Whole Brain High Resolution Metabolite Mapping Using ^{1}H FID MRSI with Dynamic B_0 Shimming at 9.4T

***Sahar Nassirpour*, Paul Chang, Anke Henning**
Max Planck Institute for Biological Cybernetics, Tuebingen, Germany

Introduction

Whole-brain metabolite mapping with volumetric coverage is a valuable tool for the evaluation of metabolite levels across different regions in the human brain. Previously, several whole-brain 1H MRSI studies have been performed at 3T[e.g. 1, 2] using the EPSI sequence[3]. However, so far, similar studies have not been done at higher field strengths despite the many advantages of higher fields for spectroscopy applications. In this study, we combine a robust in/plane acceleration technique with dynamic slice-wise B_0 shim updating and present whole-brain metabolite maps acquired with a high resolution at 9.4T.

Methods

All experiments were conducted on healthy volunteers with a 9.4T whole-body human Siemens scanner with an in-house developed 18Tx/32Rx RF coil[4] and dynamic 2nd order B_0 shim updating. ^{1}H MRSI data were acquired from a total of 10 slices (of 8mm thickness each) covering the entire Cerebrum. A multi-slice ultra-short TR and TE ^{1}H FID MRSI[5-8] sequence with no lipid or outer volume suppression with the following parameters was used for data acquisition: FOV = 205mmx205mm, TR = 300ms, TE = 1.5ms, in-plane matrix size = 64x64, slice thickness = 8mm, slices = 10. The MRSI acquisition was accelerated using a modified GRAPPA acceleration technique with an effective acceleration factor of R~6 (in-plane). This led to a total scan time of ~25 minutes for the whole brain. After each MRSI scan, a highly accelerated water reference image with the same spatial resolution as the original MRSI data was acquired from each slice. The total acquisition time of the water reference scan for the entire brain was about 7 minutes. The GRAPPA accelerated data was reconstructed using a machine-learning bases neural network prediction.

Results/Discussion

Figure 1 shows the metabolite maps of four metabolites (/Cre) for slices 3 to 10. All maps show high SNR and great anatomical details across the slices. Note that despite the high in-plane acceleration factor (R=6) there are no visible residual aliasing artifacts in the metabolite maps. Figure 2 shows the metabolite maps of 3 metabolites from the central slice in the transversal, sagittal, and coronal directions.

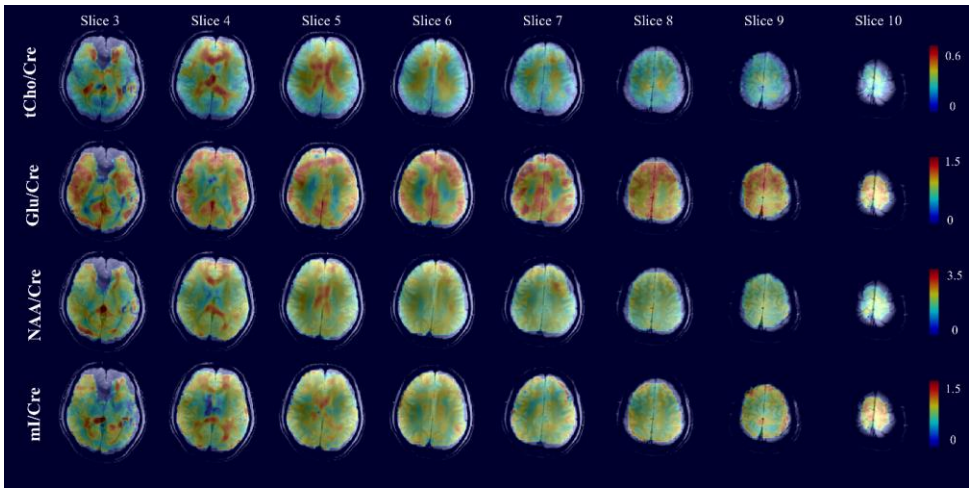

Figure 1- *whole-brain metabolite maps of four metabolites (/Cre) from a representative volunteer are shown.* All maps show high SNR and great anatomical details across the slices. Despite the high in-plane acceleration factor there are no visible residual lipid aliasing artifacts in the metabolite maps.

Conclusion

In this study whole-brain and high resolution metabolite maps acquired at 9.4T were presented. Using dynamic slice-wise B_0 shim updating and a robust acceleration method, high quality whole-brain metabolite maps with a nominal voxel size of ~80μL were acquired in about 25 minutes.

References

[1] Sabati et al, MRM 2015. [2] Maudsley et al, NMR in Biomed 2011. [3] Posse et al, MRM 1995. [4] Avdievitch et al, NMR in Biomed 2017. [5] Boer et al, MRM 2011. [6] Henning et al, NMR in Biomed 2009. [7] Bogner et al, NMR in Biomed 2012. [8] Nassirpour et al, NeuroImage 2017.

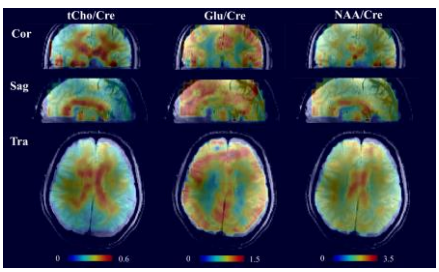

Figure 2- *Metabolite maps of three major metabolites (/Cre) shown from a representative volunteer on the central transversal, sagittal, and coronal slices.*