Functional MRS in the Anterior Cingulate

Reggie Taylor[1,2], Peter Williamson[1,3], and Jean Théberge[1,2]

[1]*Medical Biophysics, University of Western Ontario, London, ON, Canada,* [2]*Medical Imaging, Lawson Health Research Institute, London, ON, Canada,* [3]*Psychiatry, University of Western Ontario, London, ON, Canada*

Introduction: Proton magnetic resonance spectroscopy (1H-MRS) is a valuable tool for non-invasively determining *in vivo* human brain metabolite concentrations. By suppressing the brain water and appropriately applying slice select gradients it becomes possible to attain metabolic information from a voxel (volume element) in a localized region of the brain. The signal to noise ratio (SNR) in ^{1}H-MRS is inherently low and so it often requires very long scan times to average together enough spectra to achieve an adequate SNR. Due to this temporal limitation MRS has historically been performed as an analysis of a single spectrum over a broad time scale. It has been demonstrated recently that at an ultra-high magnetic field strength of 7T the SNR is adequate enough to repeatedly acquire MRS spectra providing a time course of metabolic information[1]. This technique is termed functional MRS (fMRS). fMRS can provide valuable information that conventional MRS cannot, such as the dynamic rate of concentration change. To this author's knowledge it has only ever been demonstrated at 7T in the occipital lobe. This is likely due to its close proximity to the brain, along with its robust response to visual activation. The anterior cingulate cortex (ACC) is a more challenging brain region to get quality reliable data from due to its close proximity to the sinuses. To functionally activate the ACC is also a little more difficult. However, it has potential to provide very important information into psychiatric disorders where metabolites such as glutamine have been shown to be abnormal[2]. The purpose of this work is to demonstrate that fMRS is possible in the ACC during the performance of a task. The Stroop task is a common assessment in neuropsychiatry where the subject is shown a list of the names of colours that are written in a different colour ink. The subject is then asked to read aloud the colour of the ink. It has previously shown that there is significant left ACC activity upon performance of the Stroop task[3], and so subjects will perform this task while in the 7T.

Methods: Three subjects were scanned on an Agilent/Magnex 7-T head-only scanner with Siemens AC84 head gradient coil, located at the Center for Functional and Metabolic Mapping (CFMM) at the University of Western Ontario, using a 15ch-transmit/receive head coil described in the literature[4]. A voxel was placed in the left ACC after being aligned with anterior-posterior (AP) line in the brain and angled so the voxel would be placed in the same brain area in each person. A STEAM sequence based on the literature[5] was applied with TE=8.1ms, TM=32ms, and TR=3s with VAPOR water suppression and OVS. Prior to acquisition, the voxel was B_1 shimmed, followed by a B_0 shimming using rastamap. The fMRS protocol involved 2 min of rest, then 4 minutes of activation, rest, activation, and rest, totalling 18 minutes. 90 spectra were acquired with 4 averages each (Fig.1) using online averaging, giving us a 12s temporal resolution. The subjects were asked to stare at the word "Rest" on a black screen during the resting period. During the performance of the Stroop task, subjects were asked to lightly mutter their responses to avoid possible motion artefacts while still executing the task. A 16 average water suppressed spectrum was also acquired, along with a 64 average metabolite suppressed spectrum[6] to account for the macromolecules, which would later be modelled into the fitting of the metabolites. Post-processing included QUECC lineshape correction[7] prior to being fit by our time domain fitting algorithm, fitMAN[8]. A time-domain fitting algorithm is useful for fMRS as it returns the amplitude in the time domain. Therefore, the lineshape change due to the blood-oxygen level dependant signal (BOLD) response should not influence our results.

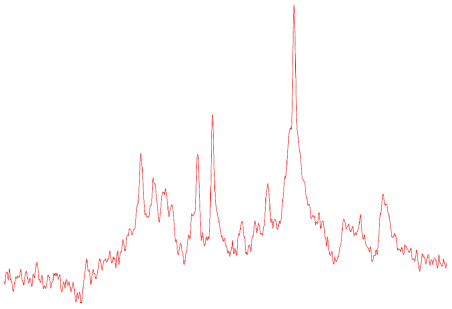

Figure 1. An example spectrum acquired from the left ACC with 4 averages at TR=3s. 5Hz line broadening has been applied.

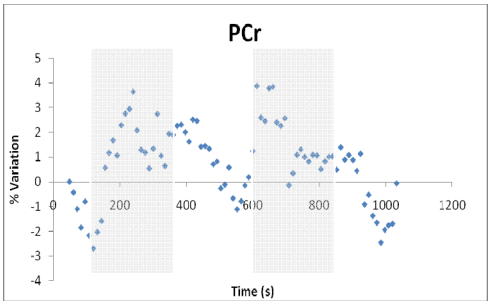

Figure 2. A time course of PCr activation in the ACC during the performance of the Stroop Task. Data points are moving averages of 8 spectra with 4 averages each. The shaded areas indicate activation.

Results and Discussion: With only N=3 and 12s temporal resolution we were able to model the Phosphocreatine response very nicely, as can be seen in Figure 2. It was difficult to reliably extract some of the metabolic patterns similar to what has been seen previously in the occipital lobe from other metabolites. However, with more subjects we would expect to be able to observe other metabolic activations from metabolites such as glutamate, glutamine, aspartate, lactate and glucose. This work will be extended to include more subjects and offline averaging. There appears to be a decrease in signal intensity over the course of the second activation period. This is likely either an attention issue, such that the subjects were getting bored of the Stroop task, or it is more likely a practice effect, such that the subjects got better at the task and so there was less strain on the anterior cingulate. There is still significant activation during the course of the task. This is encouraging, as it seems dynamic metabolite changes can be on the order of minutes[1]. It will be interesting to see how this extends to other metabolites.

Conclusion: We have successfully demonstrated that using fMRS in the ACC it is at least possible to detect PCr changes. There is potential that this technique could provide very useful information on the metabolic dynamics in neuropsychiatric disorders.

References: [1] Mangia et al. *J Cereb Blood Flow Metab* 27: 1055-1063 (2007). [2] Theberge et al. *Am J Psychiatry 160:2231-2233* (2003). [3] Barch et al. *Cerebral* Cortex 11:837-848 (2001). [4] Gilbert et al. *NMR Biomed* 24:815-823 (2011). [5] I. Tkáč and R. Gruetter. *Appl Magn Reson*. 2005 March; 29(1): 139–157 [6] Penner et al. *Proc. Intl. Soc. Mag. Reson. Med.* 18 (2010) [7] Bartha et al. *NMR Biomed* 12:205-216(1999). [8] Bartha et al. *Magn Reson Med* 44:641-645(2000)