JAM-PRESS: improving the resolution of J-resolved PRESS with editing pulses

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Spectral resolution, a major limitation of ^{1}H-MRS, can be improved by spreading t he information content of the spectrum into an additional dimension e.g. by J-PRESS[1], or by using known coupling relationships to edit the 1D spectrum e.g. by MEGA-PRESS[2]. In J-PRESS, a second dimension is achieved by acquiring PRESS at a range of echo times. Since couplings evolve during TE, this indirect dimension contains coupling information and multiplets appear diagonally in the 2D spectrum (e.g. in Fig 2 above right). In spite of the gain in resolution that results, the reproducibility of GABA measurements at 3T using J-PRESS has been reported to be worse than when using a targeted editing approach[3]. As the main inhibitory neurotransmitter in human cortex, GABA is a neurochemical of wide clinical and neuroscientific interest. In this abstract, we introduce a **new experiment**, JAM-PRESS, that retains the benefits of J-PRESS while enhancing resolution for GABA using editing.

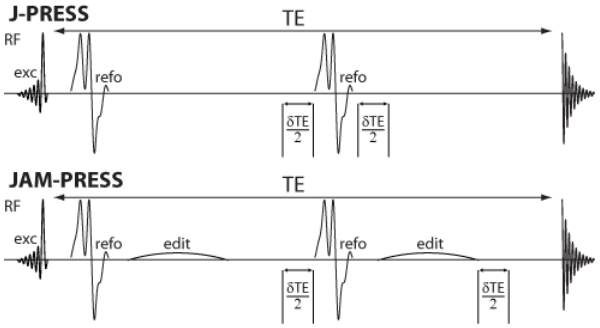

Figure 1: Pulse sequences of J-PRESS and JAM-PRESS.

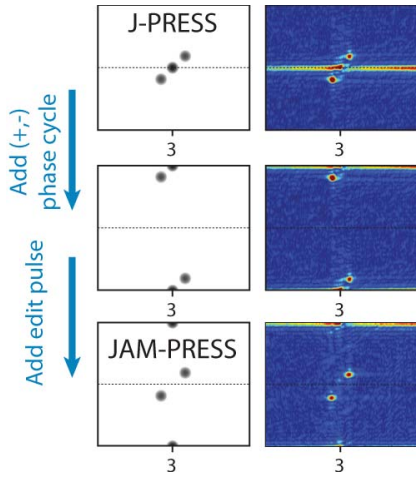

Figure 2: Schematic comparing J-PRESS and JAM-PRESS (left) and phantom data (right).

Theory In a J-PRESS spectrum, singlet signals lie along the F_1=0 line, as these signals are not modulated with respect to the echo time (t_1). If a [0°,180°] phase cycle is added to alternate increments of t_1, singlet signals are now modulated by the maximum sampled frequency $F_{1,max}$ and the whole J-PRESS spectrum is shifted by 'half the spectral width' in F_1. An additional editing pulse, applied to the GABA spins at 1.9 ppm in every second t_1 increment, will refocus coupling modulation of the GABA signals at 3 ppm. This modulates those signals by an additional increment of $F_{1,max}$ and the outer two peaks of the 3ppm triplet will be returned to the center of F_1. These steps are illustrated by the schematic left. Thus *in vivo*, rather than being separated from the overlying creatine signal by J~7 Hz in F1, they are separated by $F_{1,max}$ and resolution of GABA is enhanced.

Methods The JAM-PRESS pulse sequence above may be viewed as a MEGA-PRESS sequence in which TE is incremented - the third PRESS pulse (marked refo) is shifted as TE increases to refocus chemical shift (as in J-PRESS) and the second editing pulse is shifted by the same amount to refocus GABA couplings. In a 10mM GABA phantom, J-PRESS and JAM-PRESS spectra were acquired with the following parameters: TR=2s; TE=70 to 457.5ms in increments of 12.5 ms; excitation water suppression; (3 cm)[3] volume; 2k datapoints; 2 kHz spectral width; 8 averages; 14 ms editing pulse in JAM-PRESS (applied at 1.9 ppm in alternate TE increments). In two healthy volunteers, the same protocol was acquired in medial parietal cortex with the following parameter changes: TR 2.4s; VAPOR water suppression; experiment time 15 min.

Results As shown in Figure 2, GABA signals in phantom J-PRESS and JAM-PRESS spectra are modulated as expected (cf data and schematic). In the *in vivo* JAM-PRESS data shown in Fig 3, the singlet signals of creatine and choline lie on F_1=$F_{1,max}$ as expected, whereas the NAA signal (which is suppressed in every other t_1 increment by the editing pulse) is split between F_1=0 and $F_{1,max}$. The GABA signal at 3 ppm and the co-edited Glx signal at 3.75 appear centrally in F_1 as expected.

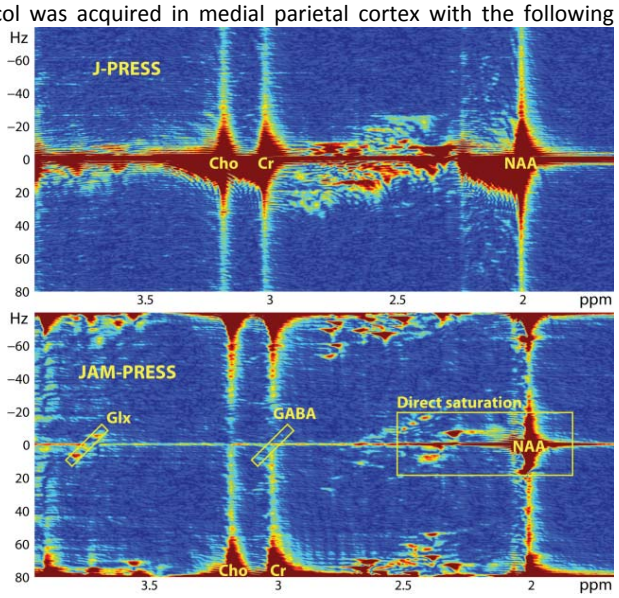

Figure 3: *In vivo* J-PRESS and JAM-PRESS spectra.

Discussion We have demonstrated that combining J-resolved spectroscopy with J-editing works as proposed. The improved signal resolution of J-PRESS is augmented by the additional editing pulses, as edited signals are shifted in F_1. The main drawback of the JAM-PRESS approach is the increase in minimum TE (from ~35 ms to 70 ms) that is required in order to accommodate editing pulses. However, omitting the editing pulses from the first 1-3 increments of TE is a solution that would not drastically alter the appearance of the spectrum. Although this method is demonstrated for GABA, it would be equally well applied to other 'editable' metabolites that J-PRESS incompletely resolves, such as glutathione. Quantitative analysis of 2D spectra is possible through linear combination fitting approaches, such as ProFit[3], and we anticipate that the JAM-PRESS method will be a useful tool particularly for studying GABA and glutamate (which is resolved from glutamine by J-PRESS).

References 1. Ryner LN et al. MRI 1995 13:853. 2. Mescher M et al. NMRB 1998 11:266. 3. Zolch N et al. ISMRM 2011 1407. 4. Schulte RF et al. NMRB 2006 19:255.

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