T_2 relaxation times of 18 brain metabolites determined in 83 healthy volunteers in vivo

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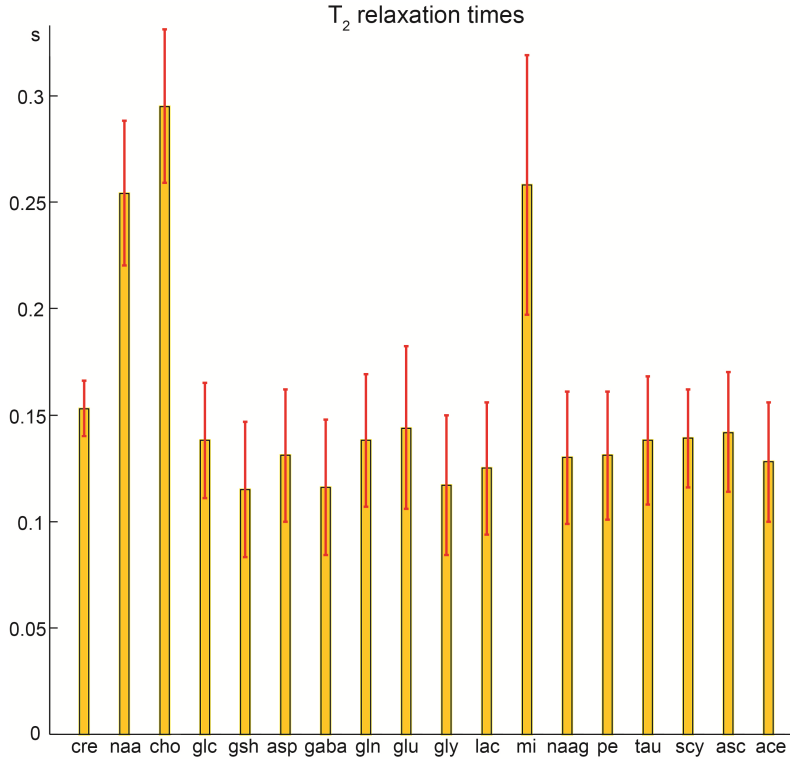
Introduction

The determination of accurate transverse (T_2) relaxation times for brain metabolites is essential for volume tissue composition correction methods, including relaxation correction (1), that aim at quantitative MR spectroscopy analyses to obtain metabolite levels in mM concentrations. Therefore, T_2 relaxation times of the singlet resonances of N-acetyl-aspartate (naa), creatine (cr) and total-choline (cho) were investigated in several publications (2). The T_2 relaxation time of the coupled spin system of gamma-amino-butyric acid (GABA) has also been recently determined based on a MEGA PRESS editing approach using 3 TE steps in five healthy volunteers (3). Additionally, the T_2 relaxation times of myo-Inositol (mi) and glutamate (glu) were identified using PRESS at four echo times in five healthy volunteers at 3T (4). However, for the majority of J-coupled metabolites detectable in the human brain, this property is still unknown. **The aim of this investigation was** to determine T_2 relaxation times for a wide range of brain metabolites and for a large volunteer cohort at 3T. For this, J-resolved PRESS with 100 TE steps and the recently developed ProFit2 (4) fitting routine was utilized.

Methods

With approval from the local ethics committee, 83 healthy volunteers were included in the study. Based on a high resolution 3D T_1 weighted scan (resolution: 1x1x1 mm^3), the spectroscopic voxel (25x20x20 mm^3) was placed in the bilateral pregenual anterior cingulate cortex (pACC). A maximum echo J-resolved ^{1}H MRS (JPRESS) protocol (5) combined with inner volume saturation (6) and VAPOR water suppression was used to determine T_2 relaxation characteristics of 18 brain metabolites at 3T (Philips Achieva). J-coupling evolution was monitored by increasing the TE from 24 ms (TR-Head coil used for 53 volunteers) or 30 ms (8-channel sense coil used for 30 volunteers) over 100 TE steps (8 averages/step + 1 w/o water suppression for phase and eddy current correction)) to 222 ms or 228 ms, respectively, with a TR of 1.6 s. The JPRESS data were quantified using ProFit2 (7) including metabolite basis sets of aspartate (asp), cho, cre, gaba, glutamine (gln), glutamate (glu), glutathione (gsh), myo-inositol (mi), lactate (lac), naa, N-acetyl-aspartylglutamate (naag), phosphoethanolamine (pe), scyllo-inositol (scy), glycine (gly), glucose (glc), acetate (ace), ascorbic acid (asc), and taurine (tau). The parameter ϑ_e in the fit model of ProFit2 (7) reflects the homogeneous line broadening ϑ_e is related to the T_2 relaxation induced exponential decay $\exp(-t/T_2)$ by $T_2 = 1/(\pi \cdot \vartheta_e)$. Thus T_2 relaxation times for all metabolites included in the fit model can be extracted from the metabolite specific ϑ_e s. The actual grey and white matter and CSF content of the VOI was calculated using the Statistical Parametric Mapping (SPM; Wellcome Trust Centre for Neuroimaging, London, UK) segmentation routine and own MATLAB-based scripts to obtain corresponding voxel statistics.



Results and Discussion

The tissue composition within the spectroscopic voxel, calculated based on the high resolution T_1 weighted image, was 71%±4% grey matter, 12%±3% white matter and 18%±4% CSF. Mean values and standard deviation of the T_2 relaxation times of all detectable metabolites are displayed in Fig. 1. The results are in very good accordance with previous 3T T_2 relaxation times in the literature: NAA 254±34ms vs. 247±19ms (2), cre 153±13ms vs. 152±7ms (2), cho 295±36ms vs. 207±16ms (2), gaba 116±32ms vs. 88±12ms (3), glu 144±38ms vs. 180±12ms (4) and mi 258±61ms vs. 196±17ms (4). In addition, a previous rat study at 9.4T found very similar T_2 values for most of the coupled spin systems around 89-116 ms (8), which is in line with our 3T findings. However, the influence of the choice of fit constraints on the resulting T_2 relaxation times has to be investigated in more detail in order to avoid bias.

Conclusion

T_2 relaxation times of 18 brain metabolites at 3T are presented for the first time as measured in the predominantly grey matter of 83 healthy volunteers.

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