Magnetization Exchange (MEX) MRI: a Clinically Viable Protein-based Imaging Method

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Introduction: In previous works we showed the possibility of obtaining a protein-based image, based on the selective filtering of NMR signal of water protons in chemical exchange with heavy macromolecular structures (1). This was achieved by generating a double quantum coherence on the immobile protons, which is then transferred to the bulk water protons through magnetization transfer (MT) where the MT operates through either dipole-dipole interaction or chemical exchange. A strong requirement for the DQF-MT sequence to generate signal is that the RF pulses be short, generally less than 100us. In this work we show a different approach for imaging water protons exchanging with macromolecular structures by using selective excitation of the macromolecules with pulses available on human scanners. The pulse sequence (figure 1) consists of preparation of the magnetization with a composite pre-pulse, devised to null the magnetization, and a longitudinal magnetization evolution period (t_{ZQ}), during which the longitudinal magnetization coherence is built.

The images are obtained by *subtraction of the results of running the above sequence under two different conditions:*

a) Relatively long (0.4-0.8ms) 90° pulses are adjusted so that they that tilt *only the magnetization of the water to the transverse plan*. The signal is subsequently suppressed by the crusher gradients. The macromolecular magnetization remains parallel to the magnetic field. Thus, magnetization-transfer from the macromolecules to the water occurs during the period t_{ZQ}. A typical length of such 90° pulses in biological tissues is in the range of 0.4-0.8 ms.

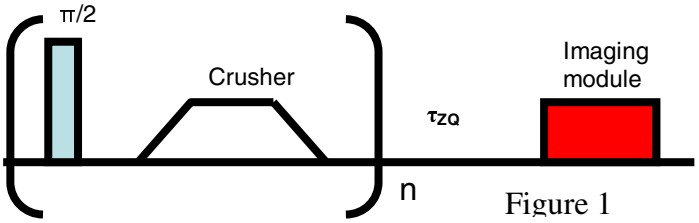

Figure 1

b) Pulses that suppress the magnetizations of the water and macromolecules. Typical examples are short 90° pulses of a length in the range of 0.2ms. On this time scale the macromolecules are excited to a sufficient degree so that spin diffusion along with the application of crushers bring about the suppression of the magnetizations of the water and the macromolecules. Since in the clinical setup the macromolecules are selectively excited (pulse lengths of 0.2ms are available) a full suppression can be achieved only after a repeated application of r.f. pulses followed by crushers.

The subtraction described above *eliminates from the spectrum or image contributions that originate from components that do not exchange magnetization with water*. In this work we show preliminary results that demonstrate it is feasible to implement this sequence on a clinical scanner and that the resulting image, in this case of a human brain, is particularly sensitive to regions rich in macromolecular structures (in this case, the myelin in the white matter of the human brain).

Materials and Methods: Experiments were performed on a 3T Philips Intera scanner. The pre-pulse used consisted of 8 π/2 pulses, with 6ms delays between them. Crusher gradients with varying intensities along different axes were applied after each pulse to eliminate any residual transverse magnetization. The zero-quantum coherence delay (t_{ZQ}) was varied as described below. The imaging sequence used was a RARE (TSE factor = 15, TE/TR = 80/4000ms.). Data matrix: 128x128, FOV of 230mm in plane and a slice thickness of 5mm. The sequence was tested on a healthy volunteer using the transmit/receive head coil. Pulse width of the selective excitation was 0.7ms and that of the non-selective excitation was 0.2ms.

Results: in figure 2a, the corrsponding T_2 Weighted image of figure 2c is shown. Two regions of interest (ROIs) on which the preliminary ROI analysis was carried out are encircled by yellow mark: one ROI is centered on a white matter region, and the other one on cortical gray matter. Figure 2b shows the MEX signal intensity measured for the white and gray matter ROIs as a function of t_{ZQ}. It is seen that the white matter ROI generates a significantly stronger contrast than the gray matter ROI, and that the maximum difference is obtained at about t_{ZQ}=400ms. Figure 2c shows the actual MEX image obtained at the optimal conditions of t_{ZQ}=400ms. It is seen that CSF in the inter-hemispheric fissure and in the sulci is not visible in the MEX image.

In **conclusion**, the MEX sequence provides a clinically-feasible approach to magnetization-exchange imaging, and can thus be used to non-invasively explore tissue-specific chemical exchange processes, and hopefully enable compartment preferential MR acquisition, based on macromolecular content.

Reference: 1. Neufeld A, Eliav U, Navon G. Magn Reson Med 2003;50(2):229-234.