Metabolite-Cycled, ECG-Triggered and Navigator-Gated ^{1}H MRS With Optimised Image-Based B_0 Shimming Achieves High Spectral Quality In the Myocardium at 3T

Donnie Cameron[1], Ariane Fillmer[2], Andreas Hock[2], Thomas W. Redpath[1], Michael P. Frenneaux[1], Dana Dawson[1], and Anke Henning[2,3]

[1]The University of Aberdeen, Aberdeen, United Kingdom, [2]Institute for Biomedical Engineering, University and ETH Zurich, Zurich, Switzerland, [3]Max Planck Institute of Biological Cybernetics, Tübingen, Germany

INTRODUCTION: Cardiac ^{1}H magnetic resonance spectroscopy (MRS) is a powerful tool for assessing myocardial lipid content, with the potential to provide further significant insight in the pathophysiology of heart failure. However, spectral quality can be severely impaired by cardiac and respiratory motion, as well as static field inhomogeneities, which are particularly problematic at higher field strengths. This explains the dearth of reports on ^{1}H cardiac MRS at 3T. B_0 homogeneity can be improved using image-based shimming[1] and motion effects can be reduced through ECG triggering and navigator gating[2], which facilitate consistent positioning of the volume of interest (VOI), but motion also causes dynamic B_0 fluctuations, which increase with increasing B_0 field strength. These disrupt the phase and frequency of consecutively acquired signals, leading to incoherent averaging. Such problems can be mitigated through the use of frequency alignment and phase correction in conjunction with metabolite-cycled, non-water-suppressed MRS[3]. Metabolite cycling[4] (MC) is a technique that utilises a broadband inversion pulse to invert metabolites both upfield of water and downfield of water, in alternate acquisitions. This approach has several advantages over water-suppressed methods: the unsuppressed water peak serves as a strong reference for frequency and phase correction and for quantification; there is no need for time-consuming water suppression (WS) optimisation procedures; and the MC pulse is short compared to WS, allowing short trigger delays to be used. **This work** presents a novel combination of ECG-triggering, navigator-gating, frequency alignment and phase correction, for superlative motion compensation, with an MC ^{1}H MRS method and an improved 'Localised B_0 Shimming Tool'[1,5], and demonstrates the feasibility of MC in the heart.

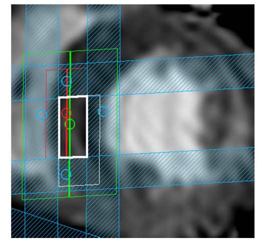


Figure 1. *Localisation of the MRS voxel (white) in the septum. IVS slabs are shown as blue bars.*

METHODS: The B_0-shimmed, ECG-triggered, navigator-gated and metabolite cycled ^{1}H MRS method was optimised in 25 healthy volunteers using a Philips Achieva 3.0T TX system (Philips Healthcare, Best, NL) with a 6-element cardiac coil. The optimised method was then applied to 5 volunteers (mean age=27, range=21-39 years) for initial validation. We performed double-triggered ^{1}H PRESS acquisitions in the interventricular septum, localising the voxel (dimensions: 40×20×10 mm^3) with a set of retrospectively-ECG- and navigator-gated bSSFP cine images (Fig. 1), which were also used to establish a suitable cardiac trigger delay. Prior to MRS, the whole heart was first-order B_0 shimmed using an image-based 'Localised B_0 Shimming Tool'. The PRESS sequences (min. TR=2500 ms, TE=41 ms, acquisition time = 512 ms) were ECG-triggered to end systole and navigator-gated with a large gating window to accept all acquisitions. Preparatory phases (resonance frequency determination, power optimisation) were also navigator-gated and ECG-triggered. In addition, a previously implemented[6] inner volume saturation (IVS)[7] scheme was used to mitigate spectral contamination from outwith the VOI. For spectral quality comparison, MC PRESS was performed with 256 NSA in 4 volunteers and with 512 NSA in a fifth volunteer, in whom an additional 256 NSA WS PRESS acquisition was also applied (with otherwise identical parameters). Scan durations: MC256 & WS~11 min, MC512~21 min. During post processing in MRecon (Gyrotools, Zurich, CH), the MC FIDs from the 512 NSA acquisition were processed in 3 different ways: (i) frequency-aligned, phase- and navigator-corrected; (ii) navigator-corrected only; and (iii) not corrected. FIDs from the 256 NSA MC and WS acquisitions were fully motion-corrected. Fig. 2 demonstrates the effect of frequency alignment and phase correction. Navigator correction was achieved through the use of a histogram of navigator positions (Fig. 3) to establish the end-expiration window (median of the histogram ± 2.5 mm). Any averages acquired outside of this window were discarded. Spectra were then trimmed to either 128 (for 512 MC/ 256 WS) or 64 (for 256 MC) NSA, by randomly removing excess FIDs, and manual averaging was performed. The resulting spectra were analysed in jMRUI 3.0[8], where AMARES was used to determine FWHM, SNR and Cramér-Rao lower bounds (CRLB) for each metabolite and spectra were apodised (5Hz Gaussian) and zero-filled to 4096 points for display.

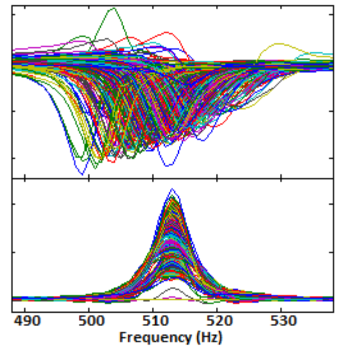


Figure 2. *Plots of real nav-corrected MC spectra which demonstrate the effect of frequency alignment and phase correction: top, uncorrected; bottom, fully corrected.*

RESULTS: Table 1 shows FWHM, SNR and CRLB data for trimethyl-ammonium (TMA), creatine (Cr) and lipid peaks from the fully corrected MC acquisitions; results are seen to improve, as expected, with increasing NSA. In the 128 NSA MC acquisition the navigator contrast boundary position ranged across 38.5 mm (-5.9 to 32.6 mm, median 9.3 mm from navigator centre) with a concomitant frequency shift of range 28 Hz; in addition, a second Cr peak at 4 ppm was resolved, a peak that is often obscured by the water resonance. This peak could be analysed along with the Cr resonance at 3.1 ppm for more-quantitative monitoring of heart failure. Fig. 4 shows MC spectra with different degrees of motion correction and a WS spectrum for comparison. Note that TMA and Cr were not resolvable in the non-motion-corrected spectra and the WS spectrum shows poor SNR, possibly due to the effect of broadband WS on the navigator.

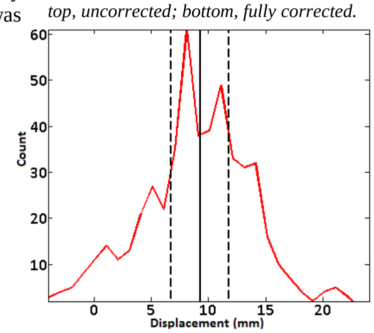


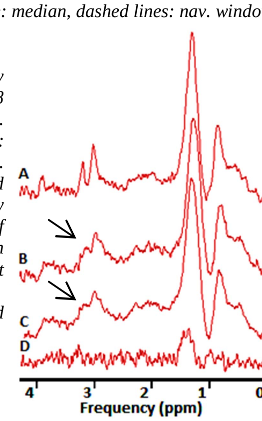
Figure 3. *Plot of nav. distribution vs. position Solid line: median, dashed lines: nav. window.*

CONCLUSION: We have demonstrated that MC ^{1}H MRS, combined with navigator gating, ECG triggering, phase correction and frequency alignment, is feasible at 3T, compares favourably to other reported 3T spectra[2], and is able to outperform WS ^{1}H MRS in terms of SNR and spectral quality. Additionally, problems associated with WS, such as stringent trigger delays or WS affecting the reliability of the navigator, are avoided through the use of MC ^{1}H MRS.

Table 1.

Metabolite	MC – 64 NSA FWHM (MEAN [SD] Hz)	MC – 64 NSA SNR (MEAN [SD])	MC – 64 NSA CRLB (MEAN [SD] %)	MC – 128 NSA FWHM (Hz)	MC – 128 NSA SNR	MC – 128 NSA CRLB (%)
Cr (CH_2), 4 ppm	-	-	-	9.8	1.4	17.4%
TMA, 3.3 ppm	18.8 [6.8]	4.7 [1.8]	14.0 [5.3]	10.2	2.5	12.6%
Cr(CH_3), 3.1 ppm	13.5 [1.7]	2.3 [1.9]	28.6 [20.6]	11.8	5.5	7.2%
Lipid (CH_2-C=C), 2 ppm	26.0 [12.7]	3.7[1.7]	16.1 [4.6]	44.9	8.5	12.5%
Lipid ((CH_2)n), 1.4 ppm	24.1 [11.8]	17.1 [18.2]	5.1 [1.2]	25.4	27.7	1.8%
Lipid (CH_3), 0.9 ppm	20.6 [8.7]	18.7 [26.1]	3.8 [1.0]	22.5	26.8	5.4%

Figure 4. ***A****: Fully corrected MC, 128 NSA.* ***B****: MC, nav. correction only.* ***C****: MC, no correction.* ***D****: Fully corrected WS. Arrows show poor resolution of TMA and Cr in spectra without frequency alignment and phase correction.*



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