Sensitivity encoded VAPOR-FIDLOVS at 7T: mapping the hidden metabolites.

A. Henning[1], A. Fuchs[1], J. B. Murdoch[2], D. Foxall[2], and P. Boesiger[1]

[1]Institute for Biomedical Engineering, University and ETH Zurich, Zurich, Switzerland, [2]Philips Medical Systems, Cleveland, Ohio, United States

Introduction

MR spectroscopic imaging is one of the most promising applications of 7T human MR systems. Theoretically, compared to lower field strengths, the SNR gain and improved spectral resolution at 7T should enable mapping of a larger number of metabolites, as well as providing a significant increase in spatial resolution. However, to take full advantage of the high field strength, severe technical challenges related to it have to be solved. One major confound is the low maximum achievable B_1 field strength, resulting in a considerable decrease in bandwidth for conventional amplitude modulated RF pulses. In combination with the large increase in spectral separation, an undesirably large chemical shift displacement artefact occurs. Previously, it has been demonstrated that frequency modulated RF pulses can overcome this problem [1-3]. However, to achieve a sufficient bandwidth, long pulse durations are required, and the achievable minimal echo time becomes very long for conventional localization methods. To make matters worse, T_2 relaxation times are significantly shorter at 7T compared to 3 T or 1.5 T due to an increased effect of susceptibility differences. At T_E = 50 ms, most fast relaxing metabolite signals have disappeared already and hardly any effective SNR gain can be found for the remaining ones.

In this work, it is therefore proposed to solve these contradictory problems by direct acquisition of the free induction decay (FID) using a broadband frequency-modulated excitation pulse for slice-selection [2,3] and a numerically optimized outer-volume-suppression scheme based on broadband saturation pulses [1,4] for skull-lipid suppression and in-plane localization (*FID* acquisition *L*ocalized by *OVS*). The striking signal-to-noise ratio (SNR) and spectral resolution that result, enable unambiguous quantification and mapping of 15 metabolites, including glutamate, glutamine, NAAG, GABA, taurine, GSH, aspartate, scyllo-inositol and PE. The high SNR is also the basis for highly spatially resolved metabolite mapping. For that, FIDLOVS can be easily combined with acceleration techniques as sensitivity encoding [7,8].

Materials and Methods

FIDLOVS has been implemented on a 7T Philips Achieva human MR system using a broadband frequency modulated excitation pulse (fremex05) [2], created using an iterative design strategy [3], and saturation pulses with polynomial phase response (PPR) [1], based on the Shinnar-LeRoux transformation. As with the SELOVS sequence proposed previously [4], B_1 sensitivity was reduced by applying two cycles of eight overlapping OVS saturation bands, which adapted an elliptical shape covering the skull. Flip angles of the saturation pulses were numerically optimized, taking into account the T_1 relaxation of skull lipid and the saturation band crossings [4]. To minimize residual water signal and gradient-induced water sidebands, an eight-pulse T_1- and B_1-insensitive VAPOR [5] sequence was interleaved with the OVS pulses for water suppression. Measurements were performed using either a Philips birdcage transmit-receive head coil or the combination of a Nova Medical birdcage volume coil for excitation and a 16 channel head array for reception. B_1 was limited to 10 µT and the specific absorption rate (SAR) was limited to 1.8 W / kg in both cases. Third-order shimming based on the FASTERMAP algorithm [6] was available. Non-accelerated FIDLOVS-MRSI was compared to four-fold accelerated sensitivity-encoded FIDLOVS-MRSI [7,8]. Spectra were phased by cyclic shifting in order to compensate for the linear phase introduced by the 5.5 ms delay in the start of sampling. Metabolite maps were created from highly spatially resolved datasets using simple peak integration. LC-model fitting using a simulated metabolite basis set [GAMMA] was applied to FIDLOVS data with medium spatial resolution.

Results and Discussion

Direct FID acquisition minimizes SNR loss due to T_2 relaxation as well as phase evolution (and signal cancellation) in coupled spin systems. As a result, fifteen metabolites per MRSI voxel could be quantified using LCModel with Cramer-Rao lower bounds < 20 (Figure 1). Hence, metabolite maps of NAA, NAAG, PCh, GPC, Cr+PCr, mI, scyllo-inositol, glutamate, glutamine, GABA, GSH, taurine, aspartate, PE and lactate can be created. Spectral quality was decent over the entire field of view, including cortex voxels (Figure 1,2). Differences between grey and white matter are evident in the high–resolution metabolite maps (Figure 2). The signal intensity of residual skull lipid in cortex voxels was comparable to that of the metabolites of interest and did not disturb interpretation and quantification of these spectra. Although conventional water suppression using frequency selective excitation and dephasing with consecutive frequency selective inversion and dephasing, that was applied before OVS, is insufficient and results in gradient induced water sidebands, the water suppression quality improved ten-fold using VAPOR (Figure 3). Third-order shimming using FASTERMAP converged robustly, a prerequisite for taking advantage of the good spectral separation at 7T. In spite of the conservative B_1 limit of 10 µT, both the excitation pulse as well as the saturation pulses generated a chemical shift displacement between water and fat less than 15% of the slice thickness. This enabled precise localization and robust skull lipid suppression. Due to the strict SAR limitation of 1.8 W / kg, the minimum repetition time was 4500 ms using slice selective excitation and 2 x 8 saturation pulses with a maximum duration of 6 ms each. Compared to lower field strength, the scan time was therefore significantly prolonged, especially for high spatial resolutions. In order to compensate for this effect, four-fold acceleration by sensitivity encoding was applied. The SNR loss due to the sensitivity encoding was moderate and seems to confirm theoretical predictions for high field strength (Figure 4). However, precise quantitative evaluation is still necessary.

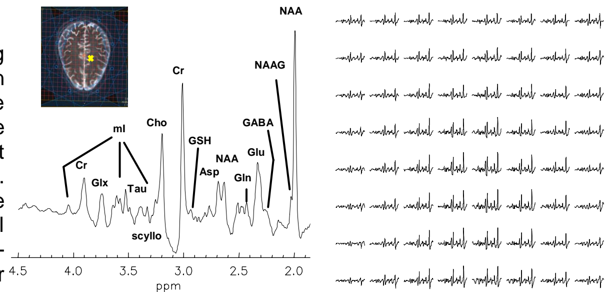

Figure 1 *FIDLOVS: single spectrum (left, no apodization) and high spectral quality in the entire FOV (right). Quantification of 15 metabolites per voxel at a medium spatial resolution (voxel size:10x10x10 mm; T_R=4500ms) was possible.*

Figure 2 *FIDLOVS: metabolite maps based on peak integration at high spatial resolution (voxel size: 6.5 x 6.5 x 10 mm; T_R=4500 ms): GM – WM differences are visible.*

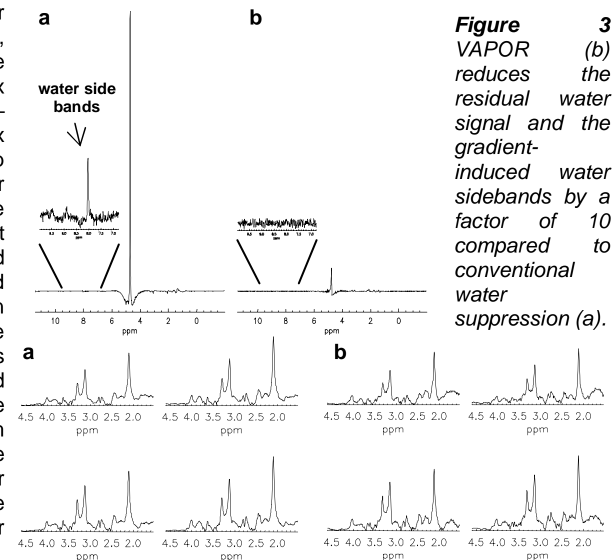

Figure 3 *VAPOR (b) reduces the residual water signal and the gradient-induced water sidebands by a factor of 10 compared to conventional water suppression (a).*

Figure 4 *non-accelerated FIDLOVS (a) versus SENSE-FIDLOVS (reduction factor: 2x2) (b): moderate SNR loss.*

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