¹H SPECIAL-MRSI at Ultra-Short TE: Improved Metabolite Detection for Multiple Voxels in Human Brain at 3T

R. Mekle¹, V. Mlynarik², B. Walaszek¹, R. Gruetter^{2,3}, B. Ittermann¹, and F. Schubert¹

¹Physikalisch-Technische Bundesanstalt, Berlin, Germany, ²Laboratory for Functional and Metabolic Imaging (LIFMET), Ecole Polytechnique Federale de Lausanne, Lausanne, Switzerland, ³Departments of Radiology, Universities of Lausanne and Geneva, Lausanne and Geneva, Switzerland

Introduction

Benefitting from full signal intensity at short TE provided by the <u>spin ec</u>ho full <u>intensity acquired localized</u> (SPECIAL) MR spectroscopy (MRS) technique (1), improved metabolite quantification was achieved in ¹H single volume studies on clinical platforms (2). However, many applications require spectra from multiple voxels as can be acquired in MR spectroscopic imaging (MRSI) (3), e.g. to avoid sampling issues in tumor diagnostics. Thus, the aim of this study was to realize ¹H MRSI using SPECIAL at ultra-short TE (< 10 ms) in human brain on a clinical scanner at 3T and to determine whether an increased number of metabolites could be quantified in multiple voxels.

Methods

Scans were performed on a 3T Verio system Medical Solutions, (Siemens Erlangen, Germany) using a transmit/receive volume RF coil. First- and second-order shims were adjusted using FAST(EST)MAP (4). 2D ¹H MRSI data were acquired for N = 5 volunteers using the SPECIAL technique with the following scan parameters: VOI = 60x60x20 mm³, FOV = 160x160 mm², matrix = 16x16, TR/TE = 4000/6.6, $T_{acq} = 512$ ms, number of averages = 2. Metabolite ratios were determined using LCModel (5). Exemplarily, for each volunteer, results were averaged over 3 selected voxels of mainly white matter (WM) and mainly gray matter (GM) each before averaging over volunteers.

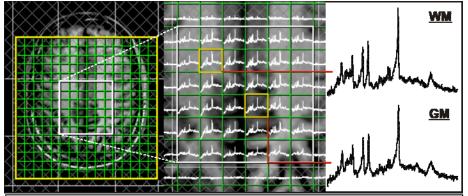


Fig. 1. ¹H MRSI grid (left) and spectra (center) from the parietal lobe of a human volunteer acquired with the SPECIAL-MRSI sequence. Sample spectra from a mainly WM and a GM-rich voxel are shown enlarged (right). Data processing for the latter consisted of zero-filling up to 4-k data points, 1 Hz Gaussian weighting of the FID, Fourier transformation, and phase correction.

Results

Localized shimming resulted in water linewidths of 7.0 ± 0.4 Hz for the VOI. Resulting spectra showed no major artifacts and no lipid contaminations (Fig. 1). The metabolites Glu, Ins, NAA, GPC+PCho, NAA+NAAG, Ins+Gly, Cr+PCr, and Glu+Gln were reliably detected (CRLB < 20%) in all usable 25 voxels from the VOI (excluding slice profile effects). On average, between 8 and 14 metabolites were reliably quantified for each voxel, and 11 metabolites for all of the selected voxels (Table 1). In addition, for the selected GM-rich voxels, the ratio /Cr for Gln was found as 0.40 ± 0.11 with CRLB = $9 \pm 4.7\%$.

Discussion

For the first time, 1H MRSI using the SPECIAL technique was realized on a clinical platform. The high data quality and minimization of T_2 losses and J-evolution effects due to the use of an ultra-short TE allowed the reliable quantification of several metabolites in multiple voxels. An increased ratio NAA/Cr in WM compared to GM was observed, as was also reported in (6). Schemes to reduce scan time, such as weighted k-space acquisitions are currently being explored to render the technique even more attractive for clinical application. It is concluded that MRSI with SPECIAL results in enhanced human brain metabolite quantification in multiple voxels.

Metabolite	WM /Cr	CRLB (%)	GM /Cr	CRLB (%)
Cr	0.76 ± 0.07	9 ± 2.5	0.71 ± 0.06	9 ± 4.3
GABA	0.38 ± 0.03	18 ± 1.3	0.34 ± 0.01	17 ± 2.3
Glu	0.83 ± 0.07	10 ± 1.3	1.21 ± 0.13	6 ± 1.0
GSH	0.19 ± 0.03	19 ± 4.0	0.18 ± 0.03	19 ± 7.2
Ins	0.95 ± 0.12	5 ± 1.2	0.89 ± 0.06	6 ± 1.0
NAA	1.41 ± 0.11	4 ± 0.4	1.29 ± 0.02	3 ± 0.6
GPC+PCho	0.32 ± 0.04	4 ± 0.6	0.23 ± 0.04	5 ± 1.2
NAA+NAAG	1.81 ± 0.19	3 ± 0.4	1.43 ± 0.08	3 ± 0.4
Ins+Gly	0.96 ± 0.12	5 ± 0.7	0.98 ± 0.09	4 ± 0.6
Cr+PCr	1.0 ± 0.0	3 ± 0.3	1.0 ± 0.0	3 ± 0.1
Glu+Gln	1.14 ± 0.07	10 ± 1.3	1.61 ± 0.22	6 ± 0.9

Table 1. Metabolite quantification of 1 H SPECIAL-MRSI spectra. Metabolite ratios and Cramer-Rao lower bounds (CRLBs) are given as mean values \pm standard deviations for selected WM- and GM-rich voxels ($n_{voxels} = 15$ each).

References (1) V. Mlynarik et al., MRM, 56(5), 965-970, 2006; (2) R. Mekle et al., MRM, 61(6), 1279-85, 2009; (3) T.R. Brown et al., PNAS, 79(11), 3523-26, 1982; (4) R. Gruetter, MRM, 43(2), 319-323. 2000; (5) S.W. Provencher et al., MRM, 30(6), 672-679, 1993; (6) S. Gruber et al., MRM, 49(2), 299-306, 2003.