**Introduction**

Constant time two dimensional methods have a feature of good time peak resolution through $^1$H decoupling along $F_1$. We have reported in vivo detection of glutamate (Glu), $\gamma$-amino butyric acid (GABA) and glutamine (Gln) in human brain using two kinds of 2D localized constant time methods, CT-COSY (1) and CT-PRESS (2). Furthermore, we have developed a quantitation method on 2D CT-COSY spectra and demonstrated quantitation of glutamate and GABA in human brain (3). This method required at least two sets of spectra for $T_2$ correction and a long total measurement time of 80 min. Since CT-PRESS is the spin echo type, SNR of glutamate C4H was improved by a factor of 1.7 in the human brain (2) and a shorter measurement time is expected. In addition to this feature of high sensitivity, we will propose $T_2$ correction and quantitation method on CT-PRESS spectra using 2D FT of shared time domain (TD) data within a shortened measurement time and demonstrate phantom experiments and human studies.

**Methods**

In ISIS version of CT-PRESS sequence (2), water suppression and outer volume suppression are followed by a module for localization; ISIS pulse (x-direction) – 90° slice pulse (y-direction) – $1/2T_1^*-180°$ non-slice pulse – $1/2(T_1^*+T_2)+\Delta t/2-180°$ slice pulse (z-direction) – (data acquisition). To meet the constant time condition, a suitable amount of zeroes were filled in front of the acquisition data (4). After $N_t$ increments by $\Delta t$, along $t_2$, 2D TD data defined by $N_1 \times n_2$ matrices are accumulated where $n_2$ is number of sampling points in FID. A part of the total TD data defined by $n_1 \times n_2$ shown as a dotted area in Fig. 1 is extracted. Reconstruction of this partial TD data generates a CT-PRESS spectrum weighted by $\exp(-t_2/T_2)$. The value of $T_2$ can be expressed as $T_2+TE2+(n_{start}+n/2)\Delta t$ by applying a window where intensity is maximized at the center along $t_2$ axis on the partial TD data. Since $T_2$ is varied with $n_{start}$, Series of $^1$H decoupled spectra along $F_1$ weighted with varied $T_2$ can be obtained by reconstruction of other parts of TD data where $n_{start}$ is incremented along $t_1$. By curve-fitting of peak volumes on these series of spectra, $T_2$ can be obtained. These peak volumes calculated using basis spectra obtained by GAMMA simulation are proportional to a model function of $A^\ast \exp(-t_2/T_2)$ even for metabolites having J coupled spin systems. By long waiting delay after the second 180° slice pulse, saturation effect due to $T_1$ can be ignored. Difference of coil-loading factors between the human brain and the reference phantom can be corrected using an internal water reference method (3). Then, absolute concentrations of metabolites can be calculated.

All experiments were performed using a 4.7 T whole-body NMR spectrometer (INOVA, Varian). A volume TEM coil was used both for transmission and reception. In phantom experiments, we used a reference phantom containing a brain metabolite mixture of 10 mM NAA, 8 mM Cr, 9 mM Glu, 3 mM Gln and 2 mM GABA. A 200-mL bottle containing this solution was placed in a water bath containing 0.9 % dissolved NaCl for mimicking an environmental condition; ISIS pulse (x-direction) – 90° slice pulse (y-direction) – $1/2T_1^*-180°$ non-slice pulse – $1/2(T_1^*+T_2)+\Delta t/2-180°$ slice pulse (z-direction) – (data acquisition). To meet the constant time condition, a suitable amount of zeroes were filled in front of the acquisition data (4). After $N_t$ increments by $\Delta t$, along $t_2$, 2D TD data defined by $N_1 \times n_2$ matrices are accumulated where $n_2$ is number of sampling points in FID. A part of the total TD data defined by $n_1 \times n_2$ shown as a dotted area in Fig. 1 is extracted. Reconstruction of this partial TD data generates a CT-PRESS spectrum weighted by $\exp(-t_2/T_2)$. The value of $T_2$ can be expressed as $T_2+TE2+(n_{start}+n/2)\Delta t$ by applying a window where intensity is maximized at the center along $t_2$ axis on the partial TD data. Since $T_2$ is varied with $n_{start}$, Series of $^1$H decoupled spectra along $F_1$ weighted with varied $T_2$ can be obtained by reconstruction of other parts of TD data where $n_{start}$ is incremented along $t_1$. By curve-fitting of peak volumes on these series of spectra, $T_2$ can be obtained. These peak volumes calculated using basis spectra obtained by GAMMA simulation are proportional to a model function of $A^\ast \exp(-t_2/T_2)$ even for metabolites having J coupled spin systems. By long waiting delay after the second 180° slice pulse, saturation effect due to $T_1$ can be ignored. Difference of coil-loading factors between the human brain and the reference phantom can be corrected using an internal water reference method (3). Then, absolute concentrations of metabolites can be calculated.

**Results & Discussion**

The proposed method in 2D gave $T_2$ value of 582 ms for a Cr peak, which was in good agreement with the value of 574 ms obtained by a conventional 1D method (Fig. 2). Figure 3 shows a result of quantitation on glutamate in the human brain. After quantitation protocol with $T_2$ correction and the internal water reference method, the concentration of glutamate was calculated as 8.0 mM which is also in good agreement with reported values.

**Conclusions**

Glutamate in the human brain can be quantitated with measurement time of 24 min on highly resolved CT-PRESS spectra at 4.7 T. This proposed method will be useful to quantitation of other metabolites having $J_{hh}$ coupled spin systems such as GABA and glutamine.

**References**