Age dependence of NAA and tCr transverse relaxation times determined in hippocampus and frontal cortex at 3T

Bernadeta Walaszek[1], Florian Schubert[1], Ralf Mekle[1], and Bernd Ittermann[1]
[1]*Physikalisch-Technische Bundesanstalt (PTB), Berlin, Germany*

Introduction

For absolute metabolite quantification at moderate to long echo times, T_2 correction is required. Most often, literature T_2 values from unspecified brain regions are applied. However, it has been shown that the metabolite T_2s can differ for different individuals and brain regions [1, 2]. In addition, the process of ageing of the human brain, as reflected by a decrease of the total number of active neurons, may affect the metabolite T_2s as determined recently using the PRESS sequence [3]. Using STEAM, however, other authors did not observe any significant age dependence of T_2 [4]. Given the increasing importance of metabolite quantification in the hippocampus as well as in cortical areas of the brain, the aim of this study was to determine T_2 values of relevant brain metabolites in these brain regions and their age dependence using PRESS.

Subjects and Methods

Ten healthy volunteers (37±11.4 years; 3 female) were scanned on a 3T Verio scanner (Siemens, Erlangen, Germany) using a 12-channel receive only head coil array. Following T_1-weighted whole brain imaging for voxel positioning and segmentation, 6 proton spectra were acquired in the anterior cingulate cortex (acc, 2.5 x 4 x 2 cm^3, 10 subjects) and hippocampus (hc, 2 x 3 x 2 cm^3, 9 subjects) using PRESS (T_E = 30, 50, 80, 135, 250, 330 ms, T_R = 3 s, n = 100 in acc, n=128 in hc). In addition, for each subject and for each voxel, 9 unsuppressed water spectra were recorded (T_E = 30, 80, 160, 276, 552, 800, 1000, 1200, 1500, 1700 ms, T_R = 10 s, n = 2). Both water and metabolite signals were quantified using LCModel, incorporating basis sets simulated for each T_E used. The T_1-weighted images were segmented using SPM5. Extraction of CSF voxel fractions was done using the program SegSpec [5]. Amplitudes returned by LCModel were fitted in QtiPlot with bi-exponential (water) and mono-exponential (metabolites) decay functions.

Metabolites	T2(ms, mean±SD) in acc, present work	T2(ms, mean±SD) in acc, [6]	T2(ms, mean±SD) in hc, present work	T2(ms, mean±SD) in hc, [6]
NAA	285 ± 29	278 ± 31	278.6 ± 48	267 ± 15
tCr	167 ± 11	179 ± 9	156 ± 17	198 ± 31
tCho	293 ± 38	282 ± 45	241 ± 32	291 ± 13
Glu	148 ± 12	194 ± 37	200 ± 48	171 ± 22
Myo-inositol	240 ± 23	---	---	---

Table 1 T2 values of acc and hc voxels (present work and literature values [6])

Results

Only metabolites that were quantified with Cramér-Rao lower bounds (CRLBs) < 20 % were included in the analysis. Resulting metabolite T_2s for NAA, tCr, tCho and Glu in the acc and hc voxels and for myo-inositol (Ins) in the acc only are presented in Table 1. T_2 values of tCr and NAA significantly decrease with age in both brain regions (Fig. 1), with p = 0.03, 0.02 for acc and p = 0.013, 0.04 for hc, respectively. Furthermore, T_2 of tCho in the acc voxel tends to decrease with age (p = 0.06). Water T_2 was (75.5±4.6) ms in acc and (75.2±2.6) ms in hc for brain tissue, and (675±117) ms in acc and (455.4±73.8) ms in hc for CSF. We observed no age dependence of water T_2 values.

Discussion

The T_2 values of five and four relevant brain metabolites were determined in the acc and in hc, respectively at 3T. Values for NAA, tCr, tCho are in agreement with previous findings [6], but in part different from those determined in other brain regions [7-9]. As measured here for the first time in acc, T_2 of Ins is longer by 20 % compared to occipital cortex [9]. The T_2 of Glu was about 50 ms lower than previously observed in acc [6], which would significantly increase Glu concentration in long T_E measurements. It was also observed that the hc T_2 values of tCr and tCho were about 50 ms lower than previously reported [6]. The age dependence of metabolite T_2 suggests the need for relaxation corrections for MRS on an individual or age-cohort basis, especially for NAA and tCr.

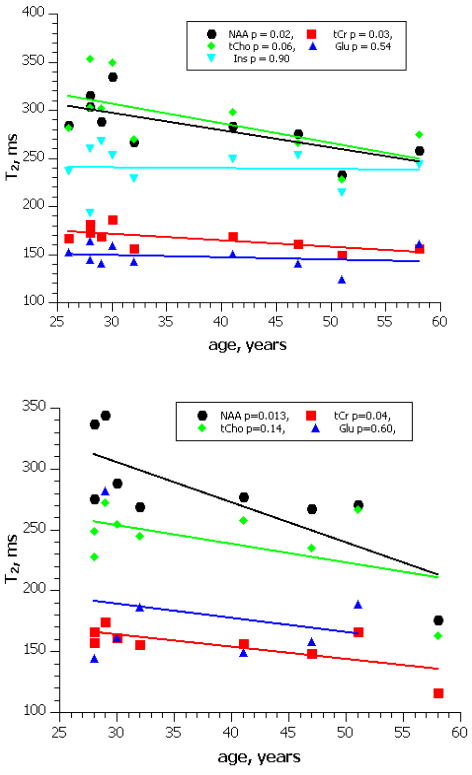

Fig. 1 T_2 relaxation times vs age. Top: acc, bottom: hc

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