Longitudinal Relaxation Times of 5 Metabolites in vivo at 9.4T – preliminary results

Andrew Martin Wright[1,2], Saipavitra Murali Manohar[1], Anke Henning[1]

[1]Max Planck Institute Biological Cybernetics, Tübingen, Germany, [2]IMPRS for Cognitive and Systems Neuroscience, Eberhard-Karls University of Tübingen, Tübingen, Germany

Introduction

Measuring longitudinal relaxation times is a requirement for absolute quantification. In this work, to more accurately measure the concentrations of metabolites in vivo at 9.4T, the relaxation of 5 metabolites was measured using an inversion recovery MC-STEAM technique[1].

Methods

In order to determine the tissue content of grey matter rich (GM) and white matter rich (WM)MRS voxels, a MP2RAGE sequence was used[2] with a 8Tx/16Rx volume coil[3], and segmented into GM, WM, and CSF tissue probability maps using SPM12 with tissue fractions within the voxel calculated by an in-house method.

The same coil was used to acquire the spectroscopy data by utilizing the three bottom channels alone to transmit by utilizing a three-way power splitter. Voxels were placed spanning the longitudinal fissure of the occipital lobe for GM and in the right occipital-parietal transition for WM. To measure the longitudinal relaxation of metabolites, a single inversion recovery MC-STEAM sequence[1] was used (TE/TM/TR = 8/50/10000ms). A series of inversion times were chosen in order to accurately characterize the T1 of 5 metabolites; the chosen TIs were [20, 100, 400, 700, 1000, 1400, 2500ms]. Basis sets were simulated using the VeSPA simulation tool with an in-house modified pulse sequence[4]. The macromolecular baseline was left flexible to fit by LCModel (dknmn = 0.5) and is uncorrected in this work[5].

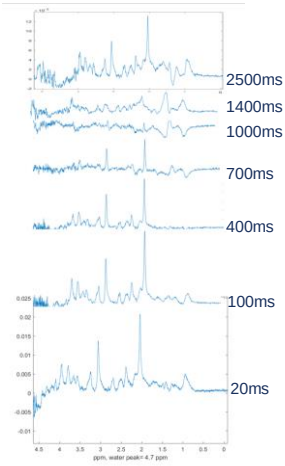

Fig.1: showing spectral quality with the ranging TIs

Results

The T1-relaxation times of 5 metabolites are reported in table 1. The average content of GM in the GM voxels was 67.4% ± 2.7% and the average content of WM in the WM voxels was 69.5% ± 9.2%.

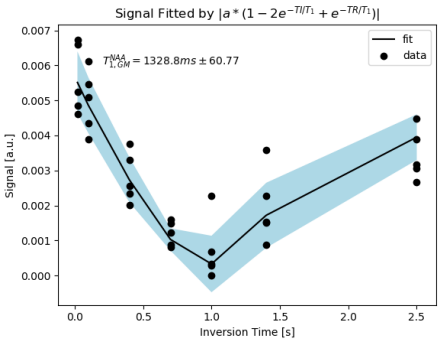

Fig.2: Fitted data for the TI series of NAA. The shaded region being the variance from the mean signal

Discussion

The advantage of utilizing a short TE is keeping a broader range of metabolites in the spectra in order to characterize their longitudinal relaxation in order to absolutely quantify these metabolites in future work. Only 5 metabolite T1-relaxation times are reported in this work due to the heavy influence of the underlying MM; in the future, the macromolecular baseline is to be corrected with a modelled subtraction scheme presented as a separate work. The current T1-relaxation times are partially in agreement with Deelchand et al[6]by having a similarly long NAA T1-relaxtion. However, the relaxation of Cre is much shorter than the values report in the previous literature.

Table 1: Relaxation Times of Metabolites		
Metabolite	GM T1 [ms]	WM T1 [ms]
NAA	1328.8± 60.77	1522.49 ± 49.12
Cr	505.68±155.15	773.3 ± 166.51
Glu	1266.75± 50.18	1376.49± 45.93
Gln	891.1 ± 114.12	933.43 ± 133.85
GPC	894.02 ± 63.04	973.62 ± 76.43

Conclusion

The longitudinal relaxation times of 5 metabolites are preliminarily reported. These preliminary results contrast previous work of 9.4Tin vivo T1-relaxation times. By characterizing metabolite T1, it will be possible to absolutely quantify metabolite concentrations in vivo, and potentiates pathology characterization with SVS and high-resolution metabolite mapping in the future.

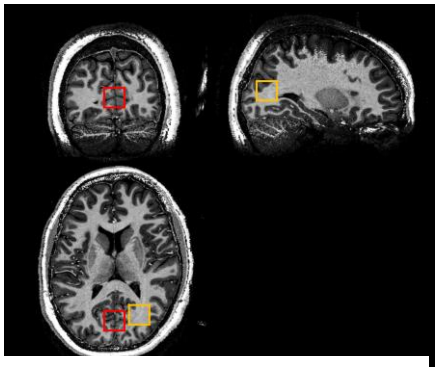

Fig. 3: Showing the voxel placement for GM(red) and WM(orange)

References

[1] Giapitzakis et al. MRM 2018. [2] Hagberg et al. Neuroimage 2017. [3] Avdievich et al. ISMRM 2017. [4] Soher et al 2018. [5] Provencher, MRM 1993. [6] Deelchand et al. JMR 2010.

Acknowledgements

Funding by the European Union (ERC Starting Grant, SYNAPLAST MR, Grant Number: 679927) is gratefully acknowledged. Special thanks also go to Sahar Nassirpour, Paul Chang, Wolfgang Bogner, Cristina Cudalbu, and Theresia Ziegs for helpful conversations and other support throughout this work.