Metabolite cycled single voxel ^{1}H spectroscopy at 9.4T

Ioannis Angelos Giapitzakis[1], Sahar Nassirpour[1], Nikolai Avdievich[1], Roland Kreis[2], and Anke Henning[1,3]

[1]*Max Planck Institute for Biological Cybernetics, Tuebingen, Baden-Wuerttemberg, Germany,* [2]*Departments of Radiology and Clinical Research, University of Bern, Bern, Switzerland,* [3]*Institute for Biomedical Engineering, UZH and ETH Zurich, Zurich, Switzerland*

INTRODUCTION: **Non-water suppressed** metabolite cycled proton magnetic resonance spectroscopy (MC ^{1}H-MRS) has been proven to enhance the frequency resolution and the signal to noise ratio (SNR) of the spectrum at 3 Tesla [1-2]. This is achieved by enabling shot-by-shot frequency and phase alignment due to the simultaneous acquisition of water and metabolite spectra. Previously the adiabatic inversion pulse for MC ^{1}H-MRS was optimized to exploit these advantages for application in the human brain at 9.4T [3]. In this work, we examine the performance of STEAM [4] based MC ^{1}H-MRS [3,5] compared to water suppressed ^{1}H-MRS using a numerically optimized short water suppression (WS) sequence with respect to spectral resolution and signal-to-noise ratio (SNR) in the human brain at 9.4T.

METHODS: All experiments were carried out using a 4 channel transceiver array coil [6] connected to a whole body 9.4Tesla Magnetom SIEMENS scanner. For ^{1}H MRS localization a STEAM sequence (TE/TM/TR: 10/50/3000ms, receiver bandwidth: 8 kHz) was used. An optimized water suppression scheme consisting of 7 excitation pulses and orthogonal spoiler gradients was developed according to the limits of our gradient system resulting in a WS scheme of 190 ms duration and 250Hz bandwidth. The WS sequence was optimized for different T_1 relaxation times (ranges from 1 to 3sec), as well as for different B_{1+} values (assuming 50% inhomogeneity) using a constrained optimization algorithm ("fmincon", MATLAB, The Mathwors, Natick, USA). The post processing of the data included in the given order: frequency alignment using the water reference [7], averaging, ECC [8], channel combination [9], zero filling using factor of 2, filtering using Gaussian and Lorenzian filters. The performance of the WS scheme was tested on a spherical spectroscopy phantom filled with an aqueous solution of acetate and lactate (fig. 1). The WS STEAM (number of averages (NEX): 64, 20x20x20mm^3) was then compared with the MC STEAM ^{1}H-MRS sequence (fig. 2) using an in-house "Braino"-like phantom containing brain metabolites in physiological concentrations in order to verify that both methods produce spectra with similar line-widths and signal to noise ratio (SNR) in absence of physiological motion. For eddy current correction (ECC) of the water suppressed data an interleaved non-water suppressed spectrum was acquired every 8 acquisitions (NEX: 16). Finally, both sequences were applied on healthy volunteers (fig. 3-5) (NEX: 128-320, voxel size: 15x15x15mm^3) placing a grey matter voxel in the occipital lobe. The optimized MC inversion pulse (IP) for the resulting B_{1+} of 22μT had a duration of 23ms and a frequency offset of 350Hz.

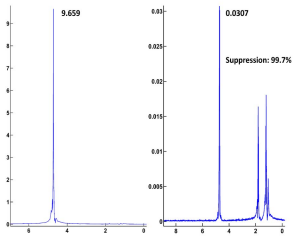

Fig 1: STEAM sequence with (left) and without (right) WS.

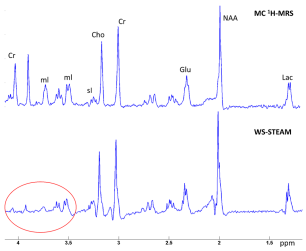

Fig 2: MC ^{1}H-MRS (up) and WS-STEAM (down) on a "Braino" phatom. The red circle indicates the frequency region affected by the WS

RESULTS-DISCUSSION: The comparison of MC and WS ^{1}H-MRS acquired from a phantom with brain metabolites showed that both of them gave similar linewidths (N-Acetyl-Aspartate (NAA) linewidth: ~7.5Hz) and SNR (fig. 2). In addition, the MC spectrum is free of gradient modulation sidebands and eddy current artefacts, while the WS-STEAM spectrum was slightly distorted. Regarding the in vivo data (fig. 3), the simultaneously acquired water reference of MC data allowed for frequency and phase alignment of the different averages (fig. 4) leading to a line width of 25.9Hz and SNR of 38.2. In addition, the MC technique provided a WS factor of 99.8%. On the other hand, theWS spectrum resulted in a line width of 28.9Hz (+3Hz difference), SNR of 33.3 (-5dB difference) and a WS factor of 99.7%. The difference in SNR and linewidth is mainly produced by physiological motion (e.g. breathing, blood flow) as well as motion of the volunteer demonstrating the importance of the simultaneously acquired water reference spectrum both for the ECC and correct averaging of the acquisitions (fig. 4). Finally the MC data enabled the reconstruction of high frequency resolution spectra similar with other studies conducted on 9.4T [10]. To sum up, **THE CONCLUSIONS OF THIS STUDY** are: 1) MC ^{1}H-MRS enables phase and frequency alignment of individual acquisitions as well as ECC of the spectrum at 9.4T 2) MC ^{1}H-MRS performs better in terms of SNR and line width and thus effective spectral resolution compared to WS ^{1}H-MRS and 3) MC ^{1}H-MRS results in a free of gradient modulation sidebands and eddy current artefacts spectrum and excellent WS performance

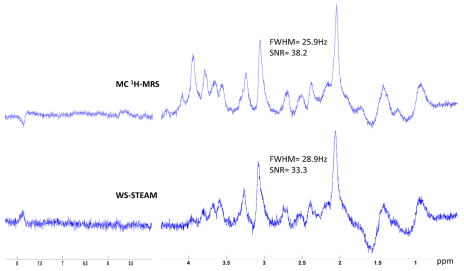

Fig 3: MC ^{1}H-MRS (up) and WS-STEAM (down) on volunteer 1. No filtering was applied on the data. NEX: 128, voxel volume: 3.375ml

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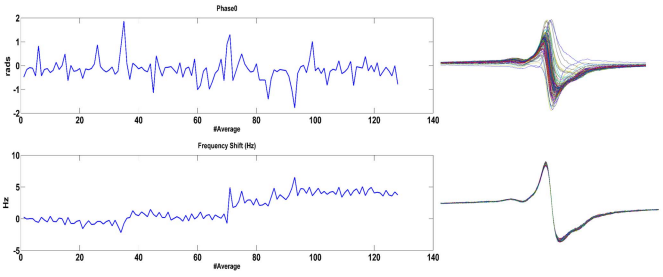

Fig 4: Left: Zero phase (up) and frequency (down) correction using the water spectrum. Right: Averages before (up) and after (down) frequency alignment

Fig 5. *MC ^{1}H-MRS resulted in a spectrum with high frequency resolution allowing the detection of several metabolites. Asp: aspartate; PE: phosphoryl-ethanolamine; Gln: Glutamine; Glu: glutamate; Tau: taurine; Glx: Gln + Glu; Cho: choline; mI:myo-inosotol; sI: scyllo-inosotol; Cr: creatine; NAA: N-acetyl aspartate; GABA: γ-aminobutyric acid. A Gaussian filter (standard deviation: 40ms) and a lorenzian filter were applied (-11.4Hz) for volunteer 2 and 3. Averages with different number of acquisitions are shown.*