Spectral resolution, a major limitation of $^1$H-MRS, can be improved by spreading the information content of the spectrum into an additional dimension e.g. by J-PRESS, or by using known coupling relationships to edit the 1D spectrum e.g. by MEGA-PRESS. 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. 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.

**Theory** In a J-PRESS spectrum, singlet signals lie along the $F_2=0$ line, as these signals are not modulated with respect to the echo time ($t_1$). If a $[0^o, 180^o]$ 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 return 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 $F_1$, 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 a 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.

**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, 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).


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