Estimation of T_2^{ρ} Relaxation Times of Macromolecules in Human Brain Spectra at 9.4 T

Tamás Borbáth[1], Saipavitra Murali-Manohar[1], and Anke Henning[1]
[1]Max Planck Institute for Biological Cybernetics, Tübingen, Germany

Introduction

Previous studies have shown, that the inclusion of a macromolecular baseline in the basis set for fitting can influence the quantification[1,2], while other studies have shown the possible clinical relevance of macromolecules (MM) in clinical diagnostics[3]. Hence, a characterization of MMs is of crucial importance[4], and knowing the apparent T_2 (T_2^{ρ}) relaxation times can lead to a better understanding of these MMs.

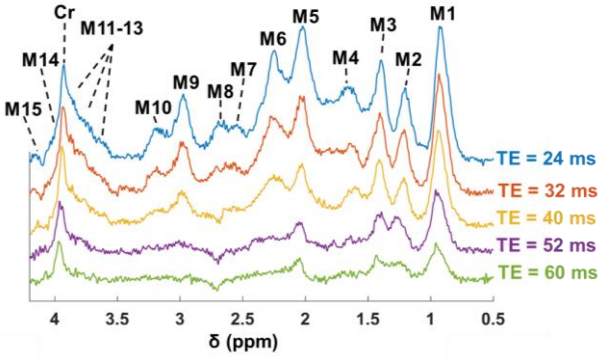

Fig. 1 The macromolecular spectra averaged across subjects measured at the different echo times. Labels mark the quantified macromolecules.

Methods

A echo times (TE) series of ^{1}H-MRS metabolite-cycled double inversion recovery semi-LASER spectra (TR 10 s / T_{Inv1} 2360 ms / T_{Inv2} 625 ms) were acquired from the occipital lobe in the human brain from 11 healthy volunteers at 9.4 T, with the TEs of 24, 32, 40, 52, 60 ms. The spectra were fitted with LCModel-v6.3[5] software using simulated spectral lines with the ppm shifts according to Giapitzakis et. al.[4] and a residual total creatine (Cr) peak at 3.92 ppm. The quantified concentrations were fitted to an exponential decay across the TE series to estimate T_2^{ρ} relaxation times.

Results

The estimated T_2^{ρ} relaxation times (Fig. 2) calculated on the summed spectra across the subjects were between 10 and 55 ms. A J-evolution of the M8 macromolecule could be visually observed over the echo times, the J-coupling constant was estimated to be around 16.6 Hz at 2.68 ppm. The confidence of the exponential decay fits was above 0.80 for most MMs, except M8 which was not modeled as a J-coupled spin system in this study, hence the low R^2 value. The estimation of the T_2^{ρ} decay of M14 and M15 is neither reliable since the spectra at longer echo times are strongly influenced by water residuals and noise in that ppm region.

	M1	M2	M3	M4	M5	M6	M7	M8
T_2* [ms]	39.82	54.45	43.42	12.16	13.82	18.73	26.34	39.66
R^2	0.95	0.85	0.94	1	0.99	0.89	0.87	0.44

	M9	M10	M11	M12	M13	M14	M15	Cr
T_2* [ms]	18.84	14.7	10.04	21.98	17	40.37	36.58	87.65
R^2	0.94	0.97	0.94	0.88	0.98	0.77	0.7	0.82

Fig. 2 Calculated T_2 relaxation times for the individual MMs and Cr, and the confidence of the exponential decay given as R-squared.*

Discussion & Conclusion

This study reports for the first time the T_2^{ρ} relaxation time of individual MMs in human brain. The reported T_2^{ρ} relaxation times are also comparable to the measured T_2 relaxation times 22.7 – 33.5 ms by de Graaf et. al.[7] and 26 ms by Pfeuffer et. al.[8], both measured in rat brains at 9.4 T. The observed J-evolution and estimated coupling constant of M8 confirms further the preliminary attribution of the M8 group according to [4] to β-methylene protons of aspartyl groups. However, the M8 has to be modeled better and the T_2^{ρ} estimation of the M11-M15 could be influenced by the residual total creatine peak at 3.92 ppm, which should have a slightly lower relaxation time of 68 ms[6].

References

1. Cudalbu C., JAD 2012
2. Schaller B., NMR Biomed 2013
3. Louis M., AIPR 2017
4. Giapitzakis I-A., MRM 2018
5. Provencher S., NMR Biomed 2001
6. Deelchand D., JMR 2010
7. de Graaf R., MRM 2006
8. Pfeuffer J., JMR 1999

Acknowledgments

For the funding by the Horizon 2020/ CDS-QUAMRI grant.