

## Toward field independent quantitative MRS

Anders Tisell<sup>1,2</sup> and Peter Lundberg<sup>1,2</sup>

<sup>1</sup>Radiation Physics, Department of Medicine and Health Sciences, Linköping University, Linköping, Sweden, <sup>2</sup>Centre for Medical Image Science and Visualization (CMIV), Linköping University, Linköping, Sweden

**Target audience:** Neuroradiologist and MR physicists.

### Purpose

Quantitative Magnetic Resonance Spectroscopy (qMRS) is an excellent and often used technique for *in vivo* assessment of metabolite levels in the human brain, and it provides direct information of the metabolic status of the investigated tissue. Unfortunately, due to coil sensitivity, coil loading *etc.*, most current used magnetic resonance technique do not provide absolute metabolite concentrations. One useful approach to obtain correct scaling is to use an unsuppressed water signal as internal reference, a method known as water scaling (WS). However, the WS calculated concentrations will unfortunately be affected by varying amount of water relaxation in different tissues. Recently a method was proposed to include a calibration of the relaxation effects based on the use of quantitative MRI (qMRI)[1]. In this work, metabolite concentrations were calculated using this latter method and they are referred to as 'qMRS concentrations'. The purpose of the present work was to investigate how large the qMRS concentration differences were between measurements obtained using a 1.5 T system, or a 3.0 T MRI-scanner. Moreover, another aim was to determine to what extent the qMRS-method would improve the accuracy of the determined concentrations, compared to the conventional WS method. An interesting aspect is to investigate to what extent the typically longer T1 values at higher field strengths affect the determined concentration values.

### Materials and Methods

Twelve healthy volunteers (7/5 F/M, age: 21-30 y) were included in this work. The subjects underwent a repeated MR examination in both a 1.5 T and a 3.0 T MRI scanner using the standard MRS protocol at our site. The 1.5 T examination was performed on a Philips Achieva (Philips, Best, The Netherlands), and <sup>1</sup>H-MRS was acquired using a PRESS sequence (TE 30 ms; TR 3 s; number of transients 128) and qMRI measured using QRAPMASTER[2] sequence (4 dynamics; TR 5 s; TE 16-96 ms; resolution 3.0x1.3x1.3 mm<sup>3</sup>). The 3.0 T examination was performed using a Philips Ingenia system (Philips, Best, The Netherlands).

Table 1. Group mean and standard error of mean (SE) metabolite concentrations calculated using the qMRS and WS methods.

	1.5 T				3.0 T			
	qMRS		WS		qMRS		WS	
	Mean	SE	Mean	SE	Mean	SE	Mean	SE
mlns	4.78 ± 0.28		4.83 ± 0.28		5.22 ± 0.26		5.70 ± 0.27	
tCho	1.87 ± 0.06		1.89 ± 0.06		1.97 ± 0.06		2.16 ± 0.06	
tCr	5.72 ± 0.11		5.78 ± 0.10		6.60 ± 0.10		7.21 ± 0.10	
tGlx	8.71 ± 0.32		8.82 ± 0.36		9.22 ± 0.30		10.10 ± 0.34	
tNA	12.34 ± 0.24		12.48 ± 0.24		13.18 ± 0.23		14.42 ± 0.24	
F <sub>ATT<sub>H2O</sub></sub>	0.692 ± 0.002		0.7†	-	0.640 ± 0.002		0.7†	-

† 0.7 is the default value for F<sub>ATT<sub>H2O</sub></sub>

parameter for attenuation of water signal (F<sub>ATT<sub>H2O</sub></sub> = 0.7). Finally, qMRS concentrations were calculated by calculating a F<sub>ATT<sub>H2O</sub></sub> value for each MRS voxel as described in [1].

<sup>1</sup>H-MRS was acquired using a PRESS sequence (TE 35 ms; TR 4 s; number of transients 96). The qMRI was measured using the QRAPMASTER[2] sequence with identical spatial parameters as for 1.5 T. Quantitative R1, R2 and water concentration maps were calculated using SyMRI brain studio (Synthetic MR AB, Linköping Sweden). The MRS signal was quantified using LCModel ver. 6.3. WS concentrations were calculated using the default

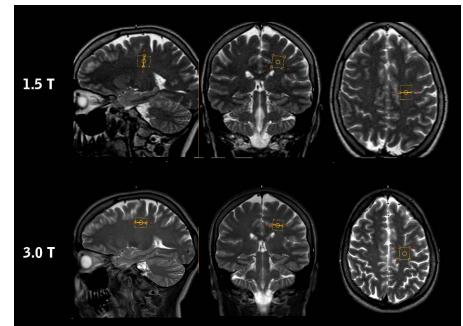


Figure 1. Typical placement of MRS voxel shown in corresponding position on the 1.5 T system and on the 3 T system.

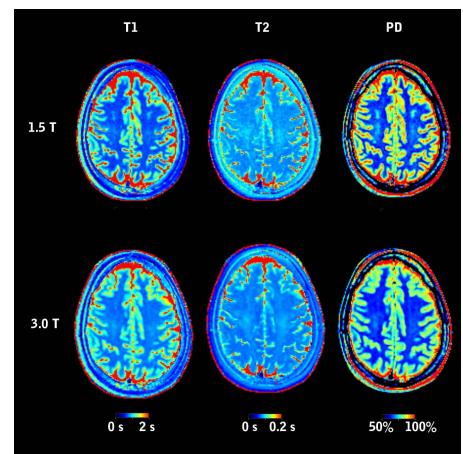


Figure 2. qMRI maps of longitudinal relaxation time (T<sub>1</sub>), transverse relaxation time (T<sub>2</sub>) and proton density (PD).

Table 2. Difference in calculated concentration between the 1.5 and 3 T system.

		Difference	SE
mlns	qMRS	0.45	± 0.24
	WS	0.88 **	± 0.25
tCho	qMRS	0.10	± 0.04
	WS	0.27 ***	± 0.05
tCr	qMRS	0.88 ***	± 0.13
	WS	1.43 ***	± 0.13
tGlx	qMRS	0.50	± 0.43
	WS	1.28 **	± 0.46
tNA	qMRS	0.84 ***	± 0.16
	WS	1.94 ***	± 0.17
F <sub>ATT<sub>H2O</sub></sub>		-0.053 ***	± 0.001

\*\* P < 0.01, \*\*\* P < 0.001

### Results

The mean difference in estimated F<sub>ATT<sub>H2O</sub></sub> between the measurements obtained using 1.5 T and 3.0 T was -0.053 with SE calculated from the qMRI data. Mean qMRS and WS concentrations are presented in Table 1 and the difference in calculated qMRS and WS concentration are presented in table 2

### Discussion

The differences in determined metabolite concentrations between the 1.5 T and 3.0 T system were significantly smaller for the concentrations calculated using the qMRS method, than with conventional WS. This showed that incorporating qMRI measurements of the water relaxation improves the accuracy of the determined metabolite concentrations. However, the qMRS concentrations were systematically higher on the 3 T system. This was likely caused by the shorter TR that was used on the 1.5 T system, leading to differentially more attenuated signals. To correct for this latter effect a method for correcting for the metabolite relaxation rates could be used, although this is not entirely straightforward due to the relatively time-consuming procedure that is required.

### Conclusion

Using qMRI for calibration of the internal water increased the accuracy of the estimated metabolite concentrations significantly. Due to the relative simplicity of such measurements we would recommend such approach whenever absolute metabolite concentrations are required.

References: [1]. Tisell, A., et al., Procedure for quantitative <sup>1</sup>H. MRM, 2012. [2]. Warntjes, J.B.M., et al., Rapid magnetic resonance quantification. MRM, 2008. **60**(2): p. 320-329.