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WALKING POSTER PRESENTATION

Correlations and validations of dual-bolus and dual-sequence quantification of first-pass myocardial perfusion CMR in humans and canines

Li-Yueh Hsu^{1*}, Peter Kellman¹, Peter Gatehouse², Hannah M Conn¹, Mitchel Benovoy^{1,3}, Matthew Jacobs^{1,4}, Andrew E Arai¹

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

Background

Dual-bolus and dual-sequence techniques have been proposed to maintain the linearity of arterial input function (AIF) in LV during first-pass CMR perfusion imaging. This study compared myocardial blood flow (MBF) estimates using both techniques in humans and in a canine model.

Methods

CMR perfusion imaging was performed in six canines and thirty patients at 1.5T using dual-bolus (0.005 and 0.05 mmol/kg Gd-DTPA) and dual-sequence techniques with 1RR, 90° composite pulse, 50° SSFP readout, saturation recovery 90 ms, TR 2.4 ms, TE 1.2 ms, matrix size 128 \times 80. A low TE 0.6 ms, low-resolution 64 \times 48 FLASH

image series was also acquired. The AIF was measured from the low-dose high-resolution series (DB), the high-dose low-resolution series (DS), and the high-dose high-resolution conventional single-bolus series (SB). Myocardial time intensity curves were analyzed on a midslice based on 6 transmural sectors and quantified by model-constrained deconvolution.

Results

In canine experiments, the Pearson's correlation between microsphere MBF and DB (r = 0.89, figure-a) and DS (r = 0.89, figure-b) estimates were excellent with small bias in Bland-Altman analysis (bias -0.19 and -0.73 ml/g/min). There was an excellent correlation and reasonable bias between DB and DS estimates of MBF



¹National Heart Lung and Blood Institute, National Institutes of Health, Bethesda, MD, USA

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



© 2016 Hsu et al. This is an Open Access article distributed under the terms of the Creative Commons Attribution License (http:// creativecommons.org/licenses/by/4.0), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited. The Creative Commons Public Domain Dedication waiver (http://creativecommons.org/publicdomain/ zero/1.0/) applies to the data made available in this article, unless otherwise stated. in canines (r = 0.97, figure-c) and patients (r = 0.98, figure-d). However, SB overestimated MBF (bias +2.50 ml/g/min, p < 0.001) despite a good correlation with microspheres (r = 0.88). In human studies, SB also overestimated MBF versus either DB or DS estimates (bias +1.47 and +1.38 ml/g/min, p < 0.001).

Conclusions

The MBF estimates by DB and DS are suitable for CMR perfusion quantification. However, SB experiments have large errors in MBF quantification with the doses and parameters studied.

Authors' details

¹National Heart Lung and Blood Institute, National Institutes of Health, Bethesda, MD, USA. ²Royal Brompton Hospital, London, United Kingdom. ³Polytechnique Montreal, Montreal, QC, Canada. ⁴Catholic University of America, Washington DC, USA.

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