

# GABA Editing without Water Suppression

Roland Kreis<sup>1</sup>, Christine Sandra Bolliger<sup>1</sup>, Erin Leigh MacMillan<sup>1</sup>, Uwe Boettcher<sup>2</sup>, and Chris Boesch<sup>1</sup>

<sup>1</sup>Depts Clinical Research and Radiology, University Bern, Bern, Switzerland, <sup>2</sup>Healthcare Sector, Customer Solutions Division, Siemens AG, Erlangen, Germany

## Introduction

The most common method to measure GABA on clinical scanners is MEGA editing<sup>1</sup> based on selective refocusing of a specific J coupling in alternating scans. Ideally, this scheme separates the satellite lines of the GABA triplet signal at 3 ppm from overlapping signals. In brain, it was found that with the basic sequence macromolecular (MM) signals coedit with the GABA signal, which can be prevented if the control pulse is placed symmetrically to the MM coupling partner at 1.7 ppm<sup>2,3</sup>. In addition, the add/subtract scheme is susceptible to small experimental instabilities that may lead to frequency shifts and amplitude and lineshape changes, as well as instable water suppression, which may all result in suboptimal cancellation of untargeted signals and an unknown signal shape for the GABA multiplet<sup>3</sup>. In this study, we have combined MEGA PRESS editing with the metabolite cycling (MC) technique suggested for non-water suppressed (nWS) MR spectroscopy<sup>4,5</sup>.

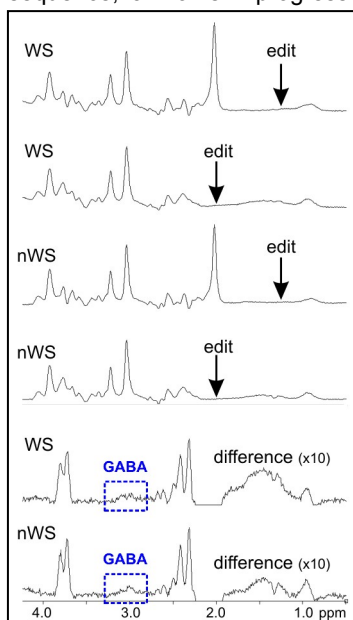
## Methods

Spectra were recorded at 3T (Siemens Verio) with a phased array head coil. Optimizations used an aqueous solution of 50mM GABA (pH 7.0). In vivo data was obtained from 6 subjects, optimizing sequence parameters (n=2) and comparing performance of editing with / without WS (n=4) in occipital cortex (midline, 25 ml) with and without intentional instabilities induced by irregular movement of one or both hands into the coil. The editing sequences were based on the manufacturers product PRESS sequence, a works-in-progress-package for editing<sup>6</sup> and MC as described in Ref. 5. For editing, parameters were set as follows: TE 70 or 71 ms, TR 2s, 128-512

acquisitions (individually stored for MC), 16 step phase cycle, Gaussian editing pulses of 42 Hz width, CHESS WS or alternating adiabatic inversion of the downfield and upfield half of the spectrum, editing pulse centered (in vivo) at 1.89 to 2.1 ppm and the control pulse symmetric with respect to 4.7 or 1.7 ppm. Signal processing in MATLAB for signal alignment and eddy current correction, in jMRUI for fitting and visualization.

## Results

In vitro parameter optimizations showed that the optimum editing frequency is ~ 2.0 ppm, if the control irradiation is symmetric w.r.t. 1.7 ppm. This offset dependence is illustrated in Fig. 1. Compared to a control editing frequency symmetric to water on the downfield side, this setting leads to a larger central peak, but overall no signal area loss in the edited spectrum. MC does not lead to significant signal loss in vitro (small loss due to T1/T1rho effects possible in vivo), but provides an inherent reference signal for alignment, eddy current correction and quantification. In vivo, alignment and eddy current correction improved the creatine linewidth in spectra of 8.5 min duration on average (4 healthy cooperative subjects) from 6.1±0.8 to 5.5±0.7Hz (original and edited spectra in Fig 2). Fig 3 shows the effect of realignment in 2 cases where occasional deliberate frequency fluctuations of up to ±9 and ±14 Hz had been induced. The resulting linewidth is drastically improved and difference spectra are much more meaningful (as suggested by



**Fig 2.** Averaged in vivo spectra (4 subjects) without extra motion obtained with WS (no alignment), and without WS (with alignment)

the coedited glutamate signal at 3.75 ppm), but in these cases the SNR of the very weak edited GABA signal would still not be sufficient for reliable quantitation.

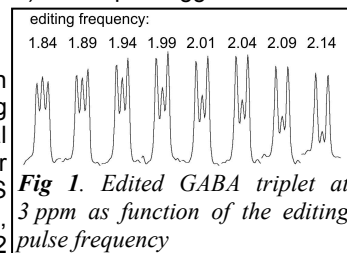
## Conclusions

Metabolite cycling was combined with MEGA PRESS editing providing excellent water signal elimination independent of the frequencies of editing and control pulses, while retaining a water-only spectrum that can be used for frequency, phase and lineshape reference, as well as continuous quantification standard. Postacquisition frequency realignment is much easier and presumably more accurate than using the low SNR metabolite signals. Even with rather severe frequency drifts, it was possible to reconstruct meaningful difference spectra – though they will have to be fitted using the knowledge of overall broadening from the water peak. With MC and the optimized parameter sets, it was found that coediting of MMs could be prevented without large penalty in GABA signal loss. Further improvements in SNR – in particular with the prevention of chemical shift related artifacts – can be achieved with combination of metabolite cycling and altered editing schemes<sup>7</sup>.

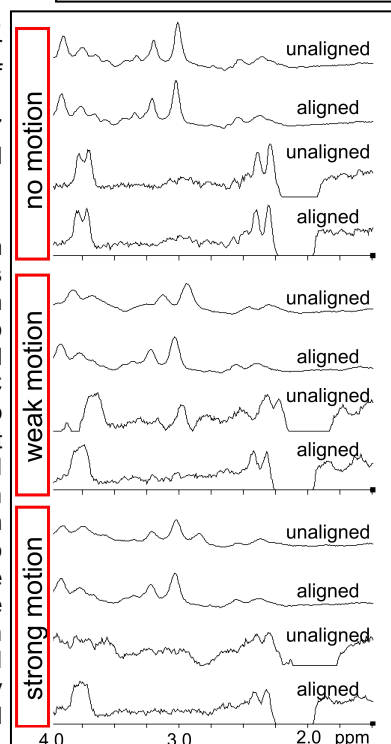
## References

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**Fig 1.** Edited GABA triplet at 3 ppm as function of the editing pulse frequency



**Fig 3.** Effect of frequency fluctuations with / without post acquisition realignment based on the full water signal