Myocardial Fat Content: Single Breath-Hold ^{1}H-MR Spectroscopy at 3 T

B. Rial[1], S. Neubauer[1], M. D. Robson[1], and J. E. Schneider[1]
[1]Cardiovascular Medicine, Oxford University, Oxford, Oxfordshire, United Kingdom

Introduction

The accumulation of lipids in the myocardium is associated with impaired myocardial function [1]. Recent studies have shown that lipids can be quantified non-invasively in the human heart by ^{1}H-MRS using cardiac triggering and respiratory motion correction [2-3]. However, poor signal-to-noise ratio (SNR), failures in water-suppression, baseline problems and poor spectral resolution are common problems encountered in the study of myocardial metabolism using ^{1}H-MRS. In addition, some techniques employed for the correction of motion artifacts from cardiac and respiratory motion are not easily implemented in combination with MRS in the clinical scanners [3-4]. Here we propose a simple and easily automated method to asses the myocardial lipid content during a single breath-hold using phased-array coils and short echo times at 3 T.

Methods

Measurements were performed in healthy volunteers on a 3 T (Siemens Magnetom Tim, A Trio, Erlangen, Germany) using the body coil in transmit mode and 6-channel anterior phased-array body coil and a 24-channel posterior phased-array spine coil. Mid-ventricular long and short-axis cine series were acquired to determine the trigger delay for the different temporal phases of the cardiac cycle and investigate the reproducibility of the myocardial water amplitude with different trigger delays. A 20 x 8 x 35 mm STEAM voxel was planned on the corresponding cine frame (Figure 1). Shim currents were adjusted based on a GRE dual echo 3D imaging data set. All sequences were cardiac triggered. Two different experiments were performed: (1) Ten sets of 7 unaveraged water-suppressed spectra were collected in 10 consecutive breath-holds at the beginning of diastole and another series 100 ms later. (2) The single breath-hold spectra acquisition consisted of: one unsuppressed spectrum (TR = 4 R-R) and three WET water-suppressed spectra (TR = 2 R-R) at mid-diastole. The other parameters of the customised STEAM method were: TE = 10 ms, TM = 7 ms, BW = 2000 Hz, 2048 data points. All slice-selective pulses in the water-suppressed scans were not centred at water, but at 3 ppm to minimize spatial mismatch because of the chemical shift displacement. The results of 3 single breath-hold acquisitions were compared to a constructively averaged spectrum obtained from 10 breath-holds in 2 volunteers. Individual coil signals were combined within Matlab using specially written modules. Frequency correction was performed between breath-holds prior to data averaging and spectra were quantified using the AMARES algorithm [6] included in the jMRUI package.

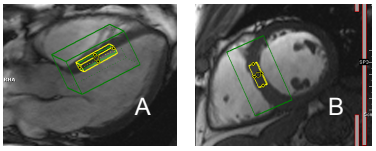

Figure 1 Cine frames at mid-diastole used for positioning the VOI in the septum. (A) Long-axis and (B) short-axis.

Results

For five volunteers the coefficient of variation of the water amplitude in 10 consecutive breath-held unsuppressed water scans acquired at start-diastole was 70 ±13 % higher than at mid-diastole. Also, acquisition at mid-diastole resulted in a 3-fold increase in water amplitude and, therefore, SNR. Figure 2A shows the spectra measured in a single breath-hold at mid-diastole in the interventricular septum of a healthy volunteer in approximately 10 seconds. The signal at ~1.3 ppm was assigned to myocardial lipids. Reproducibility of the ^{1}H-MR spectra in a single breath-hold within the same subject was good for the lipid peak, as percentage of water peak (average coefficient of variation between 3 measurements was 13 %). The mean lipid content was 0.90 ± 0.22 % (interindividual variation 24 %). Figure 2B compares the averaged spectra acquired in a single breath-hold, 10 breath-holds and a water-unsuppressed scan. Figure 2C illustrates the need for a water suppression scheme to eliminate baseline distortions improving spectral quality for quantification. Although the 10 breath-hold acquisition produced a 49 % SNR improvement (calculation based on Cramer-Rao lower bounds), the mean lipid content (0.88 ± 0.08 %) was very similar to the value obtained during a single breath-hold (0.90 ± 0.22 %).Importantly, the single breath-hold acquisition provided about 30-fold decrease in acquisition time.

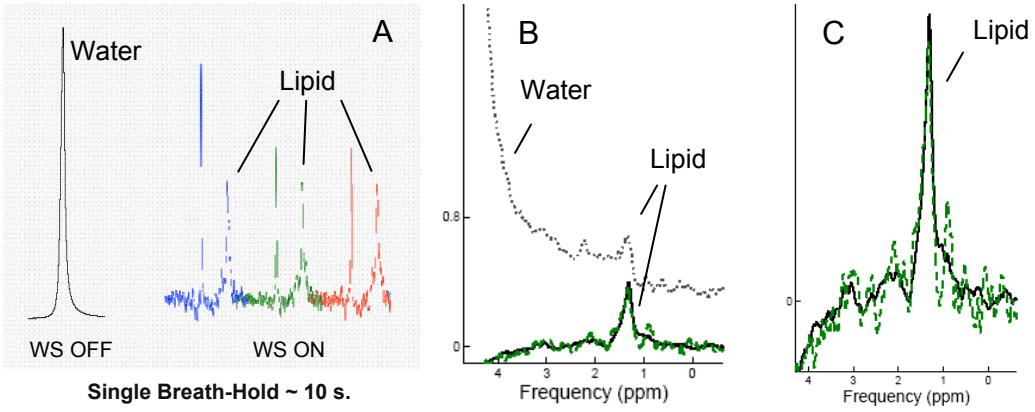

Figure 2 Proton spectra from a 5.4 ml volume in the septum of a healthy volunteer. (A) Spectra acquired during a single breath-hold scan: a single water signal and 3 water-suppressed signals. (B) Dashed grey spectrum shows the small lipid signal in the presence of a large water signal. Suppression of the water signal results in the black (10 breath-holds) and dashed green (single breath-hold) spectra. (C) Metabolites zoom. Water suppression eliminates baseline distortion leading to a reliable detection and quantification of the lipid signal.

Discussion

In conclusion, reliable quantitative ^{1}H-MRS of the human heart *in vivo* is feasible in a single breath-hold at 3 T when the lipids are at or above the normal levels, acquiring both water and water-suppressed lipid signals in less than 15 seconds. This may provide a valuable and quick tool to investigate cardiac lipid metabolism. Work is in progress to acquire data in more subjects and in patients with abnormal lipid metabolism.

References: [1] S. Sharma et al., Faseb J 18 (14), 1692 (2004). [2] R.W. van der Meer, et al.,European heart Journal 29 (12), 1516 (2008). [3] A. Redheuil et al., 12th Annual SCMR, p150 (2009). [4] M. Schar et al., Magn Reson Med 51 (6), 1091 (2004). [5] R.W. van der Meer, et al., Radiology 245 (1), 251 (2007). [6] L. Vanhamme et al., J Magn Reson 129 (1), 35 (1997).