Improved spRARE at 9.4T through water suppression with MEGA

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Introduction Spectroscopic RARE (spRARE), which was first introduced at 4.7 T [1], is a spectroscopic imaging pulse sequence that allows a short acquisition time and a good spectral resolution due to effective homonuclear decoupling. Previous studies have shown that spRARE can be implemented at 7 T and 9.4 T [2, 3]. However, several requirements such as high B_1 homogeneity and short echo spacing are mandatory at high magnetic field strength to avoid any J-evolution in the RARE module that would lead to signal loss of coupled resonances. Moreover, in these implementations CHESS or VAPOR schemes were used for water suppression (WS) before signal excitation. Consequently, as spRARE is a long echo-time sequence, the water signal may relax during the echo-time and a subsequent re-excitation in the RARE module would compromise efficient water suppression. Due to the spectral encoding scheme, an unstable or high residual water signal leads to increased noise and ringing artifacts in the spectra. The first aim of the present study was therefore to improve WS in order to reduce the aforementioned effects by implementing for the first time the MEGA WS scheme [4] in spRARE. The second aim was to assess the efficiency of spRARE at 9.4T in avoiding any J-evolution after spectral encoding by comparison of *in vitro* data with spin simulations and to determine the optimal spectral encoding time for myo-inositol, glutamate and glutamine detection.

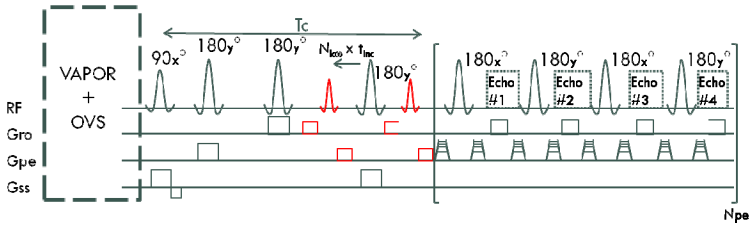

Figure 1 *Scheme of the spRARE sequence. Two 5 ms water selective refocusing pulses surrounded by spoilers (in red) were added around the chemical shift encoding pulse in order to remove all water components that may have relaxed during the long echo time.*

Methods All experiments were performed in a 9.4 T magnet (Varian/Magnex) with a quadrature transceive 25-mm diameter volume RF coil. SpRARE was implemented as previously described [3] with non-selective 180° pulses in the RARE module in order to reduce signal loss through the echo train. In order to improve water suppression, two 5-ms MEGA water-suppression pulses surrounded by spoiler gradients were added to the sequence (Fig. 1).

In vitro spectra were acquired in single high concentrated metabolite solutions or in a phantom containing: taurine, glutamine, glutamate, N-acetyl-aspartate, creatine, myo-inositol and choline with concentrations of 10-90 mM. The following acquisition parameters were used: number of spectral points $N_{k\omega}$: 370 or 480, constant spectral encoding time Tc=114 or 136 ms, TR=2 s, 1 average, matrix size 32x32, FOV 35x35 mm^2 and 1.5 mm slice thickness. Quantum-mechanical simulations based on the density matrix formalism were performed to simulate the metabolite signals acquired with spRARE.

Results and discussion The optimized WS allowed the acquisition of spectra without any residual water signal, which lead to a visible decrease in the background signal compared to spectra acquired only with VAPOR water suppression (Fig.2). This decrease in background signal reflects the reduction of noise and ringing artifacts caused by the residual water signal. Moreover, a good signal localization as well as an efficient homonuclear decoupling was achieved for all investigated metabolites (Fig.3). A comparison of the acquired spectra with the spin simulations demonstrated no loss of the major coupled resonance signals for any metabolite, which confirmed that J-evolution was minimized after spectral encoding (results for myo-inositol are presented in Fig.4). Moreover, 114 ms was determined with spin simulation as the optimal spectral encoding time for myo-inositol, glutamate and glutamine signal detection.

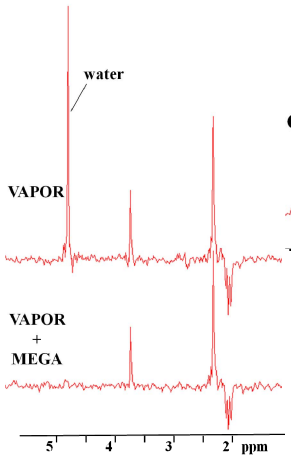

Figure 2 *Spectra of two localized glutamate maps acquired with and without MEGA in addition to VAPOR (Tc=136ms). A complete removal of the water peak at 4.7ppm was obtained with MEGA.*

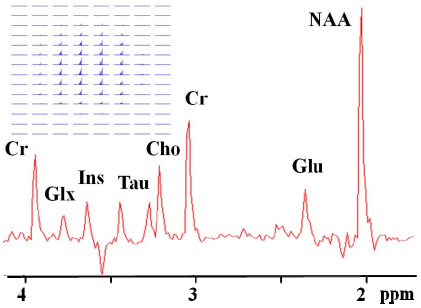

Figure 3 *Metabolite localized map and representative spectrum acquired at Tc=136ms. All major resonances are detectable in the spectrum.*

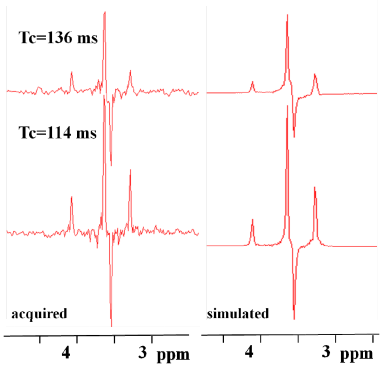

Figure 4 *Measured (left) and simulated (right) myo-inositol spectra at the optimized 114ms and at an arbitrary 136ms spectral encoding time.*

Conclusion MEGA water suppression was implemented in spRARE, which allowed the complete removal of the residual water signal, while the efficient detection of the coupled metabolites by spRARE at 9.4T was demonstrated.

References [1] Dreher W, Leibfritz D, 2002, Magn Reson Med; 47(3):5238. [2] Dreher W, Leibfritz D, Proc. ISMRM, 2010,#3377. [3] Craveiro M et al, Proc. ESMRMB, 2011,#633. [4] Mescher M et al., 1998, NMR Biomed, 11:266–272.

Acknowledgements: Supported by the EPFL-Merck-Serono Alliance, the Centre d'Imagerie BioMédicale (CIBM) of the UNIL, UNIGE, HUG, CHUV, EPFL and the Leenaards and Jeantet Foundations.