Semi-Quantitative Liver Spectroscopy with a Transmit/Receive Body Resonator at 3T

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Abstract

Abdominal spectroscopy has experienced a major push with the introduction of clinical high field MR systems. Clinical use of abdominal spectroscopy requires an acquisition and processing protocol, which is easy to use while reliably providing good spectral quality and a useful quantitative result. This can mainly be achieved with use of refined acquisition and post-processing protocols. We will demonstrate how the acquisition of liver spectra at 3T with a transmit/receive body resonator can be optimized for clinical use at 3T. A method for improved reconstruction including a semi-quantitative approach will be introduced.

Introduction

Although the increasing field strength helps to compensate for the limited metabolite concentrations and poor spectral resolution with broad lines, as found in the abdomen, spectroscopy of organs like liver, kidney or pancreas is still not in clinical use [1, 2]. This is due to the difficulty of acquiring data with acceptable quality, and a missing approach for the quantitative evaluation of the data. The unreliability of spectral quality can be related to the acquisition or the processing of the data, or to the organ itself. As the organ is given, and a major change of the acquisition sequence considered to be too time consuming, we have focused on parameters more easily accessible. We will show, that by careful preparation of the patient and an optimized acquisition and processing protocol, liver spectra can be successfully and reliably acquired in a clinical environment. A method for relative quantification of the spectra will also be introduced.

Methods

All experiments were performed on a GE Signa 3T (*General Electric Medical Systems, Milwaukee, WI, USA*), MRI scanner running under software revision VH3 (Fig.1). The integrated body resonator was used for signal transmission and reception. No additional surface or volume coils were used. A compression belt to reduce abdominal motion was put on all patients and volunteers as shown in Fig.2. Single voxel PRESS spectra of 8ml volume were acquired with TE=35ms, TR=2000ms, 128 averages and 16 additional unsuppressed water reference lines. The automatic pre-scanning for transmitter, receiver, center frequency and shim adjustments was split into two automatic and two manual phases: 1..Manual center frequency adjustment 2. Automatic setting of transmitter and receiver gains 3. Automatic shim calibration under breath hold 4. Final manual center frequency adjustment. During an initial testing phase, the length of the possible breath hold period was determined. Total acquisition time was split into consecutive blocks to match the length of a breath hold period.

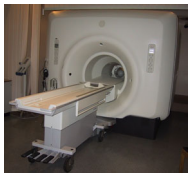

Fig.1: GE Signa 3T whole body scanner

Fig. 2: Compression belt for respiratory motion reduction.

The raw data was processed on a Sun Ultra 60 workstation (*Sun Microsystems Inc., Mountain View, CA, USA*), using a dedicated software package (*Spectroscopy Analysis of General Electric* = SAGE). Two methods for processing were initially considered: (1) clustering the time resolved acquisition into single frames with identical resonance frequency (and phase) of the water peak and removing those lines which do not match specific selection criteria or (2) frequency-shifting and phasing all frames to match the same phase and frequency before averaging all metabolite acquisitions [3]. Even though the second approach does not take local motion (resulting in spatial miss-registration) into account, the approach was chosen to gain the higher SNR while accepting lower spatial specificity. Referencing to residual internal water was applied to correct for phase, frequency, and residual eddy current distortions. The data was reconstructed using a 5 Hz Gauss filter prior to the FFT, providing typical results as shown in Fig.3.

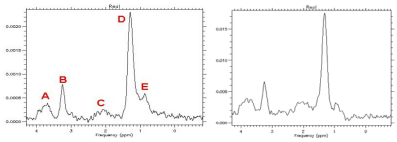

Fig.3: Typical liver spectrum (left), repeated acquisition four weeks later (right).

Semi-quantitative analysis was performed using a macro language integrated into SAGE for frequency domain fitting. First, complex data were corrected for DC offsets. During three initial passes, the amplitude, linewidth, frequency and phase of the resonance-peaks (labeled A-E in Fig.3) were adjusted using a Marquardt-Levenberg fitting (MLF) algorithm with several constraints with regard to the starting frequency and linewidths of the peaks. The parameters for all other metabolites were kept constant while fitting one specific group. In a final MLF fitting pass the amplitude was kept constant while optimizing the other parameters for all metabolites in one fitting routine. Finally, metabolite ratios were calculated and metabolite areas were normalized to the unsuppressed internal water signal.

Results

Liver spectra were acquired on 10 healthy volunteers and 10 patients. The use of a compression belt, a modified protocol of prescan and scan as well as an optimized processing protocol were all prerequisites for successful acquisition of liver spectroscopy data. Reproducibility was assessed by repeated measurements (Fig. 3). The compression belt as well as 20-30 sec breathhold periods were tolerated by all patients and volunteers. The reconstruction algorithm yielded significant improvements in spectral quality as shown in Fig.5. All lipid-resonances could be separated into the methyl- (CH_3-, 0.9ppm) and methylen protons (-CH_2-CH_2-, 1.2ppm -CH=CH-CH_2-, 2.0-2.3ppm) as shown in Fig.3, C-E, except of a case with a necrotic liver tumor shown on the right in Fig.4. The resonance at 3.2ppm assigned to choline-containing compounds and betaine (Fig.3, B) showed inter-individually varying amplitudes. The resonance at 3.7 ppm was present in the majority of the spectra, which may result from glycogen/glucose (Fig.3, A).

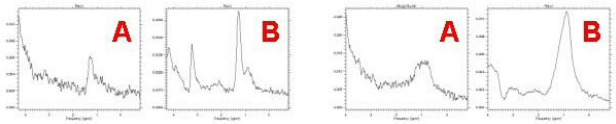

Fig.4: Comparison of processing results following the standard processing protocol optimized for (A) neurospectroscopy and (B) using the optimized processing algorithm. Left showing liver hepatocellular carcinoma (HCC), right necrotic liver tumor after therapy.

Semi-quantitative MLF provided acceptable fit results showing much good agreement with the measured. Alternatively data were analyzed using "Peak Table Analysis" (PTA) of SAGE, which is optimized for a simple quantification of brain spectra with their much smaller line-width. The average residual after MLF was about 3-6 times smaller compared to the residual after PTA (Fig.5).

Discussion

This study shows that single voxel proton spectra can reliably be acquired at 3T using the body resonator when applying appropriate protocols for acquisition, processing, and quantification. The use of phased-array coils suggested by others [3] to increase SNR, requiring more complicated data-recombination approaches, might not be necessary. A standardized clinically practical and automated protocol as suggested here covering acquisition, processing, and quantification would provide a solid base for clinical abdominal spectroscopy.

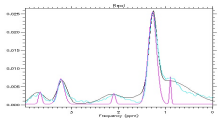

Fig.5: Marquardt-Levenberg fit result (black) of liver spectrum compared to original data (blue) and fitting result provided by "Peak Table Analysis" of SAGE (red).

Reference

[1] Tyszka JM et al. MagnResonMed 1998; 39: 1-5.
[2] Dixon RM et al. MagnResonMed 1995; 31: 482-487.
[3] Katz-Brull R et al. MagnResonMed 2003; 50: 461-467.