# In vivo two-dimensional J-resolved GABA spectroscopic imaging at 4.0T

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**Abstract:** In vivo measurements of brain GABA were obtained using a combined 2D, J-resolved, MRSI sequence at 4.0T. Spectra were extracted from the anterior-cingulate(AC), thalamus(TH), occipital-cortex(OC) and the parietal-cortex(PC) from 7 healthy volunteers. Metabolite measurements as well as standard deviations are provided in table 1. These preliminary data suggest the feasibility of this spectroscopic imaging technique in obtaining reasonable in vivo MRSI measurements of brain GABA.

**Introduction:** The in vivo measurement of γ-amino butyric acid (GABA) using non-invasive MRS techniques has been an area of considerable study and innovation. GABA is the primary inhibitory neurotransmitter in the brain and is of considerable interest in many neuropsychiatric/neurological disorders. With low concentration (~1.1μM/cc (7)), a complicated, multi-resonance spectrum and overlap by the dominant creatine, NAA and Glx resonances, reliable GABA measurements are difficult to obtain in vivo. Numerous techniques have been developed (1-7) to edit the in vivo proton spectrum as to quantify the GABA triplet centered at 3.07ppm. However, these techniques rely on complicated RF pulses, and/or are committed only to obtaining GABA measurements while sacrificing the other resonances. The 2D, J-resolved method developed by Ke et al, exploits the ~7.5Hz J-coupling constant of the GABA resonance to isolate it from the dominant uncoupled resonance of creatine (3.08ppm) to facilitate a more precise measurement of GABA, as well as the other proton metabolites that fall within the J-coupled bandwidth. The only caveat of this method is the time taken to sample enough TE-stepped points to adequately resolve GABA from creatine. The novel aspect of this work is that an optimized version of the 2D, J-resolved method by Ke et al is combined with a reduced k-space acquisition scheme to obtain MRSI data at 4.0T in a clinically-reasonable scan-time with adequate spatial resolution, thus giving this method considerable clinical utility.

**Methods:** Seven healthy volunteers were recruited (3 male, 4 female) and screened for electronic/metallic devices on or in their body prior to scanning. All data were collected on a Varian/UnityINOVA 4 Tesla(T) whole-body MR imaging system located at the Brain Imaging Center (BIC) at McLean Hospital. High-resolution $T_1$and $T_2$-weighted axial image sets (TE/TR=6.2/11.4ms, field-of-view (FOV)=24x24x16cm, readout-duration=4ms, receive bandwidth= ±32kHz, data matrix size=128x256x32, in-plane resolution=0.94x1.88mm, slice thickness=5mm, readout points=512, flip-angle=11/32°) were collected with a 3D-FLASH sequence for post-acquisition voxel placement. The GABA $^1$H-MRSI sequence employs a modified PRESS sequence with water suppression, in which a PRESS voxel is placed mid-sagittally in the brain (figure-1) as to maximize brain tissue and minimize extra-cranial tissue, and phase-encoding pulses applied to further localize an axial 8x8 matrix of individual voxels within the PRESS-defined region. To extract the GABA resonance from the in vivo spectrum, a 2D, J-resolved MRS acquisition scheme (7) was combined with the PRESS-MRSI localization scheme. For each PRESS-MRSI phase-encode step, 48 individual spectra were collected (f1-dimension), with the echo-time ranging from 30ms to 500ms in 10ms increments, providing enough J-resolved bandwidth to adequately extract the optimal GABA spectrum at a J-frequency of 7.45Hz. A reduced phase-encode scheme was used, described by 44 circularly bound k-space points instead of the standard 64, resulting in a total scan-time saving of approximately 30%. Acquisition parameters were, TR=1.4s, spectral bandwidth=2kHz, complex time-points (f2-dimension)=2048, nominal voxel volume=8cc, total scan duration=49 minutes. Optimized 1D spectra were extracted from the anterior-cingulate, left-thalamus and the left-parietal and occipital cortex for GABA(J~7.5Hz) and Cr(J=0.0Hz). Peak area estimates and standard deviations are presented in table 1.

**Results/Discussion:** Metabolite peak area estimates and standard deviations for GABA are provided in table 1. GABA measures are expressed as a ratio to Cr. Measurement precision for GABA in the 4 brain regions studied ranges from 22% to 43%. The number of subjects used in this preliminary study are small, thus our stated measurement precision for GABA could be improved. The prime drawbacks of MRSI verses single-voxel acquisition in this case are the varying shim and tip angle over the entire PRESS-defined slab, due primarily to Bo-inhomogeniety. However, our current focus on improving several aspects of the protocol includes high-order voxel shimming, improved spectral processing/fitting and a more S/N-efficient acquisition scheme allowing for smaller voxels. These developments should improve the quality of measurement in all regions, thus making this method a powerful tool for the simultaneous in vivo assessment of brain GABA in multiple voxels.

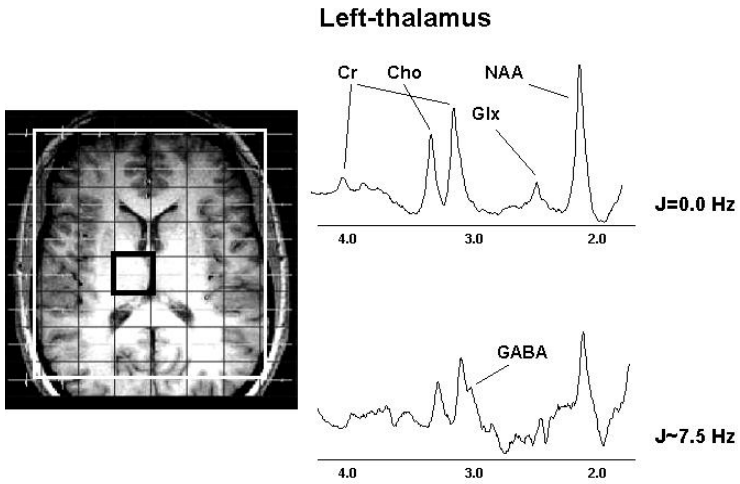


**Figure 1 –** Extracted 1D spectra from MRSI voxel placed in the left thalamus.

**Table 1** – Metabolite values, standard deviations and CV. GABA levels are expressed as a percent ratio to Creatine in each region. Anterior-cingulate(AC), Thalamus(TH), Occipital-cortex(OC), Parietal-cortex(PC).

| Region | GABA/Cr |
|---|---|
| AC | 13.7 ± 4.3 (31%) |
| TH | 11.2 ± 2.5 (22%) |
| OC | 7.5 ± 3.2 (37%) |
| PC | 6.9 ± 2.5 (43%) |

**Conclusions**: Combined 2D, J-resolved MRSI can provide multivoxel, optimized spectra for GABA as well as the other metabolites in the in vivo proton spectrum at 4.0T within clinically reasonable scan times.

**References:**

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