Long echo time *in-vivo* spectroscopy without J-modulation

Clark Lemke[1], Aaron Hess[2], Jamie Near[3], Stuart Clare[1], Peter Jezzard[1], and Uzay Emir[1]

[1]*FMRIB, University of Oxford, Oxford, Oxfordshire, United Kingdom,* [2]*OCMR, University of Oxford, Oxford, Oxfordshire, United Kingdom,* [3]*Douglas Institute, McGill University, Verdun, Quebec, Canada*

Target Audience - Scientists interested in spectroscopy of coupled metabolites (GABA, glutamate, glutamine, lactate, etc.).

Introduction – Short echo-time (TE = 1-30 ms) *in vivo* spectra can suffer from baseline contamination arising from lipids and macromolecules[1]. This can lead to significant errors in metabolite quanfitication[2] – especially in disease conditions where baseline priors may be difficult to estimate. One solution is to increase the TE such that the baseline signal has relaxed, as macromolecules have shorter T_1 and T_2 relaxation times compared with metabolites[3]. However, at long TE signal from coupled metabolites, such as glutamate (Glu), is effectively crushed due to J-modulation. While a variety of acquisition techniques can accurately measure coupled metabolites at longer TE, they are generally only able to quantify a small number of metabolites per experiment. Here we present an *in-vivo* validation of a localized method to refocus J-modulation for all coupled metabolites at arbitrary TE using a novel implementation of PRESS-JR[4].

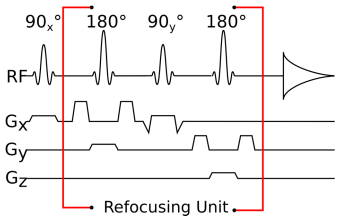

Figure 1: Pulse sequence diagram for PRESS-JR.

Methods – For an AX spin system, insertion of a 90° pulse at the midpoint of a double spin echo will refocus J-modulation caused during the first half of the sequence leading to complete refocusing of J-modulation at the end of the sequence[5-7]. For more complex spin systems (AX_n) there remains a further important constraint: TE must be less than 1/4J for the relevant structure. An elegant extension of this concept recently showed that looping "refocusing units" can circumvent the aforementioned 1/4J constraint in high resolution NMR using the PROJECT pulse sequence[8]. Here we demonstrate the effectiveness of a localized version of PROJECT entitled PRESS-JR as shown in Fig. 1.

Experimental – PRESS (TE = 30 and 60 ms) and PRESS-JR (2-refocusing units, TE = 60 ms) were implemented on a 3T whole body TIM Trio scanner (Siemens, Erlangen) using a 32 channel head coil on 3 subjects in a 20 x 20 x 20 mm voxel in the occipital lobe. Removal of unwanted coherences generated by the J-refocusing 90° pulses was accomplished with outer volume suppression (OVS) and a 4 step phase cycle. Both excitation and refocusing 90° pulses were slice-selective 2.0 ms 5-lobe hsinc pulses and all 180° pulses were optimized 7.2 ms Mao pulses[9]. Basis sets generated in VeSPA[10] were used with LCModel[11] to compare the resulting spectra and simulated macromolecule baseline.

Results – As illustrated in Fig. 2a, both the singlets and multiplets remain upright for both PRESS at TE = 30 ms and PRESS-JR (2-refocusing units) at 60 ms while only the singlets remain upright for PRESS at TE = 60 ms. As expected, the unwanted baseline and macromolecule contribution is smaller for PRESS TE = 60 ms and PRESS-JR, though at TE = 60 ms the baseline is not expected to be fully relaxed. Due to pulse imperfections and differences in coherence pathways, there is a slightly larger residual for PRESS-JR.

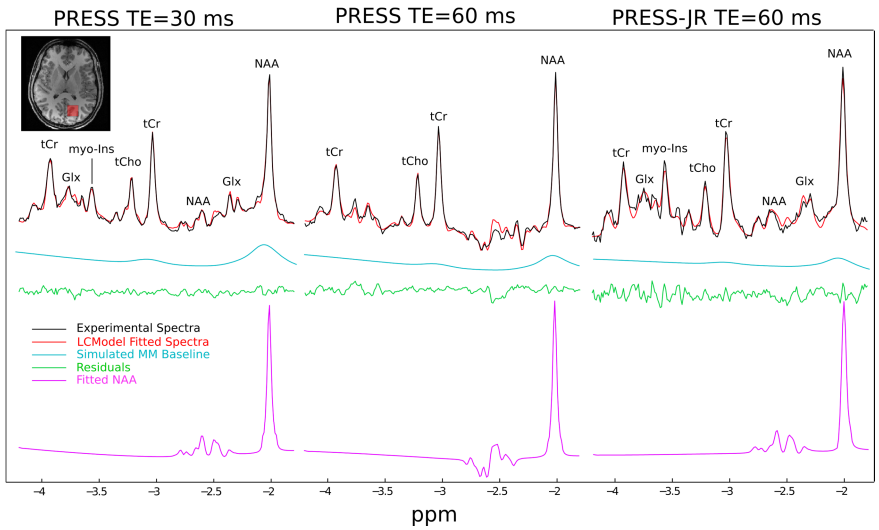

Figure 2: *In-vivo* spectra and fitted LCModel outputs from the occipital lobe for PRESS at TE = 30, 60 ms (nt=64) and PRESS-JR at TE = 60 ms (nt=256). Also shown are simulated MM baselines, residuals between fit and experiential data and the LCModel output for NAA. Note that the MM baseline is significantly smaller for longer TE and that the NAA singlet remains unaffected by PRESS-JR while the multiplets are refocused.

Discussion and Conclusion – We have shown the feasibility of PRESS-JR in clinical scanners, though some further sequence parameter optimization must still be performed. As each individual acquisition acquires signal from a spatial column, pulse phase and OVS must be set carefully to minimize signal from outside the VOI. This technique could be very useful for disease conditions such as tumors or epilepsy since larger and more complex baseline signals will result in decreased quantification accuracy for coupled metabolites at short TE. PRESS-JR is especially suited for ultra high field, as the increased spectral dispersion will lead to more accurate and reliable measurements.

References

1. Behar, K.L. et al. (1994). Magn. Reson. Med., 32, 294–302. **2**. Cudalbu, C. et al. (2012). J. Alzheimers Dis., 31, S101–115. **3**. De Graaf, R.A. et al. (2006). Magn. Reson. Med., 56, 386–394. **4**. Lemke, C. et al. (2014). Proc. 22nd Annu. Conf. ISMRM, 1424. **5**. Van Zijl, P.C.. et al. (1990). J. Magn. Reson. 1969, 89, 28–40. **6**. Takegoshi, K. et al. (1989). J. Magn. Reson. 1969, 84, 611–615. **7**. Lee, H.K. et al. (1995). Magn. Reson. Med., 34, 253–259. **8**. Aguilar, J.A. et al. (2012). Chem. Commun., 48, 811. **9**. Mao, J. et al. (1988). J. Magn. Reson. 1969, 79, 1–10. **10**. Soher, B.J. et al. (2011). Proc. 19th Annu. Conf. ISMRM, 1410. **11**. Provencher, S.W. (2001). NMR Biomed., 14, 260–264.