In Vivo MR - Spectroscopic Content: How to Validate and Test Repeatability of Short TE Proton MR Spectroscopy.

Ralph E. Hurd[1,2], Meng Gu[1], Laima Baltusis[2] and Daniel Spielman[1]

[1]Radiological Science Laboratory, Stanford University, CA, USA [2]Center for Cognitive and Neurobiological Imaging, Stanford University, CA, USA

A recent surge of interest in MR spectroscopy and standardization is documented in a recent consensus paper [1], and is further evidenced by a dramatic growth of the MR spectroscopy workgroup at the ISMRM. In addition to a developing Clinical focus based on fully automated 2-3 minute spectroscopic exams, academic support centers that cater to the application-driven synergy between functional and metabolic MR have also become popular. In these environments spectral editing and single voxel spectroscopy have both seen success. Validations of the more buried metabolites are important for these applications. This tutorial will review the metabolic content of short-TE spectra collected at 3T, along with methods for validation using phantoms and repeatability data.

In a recent comparison of PRESS and MEGA-PRESS quantification of glutathione (GSH) in human brain at 3T, Nezhad et al. [2] demonstrated a clear need for phantom validation when using basis-set fitting of metabolites such as GSH in short TE PRESS. It is not sufficient to have a repeatable fit value for a buried metabolite that is in the “physiological range”. If you don’t get a good regression over the physiological range in a phantom study, it is unlikely to magically work in vivo. In the Nezhad study, PRESS failed to achieve this criteria for GSH and MEGA-PRESS editing was found to provide a more reliable result. However, the SNR advantage of short-TE methods over long-TE editing-methods provides a compelling motivation for improving, testing, and validating a short-TE basis for glutathione that does work. Due to the complexity of the GSH resonances and their dependence on temperature [3], simulated basis spectra can be inaccurate, resulting in compromised in vivo quantification. The strategy used in this example was to add an experimental GSH (pH 7.2, 37C) spectrum to an otherwise synthetic basis illustrated here using LCModel [4]. Validation needs to consider the impact of partially overlapping metabolites that also may change under similar physiological conditions, such as ascorbate (ASC). The strategy of validation with phantoms and in vivo repeatability studies will be shown.

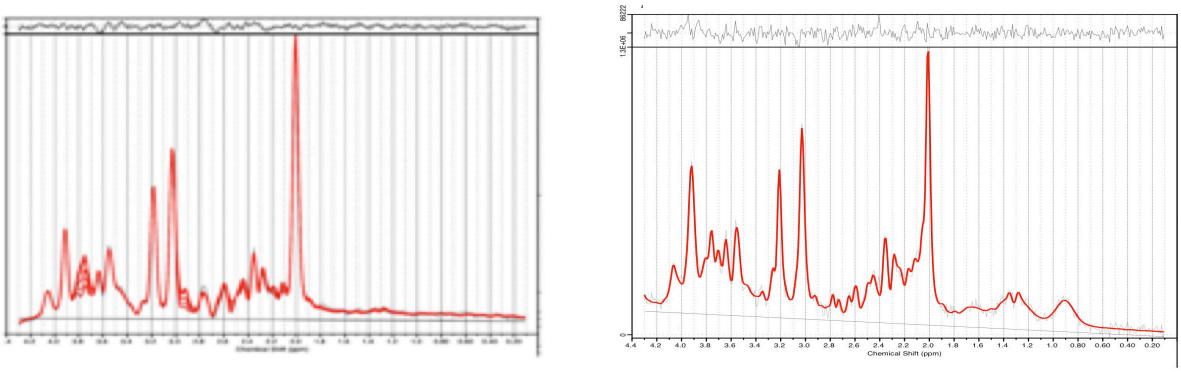

Figure 1. Left: Spectra and LCModel fits from a brain phantom in which GSH ranged from 0 to 4.0 mM in 0.5 mM steps while ASC was kept at 2.0 mM. Right: 18 x 18 x 18 mm^3 In Vivo ACC spectrum and fit.

1. Oz, G., Alger, J.R., Barker, P.B., et. al. Radiology **270**(3), 658-679 (2014).
2. Sanaei Nezhad, F., Anton, A., Parkes, L.M., Deakin, B., Williams, S.R.: Magn Reson Med **78**(4), 1257-1266 (2017).
3. Kaiser, L.G., Marjanska, M., Matson, G.B., Iltis, I., Bush, S.D., Soher, B.J., Mueller, S., Young, K.: J Magn Reson **202**(2), 259-266 (2010).
4. Provencher, S. W. (2001) Automatic quantitation of localized in vivo 1H spectra with LCModel. NMR Biomed 14, 260-264