# Measuring Glutathione using 1H MR spectroscopy at 3T: MEGA-PRESS vs. STEAM

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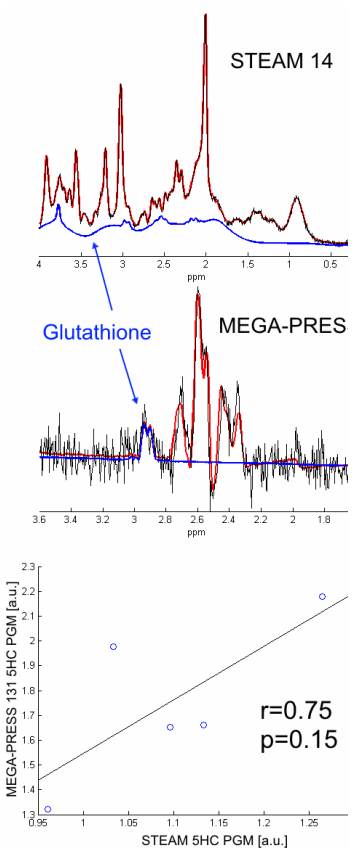


**Figure 1: Example spectra of a short echo STEAM and MEGA-PRESS. The correlation plot compares glutathione estimated in 5 HC using STEAM and MEGA-PRESS.**

**Target audience:** Researchers interested in using 1H MR spectroscopy (MRS) to measure Glutathione in the brain at 3T.

**Purpose:** To compare STEAM and MEGA-PRESS for measuring Glutathione at 3T.

**Introduction:** Amongst various key functions, glutathione is the main anti-oxidant in the brain and there is increased interest in measuring glutathione (GSH) *in vivo* using 1H MRS. Various MRS techniques have been proposed including MEGA-PRESS[1,2] and sequences using a very short TE such as ultra-short TE STEAM[3]. However on many clinical 3T systems neither of those sequences are available. In this study, we investigate if a conventional short TE STEAM sequence can be used to measure glutathione and compare the results to that of MEGA-PRESS in healthy controls (HC).

**Methods:** Written informed consent was obtained from 14 HC according to local ethics procedures. All subjects underwent a research scan on our 3T GE MR750 equipped with a 32 channel head coil. Structural MRI was acquired using a 3D T1w sequence with 1 mm isotropic voxel size. MRS voxels (35x25x20mm) were placed in grey matter around the anterior cingulate cortex (ACC) in 7 subjects and parietal medial grey matter (PGM) in the remaining 7 subjects. MEGA-PRESS (MP131) was performed using TR=2s with 128 ON and 128 OFF acquisitions and TE=131ms as previously proposed[2]. STEAM was acquired using TR=2s, TE=14ms and 128 averages. One additional HC was scanned on two separate days 4 weeks apart using the short echo STEAM sequence. On each day, the subject was scanned for two half hour scan sessions with a 5 minute break where the subject has been taken out of the scan room. In each of the half hour scan slots the STEAM sequence was run three times. MRS was placed in approximately the same location. This resulted in 12 STEAM spectra which were used to calculate the intra-subject coefficient of variation (CV) for a range of metabolites. Inter-subject CVs were calculated separately for the available ACC and PGM data as the standard deviation divided by the average metabolite proportion. Data was analysed with LCModel[4]. Pearson's correlation coefficient was calculated from the inter-subject data comparing MEGA-PRESS and STEAM. To assess the CV, MRS data were corrected for the brain parenchyma fraction by segmenting the T1w MRI into grey matter, white matter and CSF using SPM8[5].

| | STEAM repro PGM | STEAM 5HC PGM | MP131 7HC ACC | MP131 7HC PGM |
|---|---|---|---|---|
| tCho | 2.0% | 6.3% | - | - |
| Ins | 3.1% | 12.7% | - | - |
| Glx | 3.2% | 4.6% | - | - |
| Glu | 3.4% | 5.7% | - | - |
| tNAA | 4.7% | 6.4% | 9.8% | 6.9% |
| **GSH** | **5.4%** | **10.8%** | **17.2%** | **17.3%** |
| Gln | 6.4% | 10.1% | - | - |
| Cr | 6.6% | 5.8% | - | - |
| Asp | 13.8% | 8.5% | - | - |
| Tau | 15.0% | 25.8% | - | - |
| GABA | 20.2% | 22.0% | - | - |

**Table 1: CVs of the reproducibility study (12 scans 1 HC), 5 HCs using STEAM, and using MP131 in the ACC and PGM respectively.**

**Results:** Out of the 14 STEAM spectra, 9 had to be excluded due to ghosting artefacts around the critical 3.7ppm region, likely originating from not completely crushed spurious echoes. The remaining 5 spectra could be acquired artefact free in the PGM by changing the gradient order for the STEAM localisation. CVs are shown in Table 1. Figure 1 shows example spectra and a promising albeit non-significant correlation between values from the 5 STEAM spectra and the corresponding MP131.

**Discussion and Conclusion:** We have shown that a short echo STEAM sequence can give low intra- and inter-subject CVs across a number of metabolites. Due to the small number of artefact free STEAM spectra, further work is now needed to validate these initial results. Nevertheless, the low CVs and possible correlation with MP131 suggest that a short echo STEAM sequence seems well suited to estimate glutathione at half the scan time, high reproducibility and with less susceptibility to subject motion.

**References:** **[1]** Terpstra et al. Measurement of reduced glutathione (GSH) in human brain using LCModel analysis of difference-edited spectra. Magn Reson Med. 2003; 50, 19-23 **[2]** An et al. Measurement of glutathione in normal volunteers and stroke patients at 3T using J-difference spectroscopy with minimized subtraction errors. J Magn Reson Imaging. 2009; 30, 263-270 **[3]** Wijtenburg et al. Reproducibility of phase rotation STEAM at 3T: Focus on glutathione. Magn Reson Med. 2014; 72, 603-609 **[4]** Provencher. Estimation of metabolite concentrations from localized in vivo proton NMR spectra. Magn Reson Med. 1993; 30, 672-679 **[5]** Statistical Parametric Mapping, http://www.fil.ion.ucl.ac.uk/spm/

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