Quantification of Human Brain Metabolites with Different RF Coils

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Indroduction

When interpreting quantitative magnetic resonance spectroscopy (MRS) studies of pathology, knowledge of the intra- and inter-subject variations is important, especially if deviations from normal mean values are measured in a single patient. In multi-center trials, use of different hardware may be an additional source of variation. For further analysis of such issues, the same group of subjects was investigated by single-voxel MRS in repeated sessions using two different types of radiofrequency (RF) coils.

Methods

Single-voxel ^{1}H PRESS (*TR* 5 s, *TE* 30 ms, 128 acq.) spectra were acquired from a 3-mL voxel in the fronto-parietal white matter in 12 healthy young volunteers (female 8; 28 ± 3 y) at 3 T (Siemens MAGNETOM Trio). Three spectra were recorded in separate sessions from each subject using a transmit/receive birdcage head coil and another three spectra using an 8-channel array head coil. Absolute metabolite concentrations were estimated using LCModel [1] and the unsuppressed water signal as a concentration reference. Three different methods for combining the array-coil data were investigated: (I) exclusive use of the spectrum from the coil element yielding the maximum SNR, (II) summation of all spectra from the 8 coil elements with weighting factors proportional to the SNR of the corresponding spectrum [2-4], (III) weighted summation of spectra above an individual SNR threshold. Spectra with significant artifacts in the residuals or a linewidth (full width at half height, FWHH) exceeding 0.08 ppm and concentration estimates with Cramer-Rao lower bounds (CRLB) above 50% were excluded from the final analysis [5].

Results and Discussion

LCModel outputs of spectra recorded with the two coils in a 26-year-old female volunteer are shown in Fig. 1. If compared to Method I (consideration of only one coil element), the average SNR of the array data improved by 17% if all spectra from the 8 coil elements were averaged (Method II) and by 23% for Method III, which was thus used for the further analysis. The difference between Methods II and III is indicative of phase and baseline errors of fitted spectra recorded with distant coil elements and, hence, rather poor quality. Average metabolite concentrations (mean values and standard deviations, SD) and CRLB's reported by LCModel are given in Table 1 for both RF coils. The SNR almost doubled, and the CRLB's of the strongest peaks (tNAA, tCr, tCh, mI) decreased by 9-16% for the major peaks (i.e., total *N*-acetyaspartate, tNAA; total creatine, tCr; total choline, tCh; and *myo*-inositol mI) when using the array instead of the birdcage coil indicating a higher fitting precision. This improvement did not lead to consistent differences of the SD's of the pooled data for both coils, which seemed to be dominated by biological variability and errors in repositioning the voxel. Highly significant differences in the absolute concentration estimates included an overestimation of glutamate plus glutamine (Glx) by 19% mostly due to an overestimation of glutamine (Gln) and an overestimation of mI by 7% when using the birdcage coil. This confirms previous reports of a tendency to overestimate these metabolites in low-SNR spectra [4] and may be related to residual baseline errors. As additional trends, the separation of *N*-acetylaspartate (NAA) and *N*-acetylaspartylglutamate (NAAG) was improved in the array-coil spectra, and a more reasonable estimate of the normal resting-state lactate (Lac) concentration (below 1 mM) was obtained. Intersubject variation was of the order of 6% for tNAA.

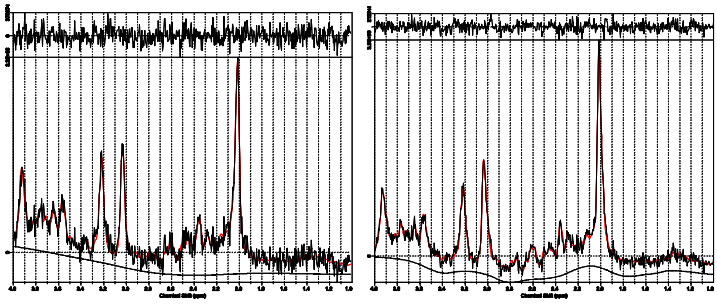

Figure 1. WM spectra recorded with the birdcage (left) and the 8-channel array coil (right).

Table 1. Average metabolite concentrations (mean ± SD).

	Birdcage coil		8-channel array coil	
Metabolite	Conc./mM	CRLB	Conc./mM	CRLB
Lac	1.42 ± 0.31	30.3%	0.95 ± 0.31	34.9%
tNAA	9.33 ± 0.35	3.3%	9.33 ± 0.82	2.8%
NAA	7.45 ± 0.42	4.6%	7.94 ± 0.59†	4.1%
NAAG	1.93 ± 0.46	20.9%	1.62 ± 0.74	24.4%
Glx	9.37 ± 0.94	9.1%	7.87 ± 1.08†	11.0%
Gln	3.12 ± 0.85	29.7%	2.34 ± 0.66*	29.9%
Glu	6.31 ± 0.80	12.0%	5.92 ± 0.73	10.1%
tCr	5.92 ± 0.40	4.9%	5.82 ± 0.59	4.1%
tCh	1.85 ± 0.26	5.3%	1.73 ± 0.36	4.5%
mI	3.81 ± 0.72	8.8%	3.56 ± 0.57*	8.0%
FWHH/Hz	6.2 ± 3.8		5.3 ± 1.3	
SNR	10.2 ± 2.9		20.0 ± 3.9†	

*$P < 0.01$; $^\dagger P < 0.001$

Conclusions

Use of a standard phased-array headcoil for single-voxel MRS offers a significant SNR benefit and yields improved precision in the fitting of signals from strongly coupled spin systems such as Glu and Gln. Alternatively, the scan time may be reduced by more than 50% even when studying WM voxels. Regarding systematic differences in the estimated concentrations of selected metabolites, care must be taken when pooling data recorded with different types of RF coils.

References. **[1]** S.W. Provencher, *Magn. Reson. Med.* 30: 672-9 (1993); **[2]** L.L. Wald et al., *Magn. Reson. Med.* 34: 440-5 (1995); **[3]** T. Prock et al., *Phys. Med. Biol.* 47: N39-46 (2002); **[4]** O. Natt et al., *Magn. Reson. Med.* 53: 3-8 (2005); **[5]** R. Kreis, *NMR Biomed.* 17: 361-81 (2004).