Journal of Cardiovascular Magnetic Resonance

POSTER PRESENTATION



T_2 -dependent errors in MOLLI T_1 values: simulations, phantoms, and in-vivo studies

Kelvin Chow^{1*}, Jacqueline Flewitt², Joseph J Pagano¹, Jordin D Green³, Matthias G Friedrich², Richard B Thompson¹

From 15th Annual SCMR Scientific Sessions Orlando, FL, USA. 2-5 February 2012

Background

Diffuse myocardial fibrosis occurs in various cardiomyopathies and can be indirectly assessed with blood and myocardial T₁ mapping at baseline and after gadolinium administration. The widely used MOdified Look-Locker Inversion-recovery (MOLLI) [1] sequence is known to underestimate myocardial T₁ at higher heart rates, but its dependence on T₂ has not been explored. We investigate MOLLI's T₁ accuracy in phantoms and confirm with simulations and in-vivo studies. T₁ values are further compared with a saturation-recovery T₁ mapping sequence [2].

Methods

Phantoms

14 NiCl₂ agarose phantoms with a broad range of T_1 and T₂ values were imaged with a gold-standard inversion-recovery spin-echo (IR-SE) sequence, MOLLI, and a new SAturation-recovery single-SHot Acquisition (SASHA) technique (Siemens Avanto 1.5T). IR-SE: 16 TIs 100-5000ms, TE=11ms, TR>5s, 90° flip. MOLLI: 2 inversion sets of 3 and 5 images, 75% partial Fourier, TImin=110ms with 80ms increment, 35° flip, TE/ TR=1.3/2.9ms, simulated HR=60bpm. SASHA: singleshot SSFP images from 10 consecutive heartbeats with incremented TI spanning the RR interval in the last 9 images (no saturation in the first image), 70° flip, TE/ TR=1.3/2.6ms, full k-space, simulated HR=60bpm. T₂: spin-echo (SE) with 7 TEs 11-200ms. Simulations: Bloch equation simulations of MOLLI and SASHA were performed in MATLAB using actual acquisition and physiology parameters and SE measured T₁ and T₂ values.

In-Vivo

For 10 healthy volunteers (5 male, 28.8±6.6yrs), blood and myocardial T₁s were measured using MOLLI and SASHA (parameters as above) in a mid-ventricular short-axis slice at baseline and 20 minutes following 0.1mmol/kg Magnevist.

Results

In blood-like phantoms with long T_2 (179-196ms), SASHA and MOLLI T₁s agree well with IR-SE (0.7 $\pm 0.5\%$ and $2.2 \pm 1.8\%$ absolute difference respectively), while shorter T₂ (46-76ms) tissue-like phantoms have greater underestimation with MOLLI (8.4±3.5%) than SASHA (0.9±0.6%) (Fig. 1). MOLLI simulations predict underestimated T_1 s, with 1.3±0.9% absolute difference from observed values (vertical lines, Fig. 1). SASHA simulations also agree well with observations $(0.8\pm0.5\%)$, not shown). In healthy volunteers (63.3±8.4bpm), MOLLI T₁s also show greater underestimation compared to SASHA in tissue than blood, although the difference is larger than observed in phantoms or predicted by simulations in all cases (Table 1).

Conclusions

MOLLI significantly underestimates T₁s in shorter T₂ tissue-like phantoms but less so in longer T₂ blood-like phantoms, as predicted by simulations. Similar trends were observed in-vivo with MOLLI, although with greater T₁ underestimation (compared to SASHA) than predicted. SASHA had good agreement with IR-SE T₁ phantom measurements and simulations and can be acquired in less time than MOLLI.

¹Department of Biomedical Engineering, University of Alberta, Edmonton, AB, Canada

Funding N/A

Full list of author information is available at the end of the article



© 2012 Chow et al; licensee BioMed Central Ltd. This is an open access article distributed under the terms of the Creative Commons Attribution License (http://creativecommons.org/licenses/by/2.0), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.



parameters is also shown, with the difference between simulated and actual results indicated with a vertical line for each phantom.

Table 1 Comparison of MOLLI and SASHA T_1 values in 10 healthy volunteers prior to and 20 minutes following 0.1 mmol/kg Magnevist. All comparisons between MOLLI and SASHA are significant (p<0.01, two-tailed, paired Student's t-test).

T ₁ [ms]	Myocardium (mean±std)		Blood (mean±std)	
	Baseline	Post Gd (20 min)	Baseline	Post Gd (20 min)
MOLLI	935.5±24.9	614.4±33.8	1514.1 ±107.5	524.9±55.2
SASHA	1175.2 ±27.6	752.9±48.2	1687.4±85.8	542.6±56.3

Acknowledgements

We acknowledge the work of Dr. Andreas Greiser in programming the MOLLI sequence used.

Author details

¹Department of Biomedical Engineering, University of Alberta, Edmonton, AB, Canada. ²Stephenson CMR Centre, University of Calgary, Calgary, AB, Canada. ³Siemens Healthcare, Calgary, AB, Canada.

Published: 1 February 2012

References

- 1. Messroghli DR, et al: MRM. 2004, 52:141-146.
- 2. Chow K, et al: JCMR. 2011, 13(Suppl 1):P31.

doi:10.1186/1532-429X-14-S1-P281

Cite this article as: Chow et al.: T_2 -dependent errors in MOLLI T_1 values: simulations, phantoms, and in-vivo studies. Journal of Cardiovascular Magnetic Resonance 2012 14(Suppl 1):P281.



- 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