Challenges in estimating T_1 Relaxation Times of Macromolecules in the Human Brain at 9.4T

Saipavitra Murali-Manohar[1], Andrew Martin Wright[1], Anke Henning[1]
[1]Max Planck Institute for Biological Cybernetics, Tuebingen, Germany

Purpose

In order to determine the T_1 relaxation times of the metabolites in human brain including the ones that have either shorter T_2 relaxation times or represent J-coupled spin systems, shorter TE times have to be chosen where there is a significant macromolecular contribution. Therefore, the behaviour of macromolecules (MMs) and their relaxation have to be understood clearly. In [1] the T_1 relaxation time of the macromolecular baseline has been determined as a whole using single inversion recovery but values have not been provided for individual MMs, in [2] it has been estimated for the MM peak at 0.93 ppm. Here we attempt to understand the T_1 relaxation pattern for the individual macromolecules at 9.4T in the human brain with a double inversion recovery (DIR) technique in order to measure the relaxation of individual MM components which relax at different rates and uniquely impact the overlying metabolite spectrum in traditional excitation approaches.

Methods

Bloch simulations for a DIR sequence with several combinations of TI_1 and TI_2 (assuming MMs and metabolites T_1 relaxation time from [1] and [3] respectively) were performed and the ones (TI_1/TI_2 = 1950/550, 2100/575, 2150/600, 2400/600, 2360/625 ms) for which the metabolites were considerably nulled were chosen. All the data were acquired on a 9.4T Magnetom, Siemens (Erlangen, Germany). 5 healthy volunteers participated in this study after signed consent. MC-STEAM [4] with DIR was used with TE/TM = 8/50 ms, averages = 32. TR, TI_1 and TI_2 were varied to acquire the data in order to get metabolite-free macromolecular spectra and to choose the correct TIs and TR.

Results and Discussion

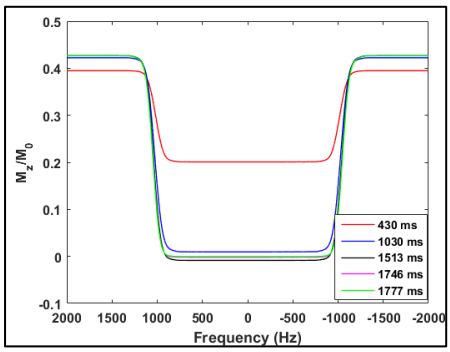

Fig.1: A representative Bloch simulation result for TI_1/TI_2 = 2150/600 ms

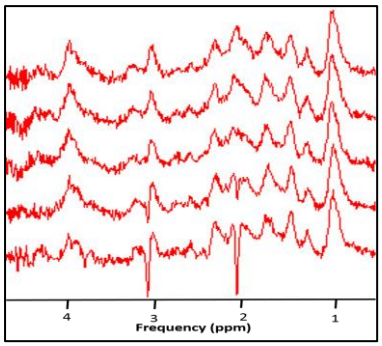

Fig. 2: MM spectra (2360/625 ms) with TR varying from 4, 6, 8, 10, 15 s from bottom to top.

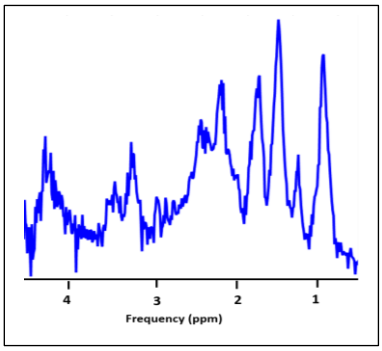

Fig. 3: MM Spectra with TI_1/TI_2 = 2150/600 ms and TR = 8s

TIs were chosen such that the need for residual metabolite subtraction was minimized. Bloch simulations helped us in finding several sets of TI_1/TI_2 (Fig.1) fulfilling this requirement. TR = 8 s seemed to be the best bet keeping in mind a comfortable scan duration and to be well within the SAR limits. The quality of MM spectra so obtained was very comparable to TR = 10/15 s (Fig.2).

Conclusion

The challenges included obtaining several sets of TI_1/TI_2 where metabolites were suppressed, choosing the right TR to allow a decent scan duration and finally to build a model which would predict the T_1 relaxation times of the MMs individually. We achieved in obtaining a set of different TIs which yield almost metabolite-free spectra and chose a feasible TR. Future steps include acquisition of macromolecule spectra using a higher number of TI_1/TI_2 covering a larger range of inversion delays in order to build a model which allows to compute the individual MMs T_1 relaxation times.

References

[1] Xin et. al., MRM 2013. [2] Behar et. al., MRM 1994.
[3] Deelchand et. al., J Magn. Reson 2010. [4] Giapitzakis et. al., MRM 2018.

Acknowledgements

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