Normal T1 Mapping values in Cardiac Magnetic Resonance Imaging in a regional cohort

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Abstract

T1 mapping represents an advanced cardiovascular magnetic resonance imaging technique, crucial for the non-invasive assessment of myocardial tissue and the early diagnosis of various cardiac pathologies. This study aims to determine the normal range of T1 mapping values in a population sample from our geographic region, using the MOLLI sequence on a 1.5T MRI scanner. In magnetic resonance imaging, establishing normal T1 ranges in mapping sequences for healthy individuals is essential to enable the early and immediate detection of abnormalities indicative of pathology. T1 normal ranges are subject to variability due to physical/biological confounders (such as magnetic field strength, temperature, sex, and patient age) and methodological factors (such as sequence type and post-processing). We analyzed 36 patients (28 male, 8 female), positioning three circular regions of interest (ROIs) on the interventricular septum at basal, mid, and apical levels in the short-axis plane for each subject. The findings indicated that the reference T1 mapping value in a healthy population from our area is 1010.2 ± 20 ms. In this study, higher T1 values were found in females compared to males; however, no significant age-related differences were found. The main limitations of this study include the small sample size and, at present, the lack of a reproducibility analysis.

Introduction

T1 mapping is a sophisticated cardiac MRI method essential for non-invasive myocardial tissue evaluation and the early diagnosis of various cardiac diseases. It enables quantitative myocardial assessment, adding to the qualitative analysis provided by standard cardiac imaging, by measuring T1 relaxation times. This technique provides detailed information about the composition of individual biological tissues, allowing improved characterization of pathological lesions and physiological processes. The present study was motivated by the need to establish normal parameters in CMR analyses to increase diagnostic sensitivity for cardiovascular diseases, which represent the primary cause of mortality in Western countries, accounting for approximately 35% of total deaths, as reported in the 2021 European Society of Cardiology guidelines [2]. T1 mapping values are altered in various pathological processes [3]. Examples include: 1. Amyloidosis – characterized by elevated T1 values relative to normal; 2. Anderson-Fabry Disease – characterized by reduced T1 values, particularly in early disease stages, due to glycosphingolipid accumulation. However, normal T1 mapping values cannot be considered universally standardized due to confounding factors, which include both physical-biological (e.g., sex, age, temperature, field strength) and methodological (e.g., sequence type, post-processing) variables [4]. This variability led to the initiation of our experimental research. The research aimed to calculate normal T1 mapping values in a population sample from our geographic area using a 1.5 T Siemens Magnetom MRI scanner at San Nicola Pellegrino Hospital in Trani (PTA Trani). The primary objective was to establish normalized T1 mapping values for healthy patients at our diagnostic center to enable characterization of potential myocardial lesions in pathological or suspected pathological patients.

Materials and Methods

Data collection and study technique

In this study, we analyzed 36 local patients (28 male, 8 female), aged 18 to 77 years; they were carried out from March to September 2024. Patients were selected by a radiologist in collaboration with a cardiologist based on eligibility criteria such as MRI compatibility and the absence of pathological abnormalities detected in standard MRI sequences. Data recorded for each patient at the time of examination included age, sex, weight, heart rate, and additional notes regarding the procedure. [5] Imaging was performed with patients in a supine

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position using a clinical 1.5T MRI scanner with a specific protocol for advanced cardiac imaging. Standard imaging sequences (Table 1) were supplemented with mapping sequences, specifically the MOLLI (Modified Look Locker Inversion Recovery) sequence (Table 2).

Table 1. *Standard Protocol sequence and parameters*

Sequence	FOV Read (mm)	FOV Phase (%)	TR(ms)	TE (ms)	Avarages	TA (min)
CINE bSSFP 2 CHAMBERS	400	81,3	36	1,15	1	0,10
TRUE FISP SHORT AXIST	400	81,3	50	1,15	1	3,10
CINE bSSFP 4 CHAMBERS	400	81,3	35	1,15	1	0,10
CINE bSSFP 3 CHAMBERS	400	81,3	35	1,15	1	0,10
GADOLINIUM MDC	/	/	/	/	/	/
TI SCOUT	350	81,3	25	1,10	1	0,23
DE PSIR SYSTOLE	460	75	700	1,00	1	0,26
DE PSIR 2 CHAMBERS	420	75	700	1,15	1	0,12
DE PSIR 4 CHAMBERS	420	78	700	1,15	1	0,10
DE PSIR 3 CHAMBERS	420	78	700	1,15	1	0,10

Sequence	Slice Group	Slice Thickness (mm)	Distance Factor (%)	Phase Encoding Direction
CINE bSSFP 2 CHAMBERS	1	86	20	A>>P
TRUE FISP SHORT AXIST	1	8	0	A>>P
CINE bSSFP 4 CHAMBERS	1	6	20	A>>P
CINE bSSFP 3 CHAMBERS	1	6	20	A>>P
GADOLINIUM MDC	/	/	/	/
TI SCOUT	1	8	20	A>>P
DE PSIR SYSTOLE	1	8	0	A>>P
DE PSIR 2 CHAMBERS	1	8	20	R>>L
DE PSIR 4 CHAMBERS	1	8	20	A>>P
DE PSIR 3 CHAMBERS	1	8	20	A>>P

Table 2. *Modified Look Loker Sequence (MOLLI) and parameters*

Sequence	Scanner	Image Type	Image View Plane	Image Technique	Acquisition scheme	Type of acquisition
MOLLI	Siemens Magnetom 1,5 T	T1 Map Pre	Short- Axis	SSFP	5 (3) 3	Synchronized ECG (diastole)

MOLLI Imaging Parameters	TR	TE	Slice Thickness	Flip Angle	TI	FOV (Field of View)
	2-3 ms	1-1,5 ms	8 mm	35°	100-200 ms	300-400 mm

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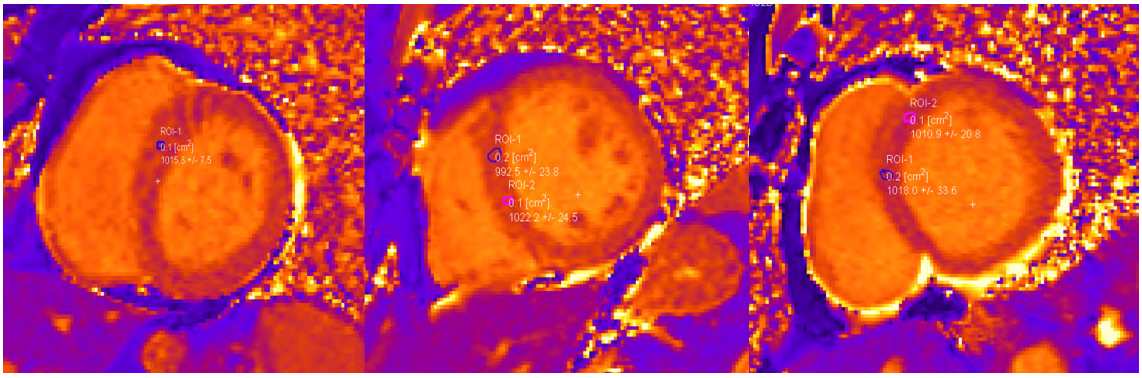
Analysis of acquired images

For each patient, image analysis was conducted using "Segment CRM_ Medviso" software (version 4.0.): three circular ROIs were positioned at basal (Figure 1a), mid (Figure 1b), and apical (Figure 1.c) levels in the short-axis plane, particularly on the interventricular septum, identified in the literature as a favorable and reproducible region as it is less affected by surrounding organs [6]. The software calculated the value of each ROI for each slice, producing a single mean result.

This normalization was fundamental because it allowed us to create an initial database of local use on the basis of these obtained normal values, it is possible to quickly identify a value of T1 mapping index of pathology.

Despite differences in gender of subjects, no significant differences in T1 values are seen. Instead, as the graphs show (Figure 3), T1 values tend to be higher in females (1028.8 ± 20 ms compared to 1010.2 ± 20 ms).



(*a*) (*b*) (*c*)

Figure 1.
The ROI has been positioned on the interventricular septum, in the short axis plane, in particular in: (*a*) *Basal Level*; (*b*) *Mid-Level*; (*c*) *Apical Level*.

Results

The reference T1 mapping value for a healthy population from our area was found to be 1010.2 ± 20 ms (Figure 2). This normalization was essential for establishing a local database, enabling rapid identification of pathological T1 mapping values. This normalization was fundamental because it allowed us to create an initial database of local use and not only, on the basis of these obtained normal values, it is possible to quickly identify a value of T1 mapping index of pathology (Fig.2)

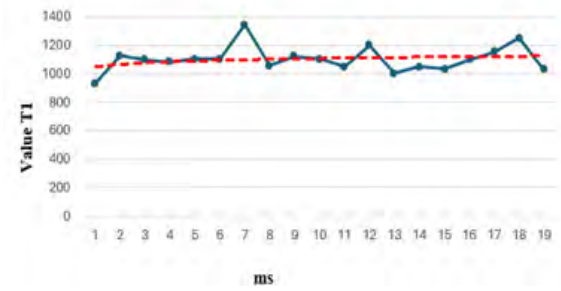
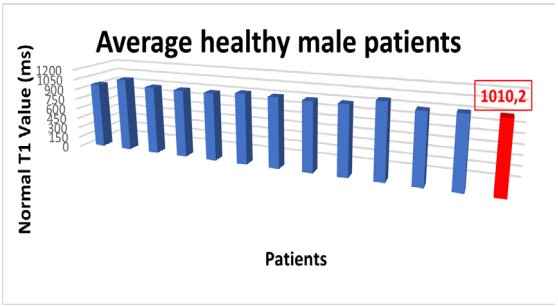
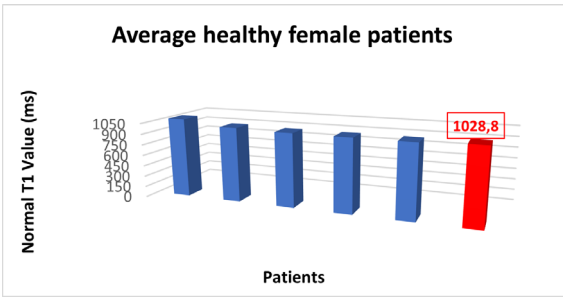


Figure 2. *Results on Line Graph*



(a)



(b)

Figure 3. (*a*) *Average healthy male patients* (*b*) *Average healthy female patients*

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Discussion

Based on our results, the clinical validity of this research can be confirmed, identifying a T1 mapping normal value of 1010.2 ± 20 ms in a population sample from PTA Trani (Figure 4). However, future studies may expand upon this research. In fact, current limitations include the small sample size, which could be expanded in the future as the number of patients undergoing cardiac MRI for diagnostic assessment increases, as well as the inability to replicate the study with the same subjects to verify that the values obtained are truly reliable and reproducible.

The results obtained confirm the validity of my clinical research. The ultimate goal has been achieved, as well as obtaining local standard values for T1 mapping in a healthy population, thus creating a starting point on which to base the distinction between "pathological" and "non-pathological" in daily patient mapping. This does not preclude further insights from future colleagues.

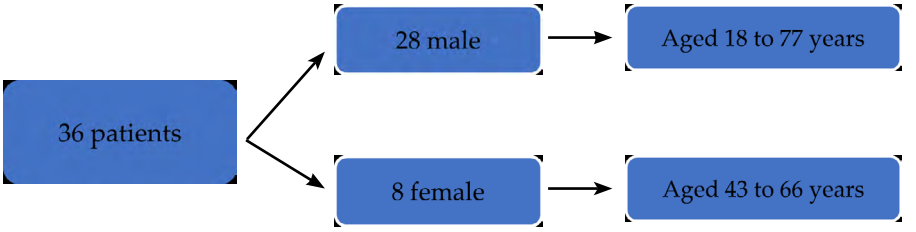

Figure 4. *Study flow chart*

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