Full title:

T1 mapping in differentiation of diffuse myocardial disease in hypertrophic and dilative cardiomyopathy

Short title:

T1 mapping and diffuse myocardial fibrosis

Authors:

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Keywords: T1 mapping, diffuse fibrosis, hypertrophic cardiomyopathy, late gadolinium enhancement
Abstract

**Background.** T1 mapping was proposed as potentially valuable in quantitative assessment of diffuse myocardial fibrosis. We aimed to determine its role in differentiation of healthy myocardium from diffuse fibrosis in clinical setting.

**Methods and results.** Thirty-nine subjects with known hypertrophic (HCM) or dilative cardiomyopathy (DCM) were enrolled (age 47±7.4 years). Twenty-five age-gender matched subjects with low pre-test likelihood of cardiomyopathy served as controls. Single equatorial short-axis slice T1 mapping was performed on a 3 Tesla scanner prior and at 10, 20 and 30 minutes after administration of 0.2 mmol/kg of gadobutrol. We quantified T1 values within the septal myocardium and calculated the relaxation rate (R1) as 1/T1 and the R1 differences between the native and post-contrast myocardium (ΔR1). R1\textsubscript{native} was significantly shorter in cardiomyopathies compared to control subjects (p<0.01). Conversely, post-contrast R1 were significantly longer in cardiomyopathies at all time-points (p<0.01). ΔR1s were significantly higher in cardiomyopathies in comparison to controls at all time-points (p<0.01). ROC analysis revealed that R1\textsubscript{native} was able to differentiate between healthy and diseased myocardium (AUC: 0.98; 95%CI: 0.96-1.00; p<0.001) with a sensitivity of 100%, specificity of 88%, diagnostic accuracy 96%, positive predictive value 93% and negative predictive value 100%. R1\textsubscript{10min} and ΔR1\textsubscript{10min} performed best among the postcontrast values, however with lower predictive values.

**Conclusions.** We demonstrate that native and post-contrast T1 values and their respective R1 values provide indices with high diagnostic accuracy for the discrimination of normal and diffusely diseased myocardium. Native imaging provides the best distinction between controls and patients with cardiomyopathy.
Introduction

Myocardial fibrosis is a fundamental process in the development of myocardial dysfunction in various cardiomyopathies, leading to myocardial remodelling and poor outcome [1-5]. Cardiac magnetic resonance (CMR) is increasingly applied as the first line investigation into the causes of cardiomyopathies [6]. Visualisation of fibrosis by CMR is based on a greater distribution volume and slower washout of gadolinium contrast agents within tissues with greater extracellular space [7]. Whereas regional fibrosis after ischaemic injury is readily distinguished by well-delineated areas of increased signal intensity on T1-weighted images by late gadolinium enhancement (LGE) [8], it may be impossible to define an area of clearly unaffected myocardium as a ‘nulled’ reference in diffuse fibrotic processes (Figures 1 A-C) [9]. As a consequence, such images may null the signal in areas of fibrosis obscuring the finding or result in images with various grey values not allowing for a clear “yes/no” decision [9,10]. Recently, several studies proposed the measurement of T1 relaxation times as potentially valuable for quantitative assessment of myocardial fibrosis [11-16]. In these studies, native myocardium of ischaemic scar showed longer T1 values compared to unaffected remote myocardium. Following contrast administration, regional and also diffusely scarred myocardium showed shorter T1 relaxation times and delayed normalization of T1 times with gadolinium washout. Whereas these observations show the potential of T1 quantification for the evaluation of myocardial fibrosis, these studies used a variety of imaging methodologies and post-processing approaches to yield a clinically robust application. In the present study we aimed to examine the value of native and post-contrast T1 relaxation times in differentiation of healthy and diffusely diseased myocardium in two model conditions, hypertrophic (HCM) and dilated cardiomyopathy (DCM).

Methods

Subjects undergoing a routine clinical CMR at King’s College London were invited to participate in this study. Groups were based on the CMR findings and consisted of subjects
with known HCM (n=22) and non-ischaemic DCM (n=17). Diagnosis of HCM was based on the demonstration of a hypertrophied left ventricle (LV) associated with a non-dilated LV in the absence of increased LV wall stress, or another cardiac or systemic disease that could result in a similar magnitude of hypertrophy [17,18]. All HCM patients had an expressed phenotype with typically asymmetric septal hypertrophy of increased LV wall thickness, permitting an unequivocal clinical diagnosis. None of the HCM subjects showed obstructive flow phenomena. Non-ischaemic DCM was defined by an increase in LV volumes, reduction in global systolic function and absence of evidence of ischaemic LGE [18]. Twenty-five normotensive subjects with low pretest likelihood for left ventricular cardiomyopathy, not taking any regular medication and with normal CMR findings including a normal LV mass index served as an age and gender matched control group [19]. Additional exclusion criteria for all subjects were the generally accepted contraindications to CMR (implantable devices, cerebral aneurysm clips, cochlear implants, severe claustrophobia) or a history of renal disease with an eGFR<30 mL/min/1.73m². The protocol of study was reviewed and approved by institutional ethics committee and written informed consent was obtained from all participants.

**CMR protocol**

We integrated native and post-contrast myocardial T1 mapping into our routine imaging protocol for the determination of the underlying aetiology of cardiomyopathy and an outline is provided in **Figure 2**. The CMR studies were performed with the patient supine using a clinical 3T scanner (Achieva TX, Philips Healthcare, Best, The Netherlands) and a 32-channel coil. After standardized patient specific planning [20], volumetric cavity assessment was obtained by whole-heart coverage of gapless short-axis slices. Thereafter, cine-images of 3 long-axis views (4-chamber, 2-chamber and 3-chamber view) and transverse axial views were acquired. All cine-images were acquired using a balanced steady-state free precession sequence in combination with parallel imaging (SENSitivity Encoding, factor 2) and retrospective gating during a gentle expiratory breath-hold (TR/TE/flip-angle:
3.4ms/1.7ms/60°, spatial resolution 1.8x1.8x8 mm). LGE imaging was performed in corresponding views in all subjects using a mid-diastolic inversion prepared 2-dimensional gradient echo sequence (echo time/repetition time/flip angle 2.0 ms/3.4 ms/25°, spatial resolution 1.8x2x10 mm reconstructed to 1.8x1.8x8 mm, with a patient-adapted prepulse delay), 20 minutes after contrast injection (gadobutrol, 0.2 mmol/kg body weight). Single breath-hold modified Look-Locker Imaging (MOLLI) was used for T1 mapping, performed in an equatorial short axis slice prior and at 10, 20 and 30 minutes following contrast administration. Imaging parameters were FOV 320x320; TR/TE/flip-angle: 3.3ms/1.57ms/50°, interpolated voxel size 0.9x0.9x8mm, phase encoding steps n=166, HR adapted trigger delay, 11 phases (3+3+5), as previously described [14-16].

Image analysis

All routine CMR analysis was performed using commercially available software (ViewForum, Extended Workspace, Philips Healthcare, The Netherlands). Endocardial LV borders were manually traced at end-diastole and end-systole. The papillary muscles were included as part of the LV cavity volume. LV end-diastolic (EDV) and end-systolic (ESV) volumes were determined using Simpson’s rule. Ejection fraction (EF) was computed as EDV-ESV/EDV. All volumetric indices were normalized to body surface area.

The LGE images were visually examined for the presence of regional fibrosis. Global enhancement was defined as % of enhanced area per total short axis stack, where enhanced area was defined by 6 standard deviations (SD) from the manually selected normal area, appearing as maximally suppressed myocardium [10].

T1 relaxation maps were obtained by RelaxMaps tools supported by PRIDE environment (Philips, The Netherlands). Whereas selective acquisition at a fixed point of the cardiac cycle in end-diastole usually largely suppressed the influence of cardiac motion, the relatively long duration of the sequence (17-heart beats to obtain a single slice map) occasionally led to some undesired breathing motion. We therefore performed a motion-correction image preparation
step using a custom-made tool developed in house based on a hierarchical adaptive local affine registration (HALAR) technique, as previously described [21], where a reference phase (source) is registered to each of the selected target phases (11 in total). A rectangular region-of-interest (ROI) being large enough to enclose the whole of the LV is manually drawn onto the source reference phase before registration. After the initial image affine registration step of the ROI, the source image is subdivided into four smaller ROIs using equal subdivisions. Each subdivision underwent an affine transformation again (each with 6 degrees of freedom) to align the features of the target image ROIs with the corresponding ROIs in the source phase image. Co-registered images were then used to derive T1 relaxation times by placing the ROIs conservatively within the myocardium avoiding ‘contamination’ with signal from the blood pool (Figure 3). T1 was determined by fitting a three parameter exponential model to the measured data and applying Look-Locker correction as previously described (Figure 4) [14]. Noise was calculated in a ROI drawn manually inside the lungs and taken into account in the T1 computation [22]. Because longitudinal relaxation is heart rate (HR)-dependent, we also applied HR-correction of T1 values when HR exceeded 80bpm, as previously described [14]. In addition to the T1 values of myocardium and blood pool, we calculated relaxation rate (R1) of myocardium as an inverse value of T1 and the difference of R1 between postcontrast and the native value (∆RR), which is proportional to the local contrast agent concentration (C) and agent-specific relaxivity constant (r) for 10, 20 and 30 minute-time-points [13]

$$\Delta RR = R1_{post} - R1_{native} = C* r.$$  

**Statistical analysis**

Statistical analysis was performed using SPSS software (SPSS Inc., Chicago, IL, USA, version 15.0). Mean differences from the control group were examined by Student t-test. Reproducibility and agreement analysis was performed using paired and unpaired Student t-test and bivariate correlations. Associations were explored by linear and logistic regressions,
as appropriate. Receiver-operating characteristics (ROC) analysis was used to select cut-off values for the best time-point to discriminate healthy and abnormal R1 values. All tests were two-tailed and a P value of less than 0.05 was considered significant.

**Results**

Patients’ characteristics, haemodynamics and cardiac function are presented in **Table 1**. All groups had a similar gender representation, HR and body surface area. In comparison to controls, HCM subjects had increased global systolic function (p=0.02) and diastolic LV wall thickness (p<0.01). Compared to controls, subjects with DCM had increased cavity volumes and reduced global systolic function (p<0.01). All patients’ groups had increased LV mass index and global enhancement (p<0.01).

**Relaxation times in native and post-contrast myocardium and blood pool**

R1 values of blood pool were similar between the groups, confirming the consistency of sampling points after the weight-adapted contrast injection. R1 relaxation times of native myocardium were significantly shorter in cardiomyopathies compared to control subjects (p<0.01, **Table 2**). Conversely, post-contrast R1 values were significantly longer in the presence of cardiomyopathy at all time-points (p<0.01). Similarly, ΔRRs were significantly higher in cardiomyopathies in comparison to the control group at all time-points (p<0.01).

**Reproducibility and agreement analysis**

In a subset of subjects (n=50), inter-observer mean differences (MD) for T1 values were 1.3ms (95%CI: -12.4-15.4) for native scans and 0.7 ms (-7.9-12.3) for overall postcontrast scans, whereas intra-observer MDs were 0.3 ms (-6.3 -5.3) and 0.1 (-3.4 to 4.2), respectively. We further demonstrate an excellent overall (pre- and postcontrast) intra- and interobserver agreement in T1 relaxation times (intraobserver: r= 0.94, p<0.0001; interobserver: R=0.91, p<0.0001). When assessed separately the postcontrast data showed better agreement within
and between observers, respectively (r~0.94, p<0.0001 for both) than in the native scans (intraobserver r= 0.81, p <0.0001; interobserver r=0.79, p<0.001).

**Analysis of relationships**

In the multivariate binary logistic regression model using native and post-contrast R1 and ΔRR values, we identified R1\textsubscript{native} as the independent discriminator of cardiomyopathic myocardium (p=0.001) with a sensitivity of 100%, specificity 88%, diagnostic accuracy 96%, positive predictive value 93% and negative predictive value 100%. Results of the ROC analysis and cut-off values for differentiation of normal from abnormal myocardium (all groups against controls) for myocardial T1s, R1s, and ΔRRs are presented in **Table 3**.

In controls and patients with DCM, R1\textsubscript{native} showed associations with indexed LV-EDV (r=0.39-0.57, p<0.05). Patients with DCM showed further associations between R1\textsubscript{native} and ΔRR\textsubscript{10min} with EF (r=-0.61, and r=-0.49, respectively, p<0.01 for both), whereas in HCM there was an association between R1\textsubscript{native} with indexed LV mass (r=-0.58, p<0.01). In both cardiomyopathies global enhancement showed associations with R1\textsubscript{native} (r=-0.47, 0.02) and ΔRR\textsubscript{10min} (r=-0.51, p<0.01); associations with variables at the other time-points were weaker (r~0.27-0.41).

**Discussion**

Our study reveals that diffusely diseased myocardium can be reliably differentiated from healthy myocardium by means of T1 mapping. We demonstrate that native and post-contrast R1s provide indices with high diagnostic accuracy, sensitivity and specificity, with R1\textsubscript{native} providing the greatest distinction between healthy and diffusely diseased myocardium. We further demonstrate that in DCM, R1\textsubscript{native} correlates with measures of LV remodelling and global systolic function, whereas in HCM it shows an association with LV mass. Our findings provide a novel and easy to use method for the detection of diffusely diseased myocardial tissue by CMR with an immediate potential for a clinical translation.
T1 mapping techniques provide quantifiable information on longitudinal relaxation through acquisition of images with different inversion times and by multi-parameter curve fitting analysis. T1 maps are derived as parametric reconstructed images, where signal intensity of a pixel depends on the absolute longitudinal relaxation properties of this voxel \[13-16, 22\]. Several methodologies were tested to acquire the myocardial T1 relaxation values including sets of inversion recovery images \[12\] with varying inversion times, and lately, the classical and modified Look-Locker sequences \[14-16, 23\]. The variant of the latter sequence, which was also applied in the present study, leads to a series of multiple images acquired within the same phase of cardiac cycle through a selective fixed delay time over successive heart beats \[14\]. Some studies using this or related methodologies suggested that native T1 myocardial values could be used to discern post-infarct scar from healthy myocardium \[15,16\]. Most of these studies however focused on the post-contrast T1 values and reported significantly shorter T1 times compared to controls. In a population of patients with mixed causes of heart failure, Iles at al reported shorter T1 times compared to controls even when excluding areas of regional fibrosis \[12\]. These authors also observed an inverse relationship between post-contrast T1 values and amount fibrosis on histology \[12\]. Ability of T1 imaging to quantify the amount of diffuse fibrosis was also confirmed by a novel technique of equilibrium contrast imaging \[24\]. Diastolic myocardial impairment, an indirect marker of diffuse myocardial fibrosis, was shown to correlate with abnormal T1 values in patients with heart failure, diabetic cardiomyopathy and also amyloidosis \[11,25-27\]. Whereas one previous study in patients with heart failure showed no significant difference in native T1 values \[12\], our findings reveal for the first time that native T1 values are significantly higher in diffusely disease myocardium. The disparity with the former findings may lie in the differences in imaging techniques and higher field strength used the present study, which leads to increased values of longitudinal relaxation in native myocardium \[15,16,28\]. As native T1 of myocardium provides the greatest distinction between healthy myocardium and diseased with high negative predictive value, development of the application (with whole heart coverage) may potentially serve as useful approach to characterise regional differences in myocardial
conditions in patients where contrast administration is contraindicated as well as an easy-to-implement test in patients with suspected diffuse fibrosis, which may be missed by the classic LGE imaging.

Our findings of native T1 respectively R1 values contrast several important aspects with regards to the post-contrast T1 mapping. As gadolinium administration greatly shortens T1 values, the overall T1 time of the tissue will depend on the dose and relaxivity of the gadolinium contrast agent, the intrinsic T1 values of the tissue [13, 23, 28] and the timing of the acquisition after gadolinium administration [7, 9]. Post-contrast T1 sampling can thus be affected by a variety of independent variables including renal function, contrast type and dose of administration, variation in sampling time-points and individual pharmacokinetics [22, 29]. Postcontrast T1 values imaging at the rigid time-points can prove cumbersome in clinical routine; we improved the inter-study comparability of the sampling time-points by consistent timing in our routine cardiomyopathy imaging protocol. Furthermore, in our study we purposefully operate with the relaxation rates R1s, as the difference between post-contrast R1 and the native R1 is proportional to the local concentration of the contrast agent whereas the absolute T1 values have no such direct meaning [12]. In view of all these factors, the derivation of ΔRRs by subtracting the native R1 somewhat improves the post-contrast T1 mapping to achieve the distinction between the healthy and diseased myocardium.

In our study T1 values were sampled in two model-conditions of diffuse myocardial fibrosis. Whereas several investigators looked at the role of T1 mapping in patients with heart failure, no previous study reports T1 values in HCM. It is well established that visualisation of LGE in HCM has an important and independent prognostic implication [5], however, recent evidence suggests that a profibrotic state through genetically driven collagen metabolism precedes the overt phenotype with LV hypertrophy or fibrosis visible on LGE images [4]. We previously demonstrated that global enhancement correlates with reduction of longitudinal ventricular deformation in HCM, even when global systolic function remains apparently unaffected [10]. Identification of early phenotypes where early fibrotic process could be
quantified and followed-up prior to the effects on cardiac geometry and function would add to
the management of this condition [4].

Some limitations apply to this study. The small sample size of otherwise well-matched
subjects may limit generalization of the present findings, and a larger multicentre study is
required to reconfirm our imaging protocol and findings for widespread clinical use.
Examination of the equivalency of multivendor sequences may also be appropriate. Next, T1
sampling in a single short axis slice is based on assumption that it can capture most of the
diffuse disease, however, future studies with multiple slices are needed to rule out relevant
regional variation. Prolonged acquisition time required for longitudinal relaxation to occur in
the native myocardium, especially at high field strengths, its HR-dependency and motion
artefacts may all amount to errors in the pixel-wise estimation of T1 values [30]. Because we
used a motion and HR-correction algorithms and a very conservative approach to T1 mapping
we believe to have controlled for the majority of these influences. Whether imaging with
shorter variants of MOLLI sequences would resolve some of the breathing motion artefacts
and still provide sufficient information on longitudinal relaxation of the native myocardium,
remains to be confirmed in future studies.

Conclusions

We demonstrate that native and post-contrast T1 values and their respective R1 values
provide indices with high diagnostic accuracy for the discrimination of normal and diffusely
diseased myocardium. Native imaging provides the best distinction between controls and
patients with cardiomyopathy. Further studies are needed to effectively translate these
findings into clinical use.

Acknowledgement

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of Cardiovascular Imaging Sciences, King’s College London, for her assistance with high
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References


Figure legends

**Figure 1.** Examples of single short axis slice of Look-Locker and respective late gadolinium enhancement images in conditions with diffuse myocardial fibrotic process (A – burnt-out hypertrophic cardiomyopathy, B-amyloidosis, C- dilative cardiomyopathy following previous myocarditis). Reduced relative difference between affected and unaffected myocardium

**Figure 2.** Routine imaging protocol in assessment of cardiomyopathies applied in the current study and sampling time-points of MOLLI sequences.

**Figure 3.** T1 map image with colour scale and region of interest within septal myocardium.

**Figure 4.** Representative images of MOLLI imaging (11 phases), motion correction step and T1 map with region of interest conservatively within the septal myocardium.
### Table 1. Patients’ characteristics, global morphological and functional measures. (Student t-test for differences from the control group: *p<0.05, **p<0.01).

<table>
<thead>
<tr>
<th>Variable</th>
<th>Control group</th>
<th>HCM (n=22)</th>
<th>DCM (n=17)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Gender (men, %)</td>
<td>16 (64)</td>
<td>14 (64)</td>
<td>12 (70)</td>
</tr>
<tr>
<td>Age (years)</td>
<td>46 ± 11</td>
<td>44±10</td>
<td>48±14</td>
</tr>
<tr>
<td>BP systolic (mmHg)</td>
<td>115 ± 12</td>
<td>118±11</td>
<td>124±13</td>
</tr>
<tr>
<td>BP diastolic (mmHg)</td>
<td>78 ± 12</td>
<td>77±9</td>
<td>81±17</td>
</tr>
<tr>
<td>Heart rate (bpm)</td>
<td>67±7</td>
<td>69±11</td>
<td>64±10</td>
</tr>
<tr>
<td>Body mass index (m/kg²)</td>
<td>24±4</td>
<td>25±3</td>
<td>23±2</td>
</tr>
<tr>
<td>LV – EDV index (mL/m²)</td>
<td>79±8</td>
<td>70±10</td>
<td>103±16**</td>
</tr>
<tr>
<td>LV-Ejection fraction %</td>
<td>63±6</td>
<td>71±8*</td>
<td>31±8**</td>
</tr>
<tr>
<td>LV mass index (g/m²)</td>
<td>55±8</td>
<td>96±17**</td>
<td>102±12**</td>
</tr>
<tr>
<td>Maximal LVWT (mm)</td>
<td>9±2</td>
<td>18±2**</td>
<td>10±2</td>
</tr>
<tr>
<td>Global enhancement (%)</td>
<td>5±7</td>
<td>12±9**</td>
<td>11±12**</td>
</tr>
<tr>
<td>eGFR (mL/min/1.73m²)</td>
<td>81±12</td>
<td>83±9</td>
<td>77±14</td>
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<tr>
<td>Haematocrit (%)</td>
<td>43±2</td>
<td>44±1</td>
<td>41±2</td>
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Table 2. T1 relaxation times in native and post-contrast myocardium (Student t-test for differences from the control group: *p<0.05, **p<0.01).

<table>
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<tr>
<th>Variable</th>
<th>Control (n=25)</th>
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<th>DCM (n=17)</th>
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<tr>
<td>Native</td>
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</tr>
<tr>
<td>T1 Myocardium (msec)</td>
<td>1095±55</td>
<td>1250±41**</td>
<td>1329±57**</td>
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<tr>
<td>T1 Blood (msec)</td>
<td>1892±88</td>
<td>1861±97</td>
<td>1914±82</td>
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<tr>
<td>R1 myocardium (msec⁻¹*10⁵)</td>
<td>92±7</td>
<td>80±5**</td>
<td>75±4**</td>
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<td>10 minutes</td>
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<td>T1 Myocardium (msec)</td>
<td>407±38</td>
<td>317±35**</td>
<td>298±28**</td>
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<td>T1 Blood (msec)</td>
<td>253±24</td>
<td>247±29</td>
<td>235±28</td>
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<tr>
<td>R1₁₀min myocardium (msec⁻¹*10⁵)</td>
<td>249±31</td>
<td>315±24**</td>
<td>348±31**</td>
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<td>ΔRR₁₀min</td>
<td>157±31</td>
<td>237±24**</td>
<td>272±32**</td>
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<td>20 minutes</td>
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<td>T1 Myocardium (msec)</td>
<td>425±56</td>
<td>362±67**</td>
<td>350±74**</td>
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<td>T1 Blood (msec)</td>
<td>296±27</td>
<td>300±37</td>
<td>292±34</td>
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<td>R1₂₀min myocardium (msec⁻¹*10⁵)</td>
<td>229±34</td>
<td>285±51**</td>
<td>289±29**</td>
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<tr>
<td>ΔRR₂₀min</td>
<td>137±35</td>
<td>205±53**</td>
<td>213±34**</td>
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<td>30 minutes</td>
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<td>496±68</td>
<td>433±59*</td>
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<td>T1 Blood (msec)</td>
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<td>347±41</td>
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<td>R1₃₀min myocardium (msec⁻¹*10⁵)</td>
<td>199±18</td>
<td>233±20**</td>
<td>228±22**</td>
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<tr>
<td>ΔRR₃₀min</td>
<td>107±18</td>
<td>153±19**</td>
<td>153±22**</td>
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Table 3. Results of Receiver-operating curve analysis with cut-off values in differentiation of normal myocardium from abnormal (all groups against controls), sensitivity and specificity and predictive values; AUC (95%CI): area-under-the curve (95% confidence interval).

<table>
<thead>
<tr>
<th>Variable</th>
<th>Cut-off value</th>
<th>AUC (95%CI)</th>
<th>Sig. (p-value)</th>
<th>Sensitivity (%)</th>
<th>Specificity (%)</th>
<th>Diagnostic accuracy (%)</th>
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<th>NPV</th>
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<td><strong>T1 value (msec)</strong></td>
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<td></td>
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<tr>
<td>Native</td>
<td>1184</td>
<td>0.98 (0.96-1.00)</td>
<td>0.000</td>
<td>100</td>
<td>88</td>
<td>96</td>
<td>93</td>
<td>100</td>
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<tr>
<td>10 minutes</td>
<td>343</td>
<td>0.94 (0.87-0.99)</td>
<td>0.000</td>
<td>94</td>
<td>84</td>
<td>91</td>
<td>88</td>
<td>89</td>
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<tr>
<td>20 minutes</td>
<td>402</td>
<td>0.86 (0.79-0.96)</td>
<td>0.000</td>
<td>82</td>
<td>64</td>
<td>75</td>
<td>82</td>
<td>64</td>
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<tr>
<td>30 minutes</td>
<td>477</td>
<td>0.84 (0.74-0.96)</td>
<td>0.000</td>
<td>72</td>
<td>68</td>
<td>70</td>
<td>72</td>
<td>68</td>
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<tr>
<td><strong>R1 value (msec-1*10^5)</strong></td>
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<tr>
<td>R1native</td>
<td>85</td>
<td>0.98 (0.96-1.00)</td>
<td>0.000</td>
<td>100</td>
<td>88</td>
<td>96</td>
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<td>R110min</td>
<td>272</td>
<td>0.94 (0.86-0.99)</td>
<td>0.000</td>
<td>95</td>
<td>88</td>
<td>92</td>
<td>91</td>
<td>92</td>
</tr>
<tr>
<td>R120min</td>
<td>250</td>
<td>0.86 (0.79-0.96)</td>
<td>0.000</td>
<td>82</td>
<td>64</td>
<td>75</td>
<td>72</td>
<td>80</td>
</tr>
<tr>
<td>R130min</td>
<td>210</td>
<td>0.84 (0.74-0.96)</td>
<td>0.000</td>
<td>72</td>
<td>68</td>
<td>70</td>
<td>68</td>
<td>70</td>
</tr>
<tr>
<td><strong>ΔRR (msec-1*10^5)</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>ΔRR10min</td>
<td>208</td>
<td>0.96 (0.94-1.00)</td>
<td>0.000</td>
<td>95</td>
<td>89</td>
<td>93</td>
<td>91</td>
<td>94</td>
</tr>
<tr>
<td>ΔRR20min</td>
<td>159</td>
<td>0.89 (0.81-0.97)</td>
<td>0.000</td>
<td>89</td>
<td>80</td>
<td>85</td>
<td>83</td>
<td>88</td>
</tr>
</tbody>
</table>
Figure 1-C

Look-Locker (T1 scout)

Late gadolinium enhancement

Apical SAX

Equatorial SAX

Basal SAX

2CH

3CH

4CH