Evaluation of Minimum Scan Time for High Quality Quantitative *in vivo* ^{1}H MR Spectroscopy at 16.4T

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Introduction

One of the critical problems in localized *in vivo* ^{1}H NMR spectroscopy is the inherently low signal-to-noise ratio (SNR), because of the low concentration of metabolites, in the order of 10^{-3}-10^{-5} compared to the water signal [1]. Increasing the field strength is a promising approach to minimize the SNR problem. The purpose of this study was to investigate and determine the minimal number of averages necessary for achieving reasonable quantification accuracy, indicated by the Cramér-Rao lower bounds (CRLB) in LCModel [2], at 16.4T.

Methods

Two male Wistar rats weighing 234 g and 220 g were used in this study. All measurements were performed on a 16.4 T/26 cm magnet interfaced to a Bruker spectrometer (Bruker BioSpin GmbH, Ettlingen, Germany). An ultra-short TE STEAM sequence (TR 5000 ms, TE 1.7 ms, TM 20 ms, 2048 data point, 512 averages) was employed to obtain *in vivo* ^{1}H NMR spectra from the rat brain under isoflurane anesthesia. A volume-of-interest was placed in two brain regions, thalamus (6.5 x 3.5 x 2.5 mm^3) and striatum (7.7 x 3.0 x 3.0 mm^3). Phase cycling was used to compensate imperfections of spoiler gradients and each fid was saved separately. Before averaging, automatic phase correction [3] was applied to each fid and the frequency shift was corrected with reference to the NAA signal at 2.02 ppm. Then eddy current correction [4] was carried out based on a reference scan (8 averages) without water suppression. Finally, fids were summed to produce 32, 64, 128, 256, 384, 512 averages spectra. All post-processing and data reconstruction was done using an in-house program written in Matlab (MathWorks, Natick, MA, USA). Totally twenty four spectra (32, 64, 128, 256, 384, 512 averages x two brain regions x two rats) were quantified with LCModel.

Results

Fig. 1 shows spectra in the striatum illustrating increased SNR as function of number of averages. The amplitude of metabolite signals increases gradually while FWHM represents consistent values regardless of increasing averages, implying well corrected frequency shifts during measurements (Table 1). CRLBs according to increasing averages are shown in Fig. 2 (striatum) and in Fig. 3 (thalamus). Most metabolites except Gly, Ala, PCh were quantified with CRLBs below 20% at 64 averages. It is noticeable that NAAG, containing low concentration and heavily overlapping with NAA, GABA, and GSH, was quantified reliably even at 32 averages in contrast to results at 9.4T [5].

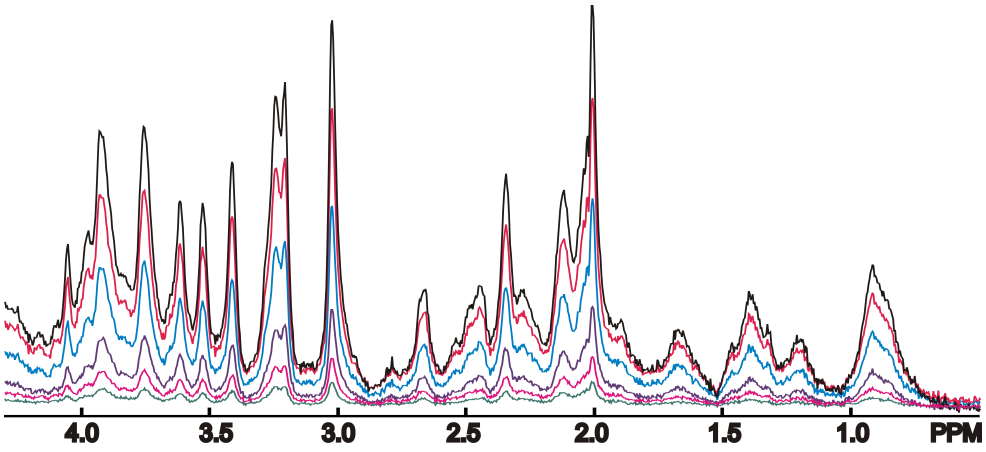

Figure 1. Series of *in vivo* ^{1}H NMR spectra acquired in striatum with averages of 16, 32, 64, 128, 384, and 512 (from bottom to top). All spectra were processed as described in the methods part and scaled identically.

Discussion

The high sensitivity at 16.4T allowed reliable quantification of most metabolites with only 64 averages, indicated by CRLBs below 20%. Acquiring more than 256 averages showed no benefits on quantification, except increasing the SNR. These results demonstrate the high sensitivity of ultra-high fields, which could provide significant decrease in measurement time and enhanced temporal resolution, an essential factor in functional MRS studies.

Averages	32		64		128		256		384		512	
	SNR	FWHM	SNR	FWHM	SNR	FWHM	SNR	FWHM	SNR	FWHM	SNR	FWHM
Striatum	16	0.029	22	0.029	29	0.029	36	0.029	40	0.027	43	0.029
Thalamus	18	0.024	24	0.023	29	0.025	37	0.027	41	0.027	45	0.025

Table 1. SNR and FWHM in striatum and thalamus, found in LCModel analysis.

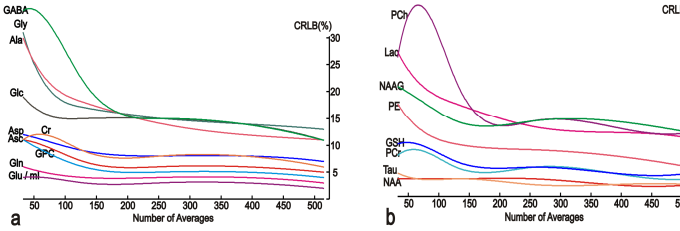

Figure 2. Series of CRLBs in striatum as a function of averages

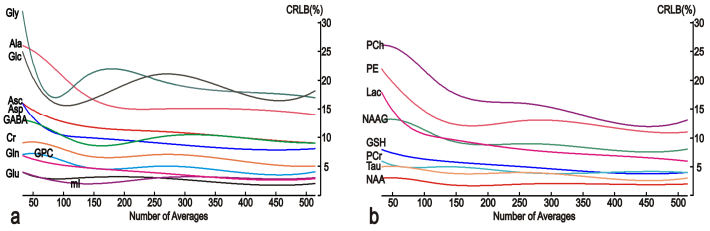

Figure 3. Series of CRLBs in thalamus as a function of averages.

References [1] Salibi N et al., Clinical MR Spectroscopy. Wiley;1998. p.3. [2] Provencher SW. MRM 1993;30:672-679. [3] Chen L et al., JMR 2002;158:164-168. [4] Klose W. MRM 1990;14:26-30. [5] Mlynárik V. et al., ISMRM 2007;3173.