Measuring Glucose Concentrations in the Rat Brain Using TE-Averaged PRESS at 7T

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Introduction

Glucose in the brain has multiple roles, and glucose consumption in the brain can be used for tumor imaging and characterization of dementia. While brain glucose consumption can be measured using positron emission tomography (PET), PET can only measure the uptake of glucose and not the current concentration. Thus, there is interest in using proton magnetic resonance spectroscopy (MRS) to measure changes in brain glucose concentrations due to pathology or physiology. Fitting in MRS is typically done through the use of a spectral model to match peak structures with corresponding metabolites. Typical 1D approaches using point resolved spectroscopy (PRESS) are insufficient because the glucose signals in the 3.2-3.9 ppm range overlap with taurine, myo-inositol, glutamate, and glutamine signals. Glucose cannot be reliably estimated from the 4.6 and 5.2 ppm peaks since water suppression will partially or completely suppress these signals. By using a technique originally developed by Hurd et al [1] called TE-averaging, multiple in phase resonance glucose signals at different TE values can be summed constructively to allow identifiable peaks to emerge in the spectrum.

Materials and Methods

The hippocampi of six rat brains were scanned on a Bruker ClinScan 7T MRI. The scans consisted of a standard 13 ms TE PRESS scan and a TE-averaged scan, which takes an equal number of averages for eight separate TE values ranging from 60 to 95 ms in increments of 5 ms as shown in figure 1. This range was chosen since the glutamate and glutamine signals at 3.75 ppm are minimized in the range, while the glucose-α peak at 3.68 ppm is maximized. Moreover, the glucose-β peak at 3.85 ppm is largely negative in the real spectrum, and it is easy to identify since no metabolite signal is also negative nearby. The total number of averages taken for the TE-averaged and the TE-13 spectra was 64, 128, and 256. The TE-13 and TE-averaged spectra were fitted in LCModel using basis files computed with a TE-averaged spectral model created using Versatile Simulation, Pulses and Analysis (VeSPA).

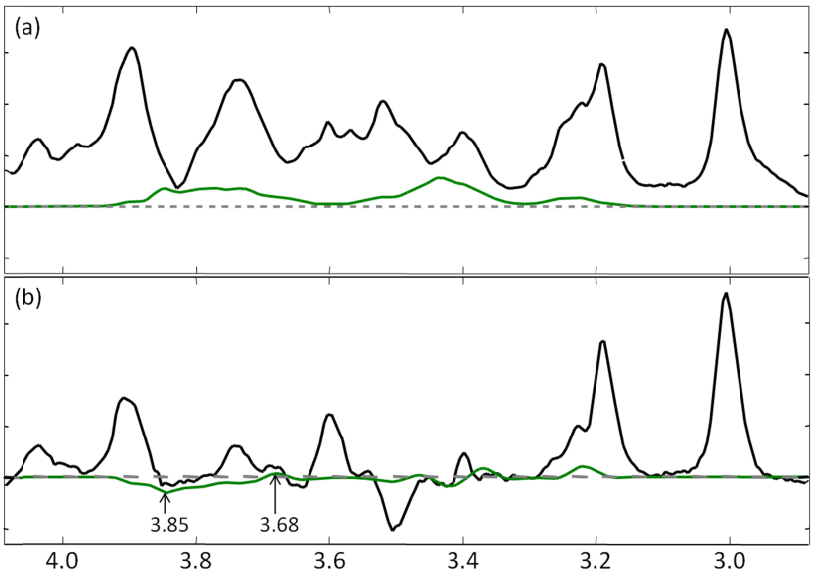

Figure 1: (a) TE 13 spectrum (black) with glucose (green); (b) TE-averaged spectrum (black) with glucose (green)

Results and Discussion

LCModel found average glucose concentrations relative to creatine to be 0.37 ± 0.35 for TE-13 spectra and 0.43 ± 0.07 for TE-averaged spectra based on the values listed in table 1. Although both averages were within the range of theoretical glucose concentrations in the rat brain, the estimates using TE-13 data ranged from 0.00 to 1.35. By comparison, the TE-averaged spectra estimated glucose in the range of 0.29 to 0.52. The higher consistency of glucose estimates using TE-averaged data was evident from the standard deviation of 16% versus the standard deviation for TE-13 data of 95%. This is due to macromolecular and metabolite signals overwhelming the glucose signals in TE-13 data (Fig. 1a), whereas a few identifiable peaks emerge in the TE-averaged spectrum (Fig. 1b).

	TE 13	TE avg
64 avg	0.00	0.43
64 avg	0.59	0.52
64 avg	0.24	0.45
64 avg	0.38	0.35
64 avg	0.48	0.52
64 avg	0.37	0.40
128 avg	1.35	0.41
128 avg	0.12	0.52
128 avg	0.48	0.29
128 avg	0.28	0.43
128 avg	0.06	0.40
128 avg	0.42	0.41
256 avg	0.00	0.40

Table 1: Glucose estimates with LCModel relative to creatine

Conclusion

TE-averaging can be used to minimize the influence of macromolecular signals and other metabolite signals to give more accurate, consistent estimates of glucose concentrations in the brain.

References

[1] Hurd R, Sailasuta N, Srinivasan R, Vigneron DB, Pelletier D, Nelson SJ. Measurement of brain glutamate using TE-averaged PRESS at 3T. Magn Reson Med 2004;51(3):435-440.