Quantitative proton MRSI of the human cervical spine at 3.0 Tesla.

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Introduction

Proton magnetic resonance spectroscopy (MRS) of the spine is a relatively unexplored area, which promises to provide important biochemical information related to myelination and axonal integrity. Spinal cord pathology is known to cause significant clinical disability in many disorders, including multiple sclerosis (MS) and amyotrophic lateral sclerosis (ALS). Although difficult (because of the spinal cord's small size and deep location), single voxel MRS and 1D-MR spectroscopic imaging (MRSI) of the cervical spine have been previously described [1,2]. This abstract describes continued technique development for 1D-MRSI of the human cervical spine and medulla oblongata at 3T, including use of the spine water signal as an internal intensity reference for metabolite concentration quantification.

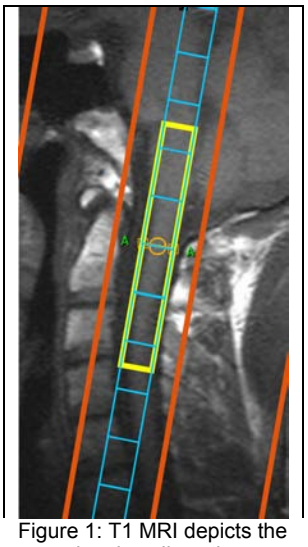

Figure 1: T1 MRI depicts the press box in yellow, the MRSI voxels in blue and the anterior and posterior OVS slabs in orange.

Materials and Methods

Images were acquired on a Philips Intera 3.0 Tesla scanner with a 2 channel flexible surface coil array. Tissue was excited by the body coil with a PRESS sequence to select a 1.0-1.3x1.2-1.3x8 cm volume. High bandwidth, frequency-modulated refocusing pulses were used to minimize the chemical shift artifact associated with slice selection. In addition, the 90˚ excitation pulse (which has a superior slice profile to the 180˚ pulses) was applied in the direction of the longest axis of the press box. The pontine-medullary junction served as a landmark to position the top of the volume (Figure 1). Exceeding the longest dimension of the press box equally on each side, a FOV of 24 cm was chosen. One-dimensional spectroscopic imaging was performed with a 16-step phase encoding scheme, TR=3 sec, TE=144 ms, nominal voxel size 1.8 to 2.5 cc, variable number of averages per step, maximum 64. Frequency selective hyperbolic-secant pulses[3] were used to achieve water and lipid suppression. Four outer-volume saturation (OVS) pulses were applied (left, right, anterior, posterior). Scan time was 18 minutes. Magnetic field homogeneity was optimized with high order shimming. Subsequently, an unsuppressed MRSI data set was recorded without water suppression (2 averages, scan time 1 minute). This scan provides information about relative coil sensitivity, B_0 field homogeneity and reference data for quantification.[4] The complex raw data of two fast gradient echo scans were recorded in order to reconstruct B_0 and B_1 field maps. The channel with the higher B_1 sensitivity profile was identified and the corresponding MRSI data processed and quantified. Metabolite peak areas were determined for N-acetyl aspartate (NAA), creatine (Cr) and choline (Cho). Quantification is based on formula 1:

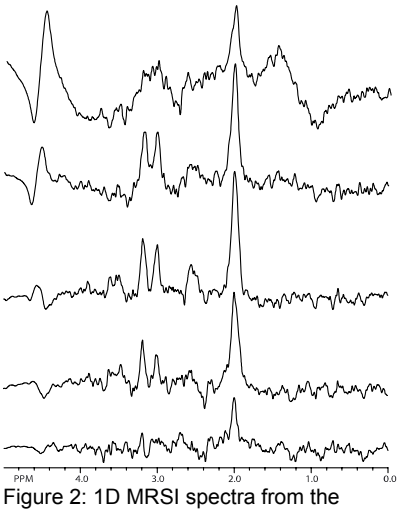

Figure 2: 1D MRSI spectra from the medulla (top) to the upper cervical spinal cord in one volunteer.

$$[\mathrm{M}] = \frac{A_{\mathrm{M}}}{A_{\mathrm{H_2O}}}[\mathrm{H_2O}]\frac{c_{\mathrm{H_2O}} n_{\mathrm{H_2O}}}{c_{\mathrm{M}} n_{\mathrm{M}}}\frac{\exp(-TE/T_{2,\mathrm{H_2O}})(1-\exp(-TR/T_{1,\mathrm{H_2O}}))}{\exp(-TE/T_{2,\mathrm{M}})(1-\exp(-TR/T_{1,\mathrm{M}}))}$$

M: metabolite, Cho, Cr, NAA, [M]: concentration of metabolite, c_{H20}, c_M: number of protons in water/metabolite resonance, [H_2O]: cerebral water content (mmol/gm wet weight), A_M: peak area of metabolite, A_{H20}: peak area of unsuppressed water, n_M, n_{H20}: number of acquisitions of metabolite/water spectra, $T_{1,M}$, $T_{2,M}$: T_1/T_2 specific for metabolite M. The number of proton resonances in the water peak is 2, in the NAA, Cr and Cho, 3, 3 and 9, respectively. T_1 and T_2 values of specific metabolites were taken from the literature, as measured in the brain. Spectra were obtained from 8 healthy adult volunteers (mean age 30.5±4.6 years, 2 females), one of which was evaluated twice and another one three times.

Results

Figure 2 shows spectra obtained with the described protocol. The locations from where the spectra were obtained are shown in Figure 1. Of the 16 phase encoded voxels, only 4 are expected to contain the full signal, namely voxels 7-10 of 16. Only half of the tissue contained in the adjacent voxels 6 and 11 is excited and thus the signal to noise expected to be reduced. Figure 1 shows that in 3 of the 4 fully excited voxels NAA, Creatine and Choline can be clearly identified. Ratios were determined: NAA/Cho=2.32±1.15, NAA/Cr=2.81±1.36 and Cho/Cr=1.26±0.42. Quantification of spectra yielded concentrations: NAA=10.20±7.30, Cr=6.37±4.99 and Cho=1.90±1.30 mmol/kg wet weight.

Discussion

The measured metabolite concentrations are similar to those previously reported in brain in the literature [5], but are somewhat lower than those reported in the previous SV study of the cervical spine [1].As we used slightly larger dimensions of the press box in the axial plane, one possible cause is partial contribution of CSF to the signal. The variability of current measurements is rather large, and this may be attributable to lower signal-to-noise due to the small size of the cord, and possible other problems such as signal loss due to CSF pulsation and/or other motion.[1] We found the combination of two flexible surface coils, that can be positioned close to the skin surface of the neck, superior to the use of phased-array or volume head coils. Careful positioning of the RF receiver coils was, however, critical in order to obtain a successful scan. Other potential sources of error in the current study could include variations in water content or relaxation times, which were taken from the brain literature, since metabolite T1's and T2's have not yet been reported for the spine at 3T.

Acknowledgment

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References

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