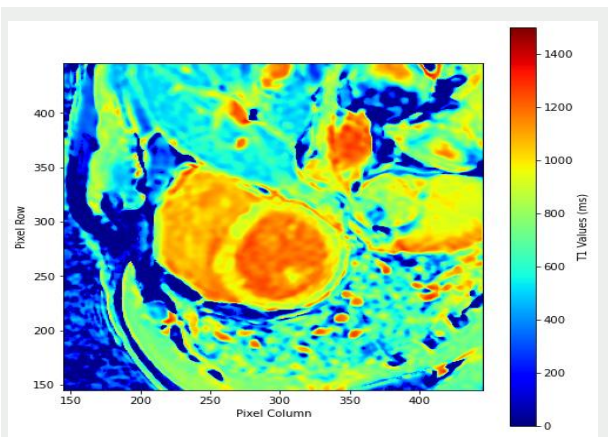


Figure 3. Representative native T1 map of a healthy volunteer using the proposed Single-Shot technique, showing homogeneous myocardial signal distribution.

T1 values obtained using the proposed Single-Shot technique were compared with reference values reported in the literature. Bland–Altman analysis demonstrated a mean bias of 5.7 ms, with 95% limits of agreement falling within a narrow and clinically acceptable range, indicating good agreement between the two methods (Figure 4).

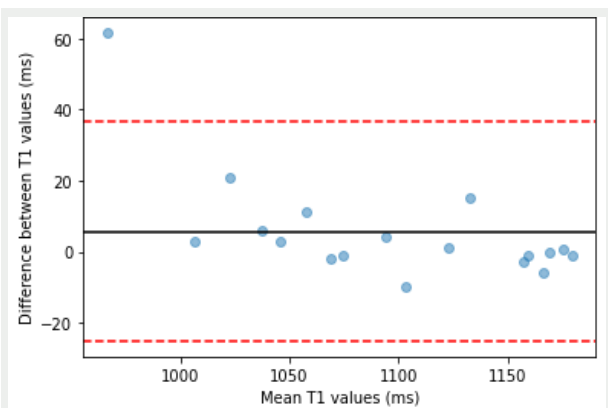


Figure 4. Bland–Altman analysis comparing T1 values obtained using the proposed Single-Shot technique with reference values in healthy volunteers.

Clinical Application of Single-Shot T1 Mapping

T1 mapping provides a quantitative and objective tool for the detection of myocardial abnormalities, including subclinical involvement through alterations in native T1 values. The proposed Single-Shot T1 mapping approach was applied to patients with myocardial infarction (MI), myocarditis, and structural cardiac abnormalities to assess its robustness in comparison with visual assessment and LGE imaging.

Representative T1 maps and corresponding LGE images are summarized in Table 2. Patient A, diagnosed with post-COVID myocarditis, presented with moderate pericardial effusion and a relative increase in native T1 values (~17%) without imaging evidence of acute myocardial inflammation on LGE. Patient B, with lateral wall myocarditis, demonstrated focal myocardial involvement on T1 mapping, with lesions measuring approximately 3–6 mm.

In Patient C, a 10-year-old with a history of myocarditis, T1

mapping revealed extensive lateral and apical involvement consistent with myocardial injury, with elevated native T1 values ranging from 1436 to 1556 ms (mean: 1521 ms), despite preserved left ventricular ejection fraction (66%). In Patient D, a 67-year-old heart transplant recipient with postoperative structural abnormalities, T1 mapping identified myocardial alterations not clearly detected on LGE imaging, suggesting increased sensitivity of the proposed method in this context.

Table 2. Native Single-Shot T1 Mapping at 3T: Representative Pathological Cases

Patients	Pathology	LGE	T1 mapping	Mean T1 value
A	Pericarditis			1217 ± 12 ms
B	Lateral Myocarditis			1531 ± 76 ms
C	Myocardial Infarction			1521 ms
D	Postoperative Structural heart defect			1515 ms

Native T1 Values and Comparative Statistical Analysis

T1 mapping provides valuable diagnostic information by enabling the detection of myocardial involvement that may be missed using conventional imaging techniques. Patients with pericarditis, acute myocarditis (AM), and MI demonstrated significantly higher native T1 values (1566 ± 65 ms) compared with healthy controls (1079 ± 80 ms) (Figure 5). The observed difference was highly statistically significant ($t = -23.67$, $p < 0.001$). In addition, the distribution histogram highlights not only increased T1 values in pathological cases but also greater inter-subject variability, reflecting heterogeneous myocardial involvement.

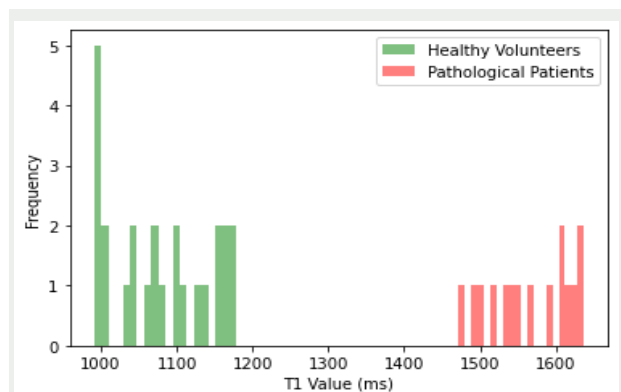


Figure 5. Distribution of native T1 values in healthy controls versus patients with cardiac pathology.

To further evaluate the robustness of the proposed method, a comparative analysis was conducted against a conventional T1 mapping post-processing reference (Circle Cardiovascular Imaging, CVI⁴²). Descriptive statistics for the four groups (X1–X4) are summarized in Table 3.

Table 3. Descriptive statistics of T1 values

	X1	X2	X3	X4
Sample size	25	25	15	15
Mean	1 078.24	1 068.24	1 557.07	1 566.07
Standard deviation	65.24	75.30	97.67	94.51
Minimum	991	912	1217	1291
Maximum	1179	1178	1618	1689
Range	188	266	401	398
1st quartile	1 008.00	1 009.00	1 564.00	1 534.50
Median	1 076.00	1 070.00	1 581.00	1 579.00
3rd quartile	1 140.00	1 145.00	1 598.50	1 605.50
IQR	132.00	136.00	34.50	71.00
Mode	1 159.00	998.00	None	None

Preliminary analysis revealed a clear separation between healthy groups (X1, X2) and pathological groups (X3, X4), particularly in terms of central tendency and variability. This motivated formal hypothesis testing to compare mean T1 values between methods under both equal and unequal variance assumptions.

Independent samples t-tests were performed for each pairwise comparison, and the full statistical results are reported in Table 4. The analysis consistently showed no statistically significant difference between the proposed method and CVI⁴² for either healthy (X1 vs X2) or pathological (X3 vs X4) groups.

Specifically, for healthy subjects, the null hypothesis ($H_0: \mu_{X1} = \mu_{X2}$) was not rejected ($t = 0.5018$, $p = 0.6180$ under equal variances; $p = 0.6181$ under unequal variances). Similarly, for pathological subjects, no significant difference was observed ($t = -0.2564$, $p = 0.7994$ for both variance assumptions). These findings indicate statistical equivalence in mean T1 measurements between the proposed method and the reference standard.

Table 4. Results of Student's t-tests comparing mean T1 values under assumptions of equal and unequal variances. Significance level set at $\alpha = 0.05$.

Null Hypothesis	Equal standard deviations		Unequal standard deviations	
	t-statistic	p-value	t-statistic	p-value
$H_0: \mu_{X1} = \mu_{X2}$	0.5018	0.6180	0.5018	0.6181
$H_0: \mu_{X3} = \mu_{X4}$	-0.2564	0.7994	-0.2564	0.7994

Beyond mean comparison, variability analysis demonstrated that the proposed approach exhibits reduced dispersion compared with CVI⁴², as illustrated in the box plots (Figure 6). This reduction in variability suggests improved numerical stability and consistency of the proposed method across both healthy and pathological populations.

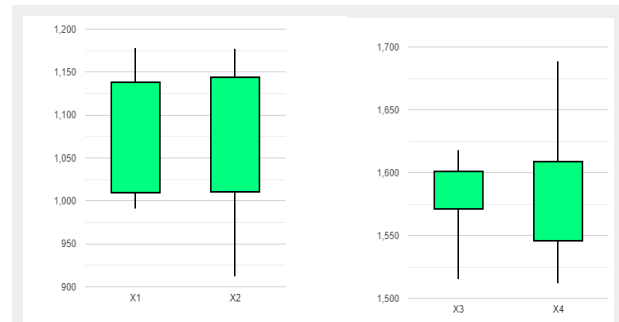


Figure 6. Box plots showing the distribution of native T1 values in healthy (a) and pathological (b) groups using the proposed method and CVI⁴².

DISCUSSION

In this study, we proposed and validated a native Single-Shot T1 mapping approach as a MOLLI-independent and more accessible alternative for quantitative myocardial tissue characterization. The main findings can be summarized as follows: (i) the proposed method demonstrated strong agreement with reference post-processing (CVI⁴²), (ii) native T1 values showed clear and statistically significant separation between healthy and diseased myocardium, and (iii) reduced inter-subject variability was observed compared with the reference approach, suggesting improved numerical stability and robustness.

A fundamental challenge in T1 mapping is the strong dependence of absolute T1 values on sequence design, reconstruction strategy, field strength, and post-processing pipeline. This variability necessitates sequence-specific normal ranges for reliable clinical interpretation. In healthy volunteers, native T1 values obtained with the proposed approach (1079 ± 80 ms) were consistent with previously reported MOLLI-based reference values, which typically range between approximately 1050 and 1175 ms across large studies [14–17,31]. This agreement supports the methodological validity of the proposed Single-Shot framework for native myocardial characterization, despite differences in acquisition strategy and reconstruction assumptions.

Beyond healthy populations, our findings are also consistent with the broader literature demonstrating significantly elevated native T1 values in pathological myocardium. Across multiple conditions, including myocarditis, myocardial infarction, and cardiomyopathies, prior studies have consistently reported increased T1 values reflecting edema, inflammation, and diffuse fibrosis (Table 5). In our cohort, pathological cases exhibited markedly elevated T1 values compared with controls (1566 ± 65 ms vs. 1079 ± 80 ms, $p < 0.001$), confirming the sensitivity of the proposed approach for detecting myocardial involvement. Importantly, this separation was not limited to focal disease but also extended to diffuse or heterogeneous myocardial alterations, highlighting the quantitative robustness of the method.

Table 5. The performance of various T1 mapping techniques for healthy controls and for the detection of cardiac clinical manifestations

Authors, Years	Sequence	Number of patients	Cardiac complication	T1 values
Piechnick et al. [14], 2010	MOLLI	10	Healthy	1166 ± 60/91 ms
		4	MI	1396 ± 27 ms
	SHMOLLI	10	Healthy	1169 ± 45/73
		4	MI	1432 ± 33 ms
Nacif et al. [19], 2011	LL	165	Healthy	1004.9 ± 6 120.3
	MOLLI	168		1034.1 ± 6 53.1
Chow et al. [39], 2012	MOLLI	10	Healthy	935.5 ± 24.9 ms
	SASHA			1175.2 ± 27.6 ms
Puntmann et al. [16], 2013	MOLLI	30	Healthy	1070 ± 55 ms
		25	HCM	1254 ± 43 ms
Rogers et al. [15], 2013	MOLLI	38	Healthy	1087 ± 60 ms septal
				1108 ± 67ms SAX
Darius et al. [40], 2014	MOLLI	102	Healthy	1052 ± 23 ms
Hinogar et al. [38], 2015	MOLLI	23	Healthy	1044 ± 18 ms
Terrier et al. [24], 2015	MOLLI	40	Fibrosis	>1250 ms
Lee et al. [25], 2015	MOLLI	15	Healthy	1169 ± 21 ms
Teixeira et al. [26], 2016	MOLLI	40	Healthy	1199 ± 28 ms
	SHMOLLI			1174 ± 37 ms
	SASHA			1487 ± 36 ms
Roy et al. [18], 2017	MOLLI	75	Healthy	1122 ± 57 ms
Heidenreich et al. [31], 2019	MOLLI		Healthy	1175 ± 72 ms
				1356 ± 43 ms
	SHMOLLI	-	Pathological:	1076 ± 100 ms
	SASHA	19	- Amyloidosis	1264 ± 72 ms
			- Acute MI	1460 ± 67 ms
Tribuna et al. [27], 2021	MOLLI	20	- Myocarditis	1687 ± 68 ms
			Healthy	1124.9 ± 55.2 ms
Lavall et al. [28], 2022	MOLLI	24	CA	1409 ± 59 ms
		21	HCM	1266 ± 44 ms
		80	HHD	1257 ± 41 ms
Guo et al. [29], 2022	MOLLI	607	Healthy	1170 ± 55 ms
Our approach, 2023	Single-Shot	40	Healthy	1079 ± 80 ms
			Pericarditis	1217 ± 12 ms
			Myocarditis	1506 ± 36 ms
			MI	1596.3 ± 48 ms

HCM: Hypertrophic cardiomyopathy. **HHD:** Hypertensive Heart disease. **LL:** look locker sequence. **MI:** Myocardial Infarction. **MOLLI:** Modified look locker inversion recovery sequence. **SAX:** Short Axis. **SASHA:** saturation recovery single-shot acquisition. **SHMOLLI:** Shortned MOLLI.

Number of participants per group, mean values (mean ± S D) are reported for the type of sequence, T1-mapping values (ms).

An additional clinically relevant observation is the reduced variability observed with the proposed Single-Shot approach compared with CVI⁴²-based post-processing. While mean T1 values were statistically equivalent between both methods, variability was consistently lower in the proposed framework, suggesting improved numerical stability. This finding is particularly important in quantitative cardiac imaging, where reproducibility across patients, scanners, and acquisition conditions directly impacts clinical utility. The reduced dispersion may be attributed to the simplified acquisition scheme, reduced dependency on complex reconstruction pipelines, and minimized post-processing variability. Agreement analysis further demonstrated minimal bias

and narrow limits of agreement between the proposed method and the reference standard, supporting their interchangeability for mean T1 estimation in clinical settings. Taken together, these results indicate that the proposed Single-Shot strategy preserves quantitative accuracy while improving robustness, which is a key requirement for translation into routine clinical workflows.

From a clinical perspective, T1 mapping has become a cornerstone technique for non-invasive tissue characterization, particularly in conditions where conventional imaging techniques such as T2-weighted imaging and LGE may be insufficient or limited. Its value has been extensively validated in myocarditis, ischemic

cardiomyopathy, and infiltrative or systemic cardiac diseases, where it provides sensitive quantification of diffuse myocardial injury [24,33–36]. Large clinical studies have reported high diagnostic performance for native T1 mapping in acute myocarditis, with reported AUC values reaching up to 0.95 and diagnostic accuracies exceeding 90% in multicenter cohorts [37,38]. Our findings are in agreement with this diagnostic performance, further supporting the role of native T1 as a robust quantitative biomarker.

Importantly, our results reinforce that a simplified acquisition strategy does not compromise diagnostic sensitivity. The ability of the proposed method to clearly differentiate healthy and diseased myocardium, while maintaining agreement with established post-processing tools, suggests that it may serve as a practical alternative in routine clinical practice, particularly in environments where access to advanced mapping sequences or proprietary post-processing platforms is limited.

Clinical implications and limitations

The proposed approach addresses an important limitation of conventional T1 mapping techniques, which often depend on specialized sequences, vendor-specific implementations, and dedicated post-processing tools. By simplifying acquisition while maintaining quantitative reliability, the Single-Shot strategy may facilitate broader access to myocardial tissue characterization, particularly in resource-limited settings. In parallel, recent advances in computational cardiac imaging and artificial intelligence have highlighted the potential of automated frameworks to enhance myocardial disease assessment from CMR data, supporting a broader transition toward more standardized and reproducible quantitative imaging workflows [41,42].

However, several limitations must be acknowledged. First, the present study did not include post-contrast T1 mapping sequences, which precluded the assessment of extracellular volume (ECV). This represents a relevant limitation, as ECV is an established quantitative marker for diffuse interstitial remodeling and fibrosis. Consequently, the current analysis is restricted to native T1 measurements, and future work should integrate post-contrast imaging to enable a more comprehensive tissue characterization and validate the performance of the proposed method in ECV estimation.

Second, the relatively small number of patients with cardiac pathology ($n = 15$) may limit statistical power and generalizability across disease subgroups. Although statistically significant differences were observed between healthy and diseased myocardium, subgroup-level interpretation (e.g., myocarditis versus infarction versus structural disease) should be considered exploratory. Future studies with larger, multicenter cohorts are required to confirm robustness across broader clinical populations and to perform adequately powered subgroup analyses. A formal power analysis was not performed in this preliminary study; however, the observed effect sizes suggest a strong separation between groups, supporting the feasibility of the

proposed approach.

Third, this work was conducted in a single-center setting, and external validation across different scanners, field strengths, and vendor platforms remains necessary to confirm reproducibility.

CONCLUSION

The proposed Single-Shot T1 mapping technique provides a reliable and accessible alternative to conventional MOLLI-based approaches for myocardial tissue characterization. It demonstrates strong agreement with reference post-processing methods, statistically significant discrimination between healthy and pathological myocardium, and reduced variability, indicating improved numerical stability. These findings support its potential utility as a practical quantitative tool for routine clinical cardiac MRI, particularly in settings where standard mapping sequences or advanced post-processing tools are not readily available.

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