

POSTER PRESENTATION

Open Access

Native T1 mapping allows for the accurate detection of the segments with chronic myocardial infarction in patients with known or suspected coronary artery disease

Yoshitaka Goto^{1*}, Masaki Ishida¹, Akimasa Yamada¹, Mio Uno¹, Shiro Nakamori², Motonori Nagata¹, Yasutaka Ichikawa¹, Kakuya Kitagawa¹, Masaaki Ito², Hajime Sakuma¹

From 19th Annual SCMR Scientific Sessions
Los Angeles, CA, USA. 27-30 January 2016

Background

Late gadolinium enhancement (LGE) cardiac magnetic resonance (CMR) is the current gold standard for the assessment of the myocardial infarction (MI). However, LGE CMR requires the administration of gadolinium contrast medium, which is contraindicated in patients with advanced chronic kidney disease (CKD). As patients with advanced CKD have higher prevalence of MI, accurate non-contrast CMR technique to detect MI is valuable. A previous study showed that visual assessment of native T1 map at 1.5T provided high specificity but only moderate sensitivity for detecting chronic MI. However, diagnosis performance of current native T1 mapping at 3.0T for detecting chronic MI has not fully understood. The aim of this study was to investigate the diagnostic accuracy of segmental native myocardial T1 mapping for detection of MI in patients with known or suspected CAD.

Methods

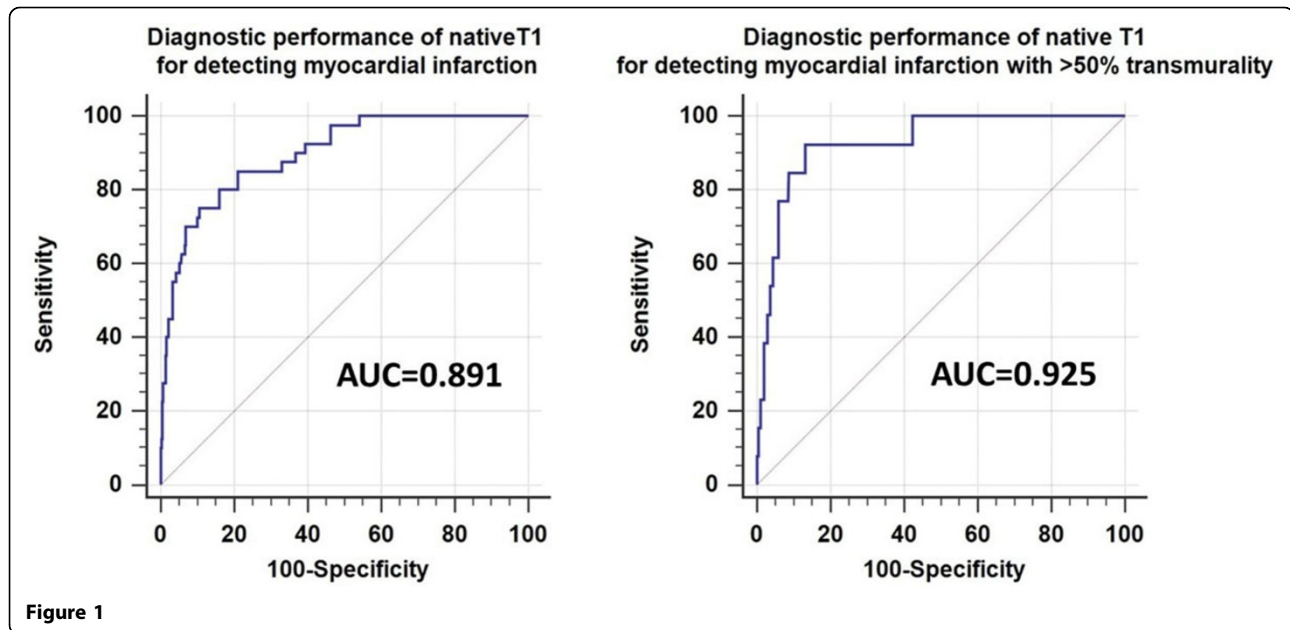
Consecutive 30 patients with known or suspected CAD who underwent CMR at 3.0T including cine, native T1 mapping and LGE were studied. Patients with acute MI, coronary artery bypass surgery and non-ischemic cardiomyopathy were excluded. T1 mapping was performed with a modified Look-Locker inversion recovery (MOLLI) sequence on 3 left ventricular (LV) short-axis slices (basal, mid, and apical). Endo- and epicardial borders of the LV myocardium were manually traced on

each slice. Myocardium was divided into AHA 16 segments. Segmental mean T1 values were quantified with a heart rate correction. On the corresponding slices of LGE images, presence or absence and transmural extent of MI were visually determined in each segment by consensus of two experienced observers. Presence or absence of severe wall motion abnormality (severe hypokinesis to dyskinesis) was also determined in each segment on the corresponding slices of cine images.

Results

MI was present in 10 of 30 patients (33.3%) in LGE CMR. Of the 480 segments, 475 segments were eligible for the analysis after excluding 5 segments due to artifacts on MOLLI images. MI was seen in 40 segments (8.4%) on LGE images. In 13 of the 40 segments, the transmural extent of MI was >50%. Native T1 was significantly greater in the segments with MI than those without MI (1491.5 ± 122.2 ms vs 1335.1 ± 95.9 ms, $p < 0.001$). The area under the ROC curve (AUC) of native T1 for detecting the segments with any MI was 0.891, providing sensitivity and specificity of 75.0% and 88.9%, with a cut-off of 1420 ms. For detecting the segments with MI with transmural extent of >50%, AUC of native T1 was 0.925 and the sensitivity and specificity was 92.3% and 86.5%, with the same cut-off. No apparent wall motion abnormality suggestive of MI was observed on cine MRI in 25 of 40 segments with MI. Native T1 mapping accurately detected the presence of MI in 17 of the 25 segment (68%).

¹Radiology, Mie University Hospital, Tsu, Mie, Japan
Full list of author information is available at the end of the article



Conclusions

The current results demonstrated that native T1 mapping at 3.0T allows for the accurate detection of the segment with MI in patient with known or suspected CAD without administrating gadolinium contrast medium.

Authors' details

¹Radiology, Mie University Hospital, Tsu, Mie, Japan. ²Cardiology, Mie University Hospital, Tsu, Mie, Japan.

Published: 27 January 2016

doi:10.1186/1532-429X-18-S1-P70

Cite this article as: Goto et al.: Native T1 mapping allows for the accurate detection of the segments with chronic myocardial infarction in patients with known or suspected coronary artery disease. *Journal of Cardiovascular Magnetic Resonance* 2016 **18**(Suppl 1):P70.

Submit your next manuscript to BioMed Central and take full advantage of:

- Convenient online submission
- Thorough peer review
- No space constraints or color figure charges
- Immediate publication on acceptance
- Inclusion in PubMed, CAS, Scopus and Google Scholar
- Research which is freely available for redistribution

Submit your manuscript at
www.biomedcentral.com/submit

 BioMed Central