How to do Cardiac Single Voxel ^{1}H Spectroscopy

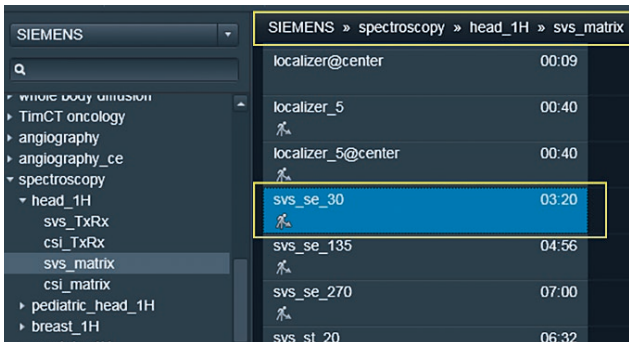
Morten Asp Vonsild Lund, M.D.[1–3]; Karen Kettless, B.Sc. Hons, PgD[4]; Xiaoying Cai, Ph.D.[5]; Maria-Alexandra Olaru, Dr. rer. nat.[6]

[1]Department of Cardiology, Rigshospitalet, Copenhagen University Hospital, Copenhagen, Denmark
[2]The Children's Obesity Clinic, Department of Pediatrics, Holbæk Hospital, Holbæk, Denmark
[3]Department of Biomedical Sciences, University of Copenhagen, Copenhagen, Denmark
[4]Siemens Healthineers, Ballerup, Denmark
[5]Siemens Healthineers, Boston, MA, USA
[6]Siemens Healthineers, UK

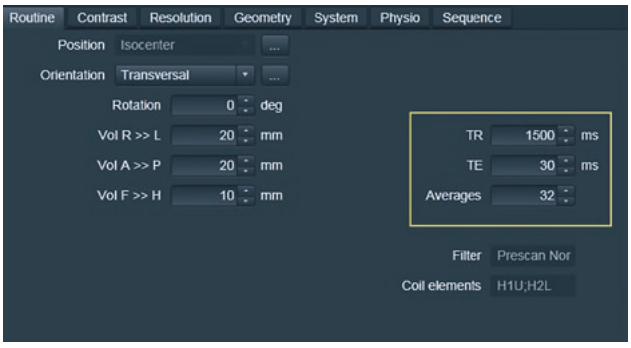
Introduction

Cardiac MR is an established method for assessing cardiac function and morphology. In the meanwhile, MR can be utilized to assess metabolism using spectroscopy, which offers many advantages compared with other imaging modalities including that it does not require additional tracer and it is free of ionizing radiation. Furthermore, in vivo spectroscopy has been used to assess cardiac energetics and myocardial metabolism. For ^{1}H spectroscopy of the heart, the commonly studied metabolites are triglycerides and creatine. Alterations in the level of these metabolites are reported in various conditions such as cardiomyopathy, heart failure, and type 2 diabetes mellitus [1, 2].

^{1}H cardiac spectroscopy can be performed using either a spin-echo (PRESS) or stimulated-echo (STEAM) excitation scheme. In this article, we describe the procedures of performing single voxel ^{1}H spectroscopy in the myocardium at our site using a MAGNETOM Aera 1.5T and a MAGNETOM Prisma 3T (Siemens Healthcare, Erlangen, Germany). The protocols we use are based on the standard PRESS sequence supplied with the Siemens Spectroscopy package and are tailored for the quantification of myocardial triglycerides content. Specifically, the integral areas of lipids and water resonance respectively are assessed via two separate scans and used to calculate the triglycerides-to-water ratio.



1 Location of the PRESS protocol used as the starting point to set up the desired protocols.



2 Routine tab of the protocol.

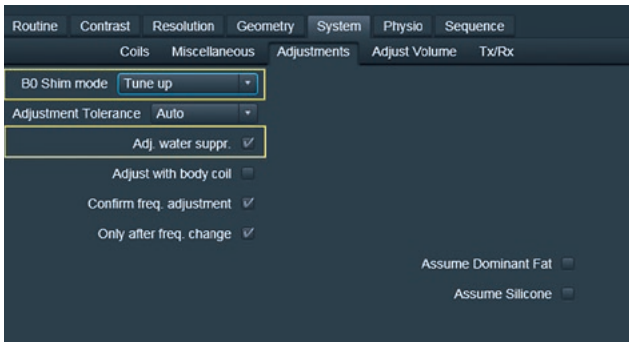
Protocol setup

A copy of the standard PRESS protocol (Fig. 1) is used as the starting point and modified to utilize both ECG and respiratory triggering along with changes to other acquisition parameters. Two protocols are set up with the first for assessing lipid resonances and the second for water resonance. Specific parameter selections for the lipid protocol are:

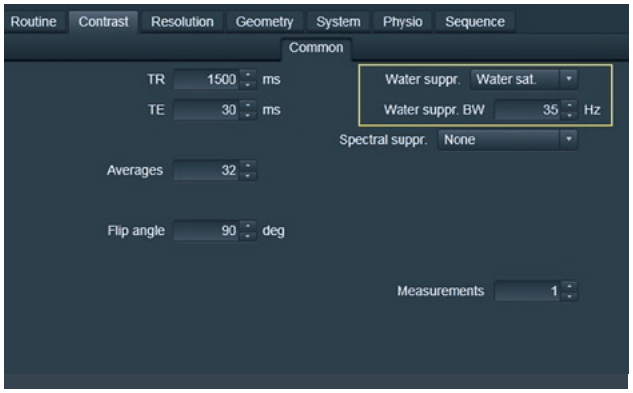
1. **Routine:** Adjust the voxel size, repetition time (TR), echo time (TE) and number of Averages (Figure 2). The voxel of interest is to be placed on the septum and approximately a size of 20 x 20 x 10 mm^3 is suitable. The choices of TR and TE need to be considered in the context of the relaxation rates of myocardial triglycerides and water, respectively. It is important to use the shortest echo time (TE) allowed by the sequence properties and a repetition time (TR) long enough to allow for full magnetization recovery. Typical parameters are TE 30 ms, TR at least 1500 ms.
2. **Contrast:** Make sure **Water sat.** is selected for water suppression (Fig. 3). With this option, a chemical shift selective (CHESS) based water suppression scheme is employed, with a typical excitation bandwidth of 35 Hz at 3T.
3. **Resolution:** Adjust the vector size to 512 for a shorter and more suitable readout duration. It is also recommended to utilize **PreScan Normalize**.
4. **Physio:** Switch on ECG triggering in **Signal1** and respiratory triggering in PACE to reduce adverse impacts of cardiac and respiratory motion to the spectrum.
5. **System:** Switch the adjustment mode to **Tune up** as the B_0 shimming will be performed via manual adjustments. Also make sure that **Adjust for water suppression** is ticked.
6. **Sequence:** Set the excitation frequency via **Delta Frequency** and adjust other parameters (Fig. 5). The frequency of the excitation pulse is centered on the interval of values corresponding to the triglyceride resonances (0.9–1.3 ppm) and it is expressed as a relative number (Delta frequency) in reference to the value corresponding to the water frequency.

After the lipid protocol is set up, the water reference protocol can be set up via:

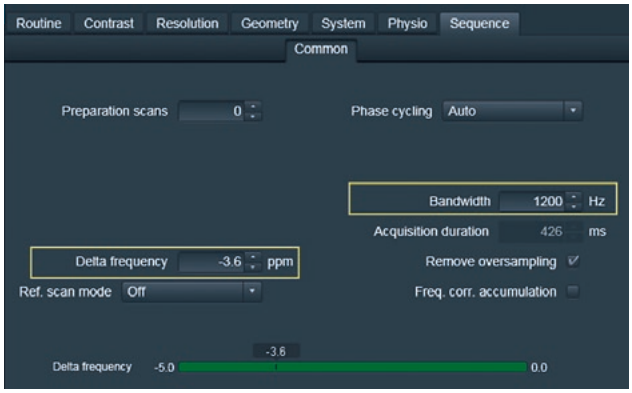
1. Make a copy of the lipid protocol.
2. Switch water suppression off in **Contrast** tab.
3. Adjust Delta frequency to 0 ppm in **Sequence** tab.
4. Make sure the B_0 shim mode is still **Tune up**.



4 Parameters in System/Adjustments.



3 Contrast tab used in the protocol employed for myocardial triglyceride detection. Important parameters are Water suppr. and Water suppr. BW.



5 Parameters regarding spectroscopy acquisition in Sequence tab. For detection of triglycerides resonances, the Delta frequency should be set on the triglyceride resonance, e.g. -3.6 ppm. For water resonance, this parameter should be set 0 ppm.

Planning the acquisition

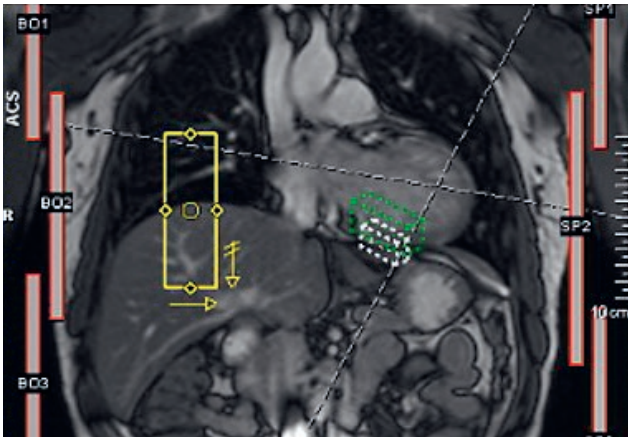
It is recommended to use the following images as reference images for planning: 3-plane localizer, short-axis stack (SAX) cine and 4-chamber cine. Planning of the voxel position and navigator can be properly using the following steps:

1. Convert the reference images to create non-distortion corrected version, as spectroscopy planning cannot be performed on images post distortion correction.
2. Load the reference images and then open the spectroscopy protocol.
3. Place the navigator (yellow box) on the liver dome and the Adjustment Volume (green) around the voxel of interest (Fig.6).
4. The voxel of interest is typically positioned in the inter-ventricular septum. The position and size of the voxel should be adjusted so that it is sufficiently large but not contaminated by the surrounding blood pool. Using as reference images (SAX) and 4-chamber cine images, position the voxel in the mid ventricular septum, avoiding the cardiac blood pool (Right-Click on LV Mid SAX: Shift to Image Plane and then make Perpendicular (Fig. 7).
5. Adjust the ECG trigger delay so that the RF pulses are trigged to end-systole. For the water reference protocol, the trigger delay is simply the time to end systole, which can be determined from the cine acquisitions. However, for the lipid protocol, the duration of water saturation needs to be taken into consideration, i.e. [trigger delay] = [time to end systole] - [water saturation duration]. The duration of water saturation train is approximately 192 ms.

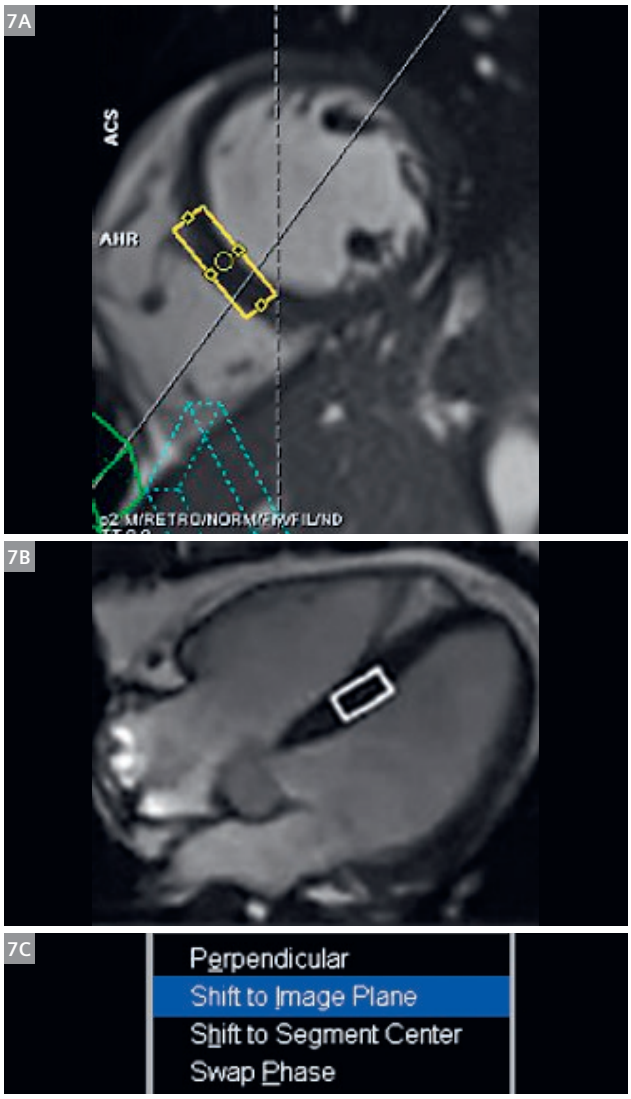
B_0 shimming via manual adjustments

Optimal field homogeneity is required for successful acquisition of quality spectroscopy data. We recommend that the values of the shim currents are adjusted interactively prior to the acquisition, via the Manual Adjustments window. The B_0 shim could be performed via the following steps:

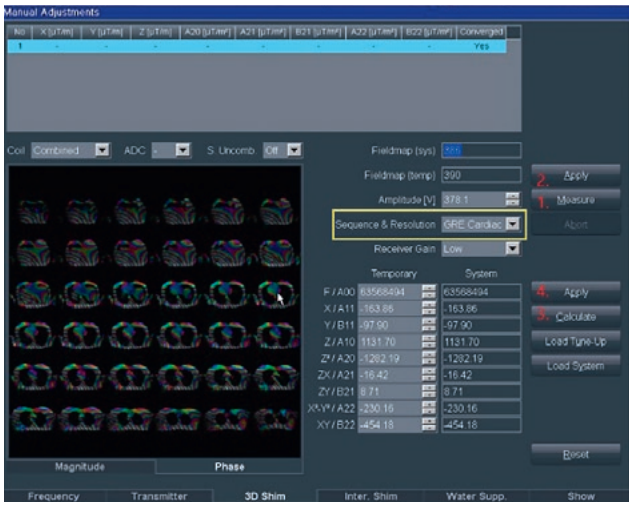
1. Set up the adjustment volume on the voxel of interest.
2. Access Manual Adjustments via the **Options** drop-down menu.
3. In 3D Shim, switch the **Sequence&Resolution** option to **GRE Cardiac** and perform shimming (Fig. 8).
   The GRE cardiac method is a gradient-echo based protocol optimized for cardiac magnetic resonance that allows the user to acquire field maps of the volume of interest.



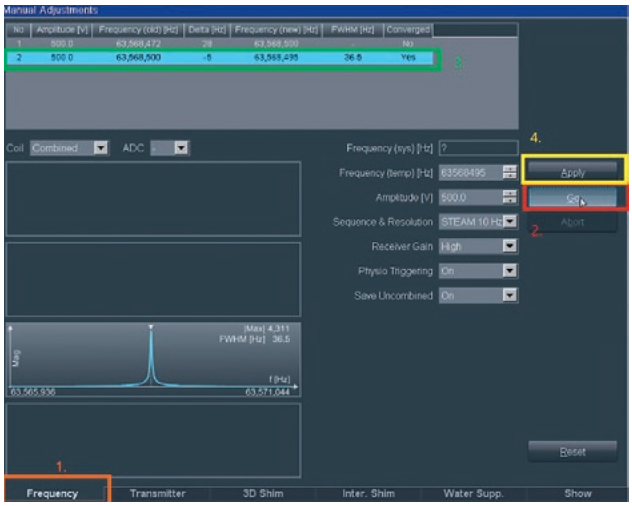
6 Positioning of the respiratory navigator.



7 Voxel geometry and placement on SAX view (7A) and 4-chamber (7B) view. The **Shift to Image Plane** function can be used to facilitate voxel localization (7C).



8 3D Shim steps: Measure a new field map (1), apply the field map as the current system field map (2), calculate new values for the shim currents based on the new field map (3) and apply them to the system (4).



9 Assess the field inhomogeneity via (1) switching to Frequency tab and (2) measuring the current FWHM. (3) The FWHM is displayed in the table and next to the water resonance. (4) If the FWHM is acceptable, confirm/accept the current shimming.

4. Switch to Frequency tab and measure the current line width at half height (typically referred to as FWHM – Full Width at Half Max) as shown in Figure 9. The purpose is to assess the field inhomogeneity after shimming. Ideally, the FWHM should be below 25 Hz, B_0 inhomogeneities cause line broadening in the spectra.
5. If the FWHM is too high, repeat step 3 and 4. Otherwise, click **Apply** to confirm the current shimming and close the manual adjustments window.

Summary

Cardiac magnetic resonance spectroscopy can be performed with combined ECG and respiratory triggering using a standard Siemens 1.5T or 3T MR system with no additional equipment or coils required.

References:

1 McGavock JM, et al. Cardiac steatosis in diabetes mellitus: a 1H-magnetic resonance spectroscopy study. Circulation 2007; 116:1170–1175
2 Faller KME, et al. 1H-MR spectroscopy for analysis of cardiac lipid and creatine metabolism. Heart Fail Rev 2013; 18:657-668
3 Wei J, et al. Myocardial steatosis as a possible mechanistic link between diastolic dysfunction and coronary microvascular dysfunction in women. Am J Physiol Heart Circ Physiol 2016; 310: H14–H19

The .exar1 protocols for
3T MAGNETOM Prisma (software version *syngo* MR E11E)
and
1.5T MAGNETOM Aera (software version *syngo* MR E11C)
are available for download at:

www.siemens-healthineers.com/magnetom-world
> Clinical Corner > Protocols > Cardiovascular MRI

Contact

Morten Asp Vonsild Lund, M.D.
Department of Cardiology
Rigshospitalet
Copenhagen University Hospital
Blegdamsvej 9
2100 Copenhagen
Denmark
morten.lund@sund.ku.dk