Investigation on magnetic resonance imaging (MRI) scanner-dependence and software-dependence of T_1 and T_2 relaxation times measurements at 1.5 T

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Authors:	D. Cicolari[1], D. Lizio[2], P. Pedrotti[2], R. Sironi[2], M. T. Moioli[2], A. Lascialfari[2], M. Mariani[1], A. Torresin[2]; [1]Pavia/IT, [2]Milan/IT
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Aims and objectives

In recent years, technological developments of MRI scanners have allowed the mapping sequences to become clinically feasible: these sequences generate parametric maps able to display tissue magnetic properties [1, 2].

Qualitative and quantitative information of tissues [3] should be obtained through the appropriate image acquisition and analysis of the body physical properties, like *spin-lattice* relaxation times (T_1) and *spin-spin* relaxation times (T_2).

A new approach to the evaluation of standardization will be necessary in order to take in to account the possibility of finding T_1 and T_2 mapping independence from the MRI scanners used.

Aim of this study was the assessment of the standardization in measuring nuclear relaxation times for ^{1}H nuclei from post-processing of phantom images acquired with different vendor clinical magnetic resonance imaging (MRI) scanners and a NMR spectrometer.

Methods and materials

Six vials (ID 2, 4, 11, 13, 14 and 15) of an Eurospin phantom (Diagnostic Sonar, Livingston, UK), filled with agarose gels doped with gadolinium, were used to compare relaxation times results obtained from measurements performed with different scanners.

Standard reference values of ID inserts were needed to be established with NMR methodology.

First, the vials were scanned with Tecmag Apollo NMR spectrometer (Tecmag, Houston, TX, USA) at University Physics Department's laboratories using standard sequences in order to restate reference T_1 and T_2 relaxation times values at 1.5 T. Saturation Recovery (SR) and Inversion Recovery (IR) for T_1 measurements and Spin Echo (SE) and CPMG (Carr-Purcell-Meiboom-Gill) for T_2 measurements were applied. Sequences were planned with the Tecmag NTNMR software and signals were analyzed with the non-commercial QTNMR software, developed by NMR-NQR group. SR and IR data were then fitted with a 3-parameters exponential recovery function [$y = A - B \exp(- x / T_1)$]; SE and CPMG data were fitted with a 2-parameters exponential decay function [$y = A \exp(- x / T_2)$] [4]. Fitting procedure was performed by means of gnuplot software (http://gnuplot.info).

The vials of the Eurospin phantom were also scanned through two MRI scanners from different vendors: a Siemens MAGNETOM Aera (1.5 T) and a General Electric Signa (1.5 T), both located in our Hospital. Phantom images were acquired with body coils and by means of standard clinical sequences SE (Spin Echo, 3 images: T_E from 20 ms to 100 ms; T_R = 1.5 s) and IR (Inversion Recovery, 8 images: T_I from 100 ms to 3300 ms; T_R = 5 s).

Images were processed with different vendor independent software (Fig. 1): cvi42 (Circle Cardiovascular Imaging Inc., http://www.circlecvi.com, CE mark) and Segment (open source, [5, 6]); a manual computation of relaxation times was also performed using the gnuplot software. For each slice, Cvi42 and Segment generated a map performing a pixel per pixel fit; measurements were executed with ImageJ and Segment by calculating the mean value (and its standard deviation) in a selected ROI on each map. Then, a weighted average was taken from relaxation times values measured in corresponding ROIs in maps of each slice. The intensities, measured with ImageJ, in corresponding ROIs selected in each image of the acquisition series were also plotted and fitted by means of gnuplot. Then, a weighted average was taken from relaxation times values obtained by the fitting procedure of each slice.

Images for this section:

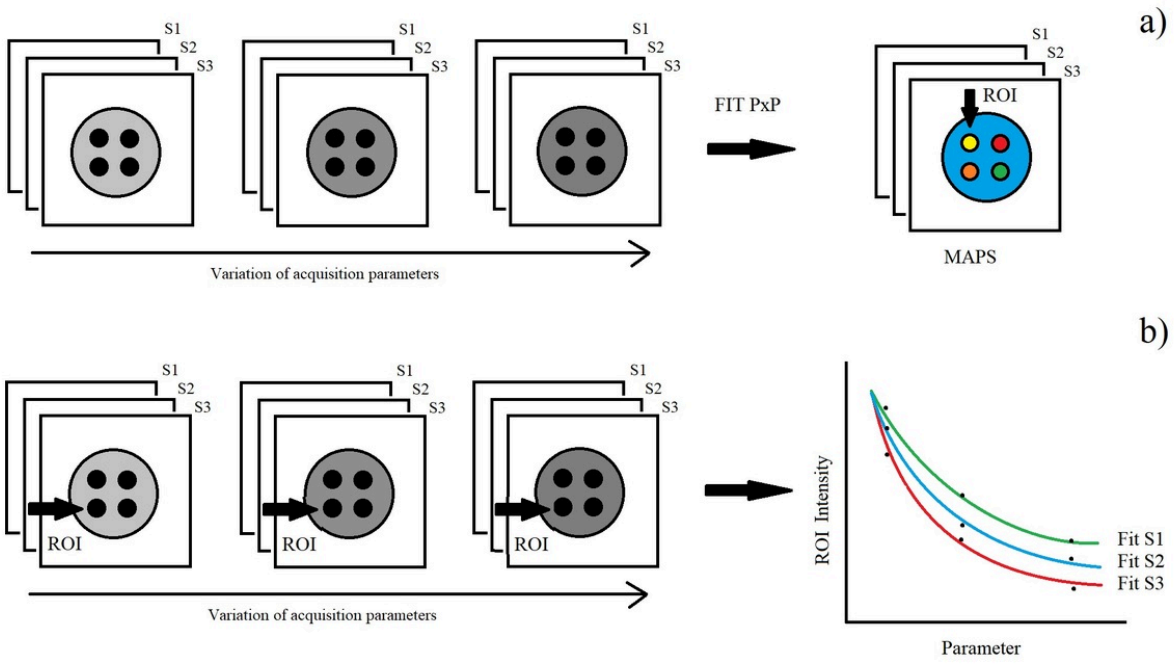

Fig. 1: a) Maps generation and measurement: for each slice (indicated by S1, S2, S3), Cvi42 and Segment generated a map performing a pixel per pixel fit; measurements were executed with ImageJ and Segment by calculating the mean value (and its standard deviation) in a selected ROI on each map. Then, a weighted average was taken from relaxation times values measured in corresponding ROIs in maps of each slice. b) Manual procedure performed with ImageJ and gnuplot: the intensities, measured with ImageJ, in corresponding ROIs selected in each image of the acquisition series were plotted and fitted by means of gnuplot. Then, a weighted average was taken from relaxation times values obtained by the fitting procedure of each slice.

Results

The NMR spectrometer results at 23°C are listed in Tab. 1.

Tab. 1. Relaxation times values of the Eurospin phantom inserts measured with the NMR spectrometer at 23°C.

Insert ID	SR - T_1 (ms)	IR - T_1 (ms)	SE - T_2 (ms)	CPMG - T_2 (ms)
2	348 ± 6	294 ± 10	20 ± 1	50 ± 2
4	507 ± 9	427 ± 12	18 ± 1	33 ± 1
11	1039 ± 20	886 ± 44	17 ± 1	71 ± 1
13	2923 ± 78	2491 ± 79	21 ± 1	156 ± 3
14	2990 ± 50	2311 ± 53	21 ± 1	89 ± 1
15	1371 ± 19	1302 ± 65	20 ± 1	113 ± 2

From the NMR spectrometer measurements (Tab. 1), IR T_1 values showed on average an underestimation of 16% compared to SR T_1 values.

T_2 values measured with the spectrometer Spin-Echo sequence (Tab. 1) were affected by a high diffusion, which suppressed the signal from the vials and it shortened the relaxation of every scanned vials to a value near 20 ms. Thus, values from SE sequences of the NMR spectrometer will not be taken as references: as reference values for the T_2relaxation time we considered the CPMG results.

As can be seen in Fig. 2, a Bland Altman analysis stated that results obtained with Cvi42 and Segment had a confidence level of ±0.7%, meaning that the algorithms to generate maps were similar for the two software.

In order to compare T_1 and T_2 values of MRI results with those estimated with the NMR spectrometer (Tab. 1), which are standard reference values, the temperature difference of the various sites in which acquisitions were performed must be considered: room temperature of spectrometer site was 23°C, Aera site was at 20°C and Signa compartment was at 21°C. The comparison (Fig. 3) was performed by reconducting values measured from cvi42 maps (Aera 20°C, Signa 21°C) at the same temperature of the standard reference values obtained by NMR spectrometer analysis (23°C), assuming a linear dependence. The comparison was not possible for T_1 values of inserts 13 and 14 because of inaccuracy and imprecision due to the chosen sampling of the response

curves (the image acquisition parameter T_I should be distributed in a temporal range which must be at least three times longer than the T_1 value of the scanned object).

Gnuplot manual fit procedure allowed the measurement of real fit errors of estimated relaxation times values. In mapping procedure all the information about fit errors is lost, as it consists in assigning a bit per pixel (BPP) value corresponding only to the estimated relaxation times values in a certain position: errors measured with Cvi42 and Segment are related only to the variability of fitted relaxation times values assigned to each pixel in a selected ROI of the maps, while errors estimated with gnuplot reflect the goodness of the sampling of the response curves.

Images for this section:

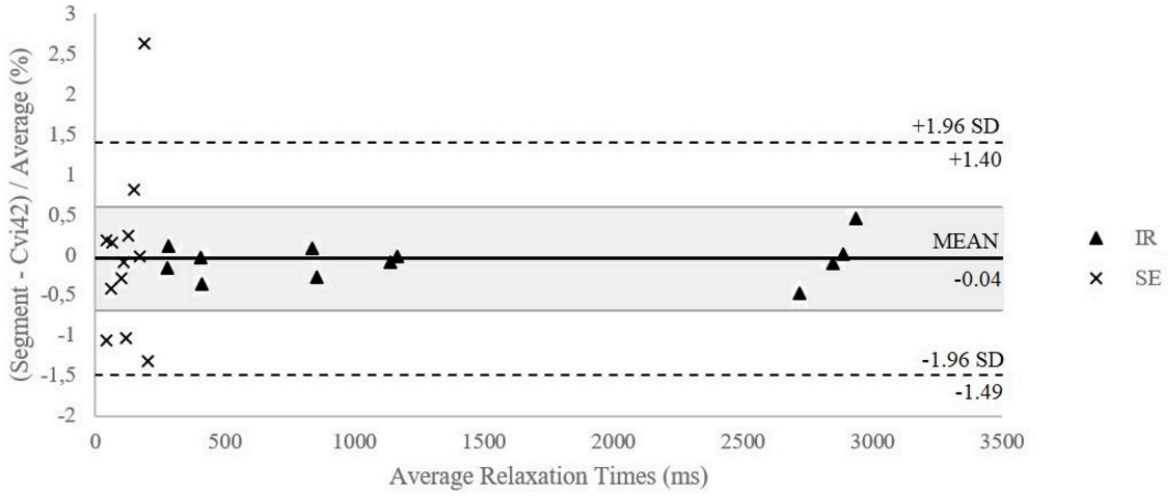

Fig. 2: Segment vs Cvi42: Bland Altman plot of the comparison of values measured on maps generated by Segment and Cvi42. The confidence limits are illustrated as the grey area (-0.68% to 0.60%).

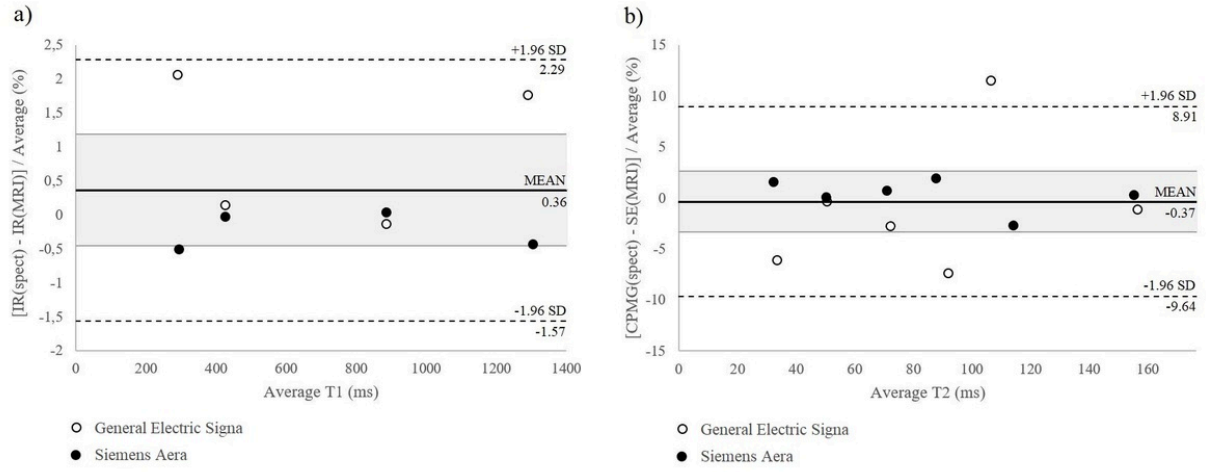

Fig. 3: a) T1 comparison: Bland Altman plot of T1 values of Eurospin inserts measured in maps generated by Cvi42 with IR sequences images acquired with both MRI scanners (Siemens Aera and General Electric Signa) reconducted at 23°C with IR NMR spectrometer T1 values taken as references. The confidence limits are illustrated as the grey area (-0.46% to 1.18%). b) T2 comparison: Bland Altman plot of T2 values of Eurospin inserts measured in maps generated by Cvi42 with SE sequences images acquired with both MRI scanners (Siemens Aera and General Electric Signa) reconducted at 23°C with CPMG NMR spectrometer T2 values taken as references. The confidence limits are illustrated as the grey area (-3.37% to 2.64%).

Conclusion

A good agreement was observed between IR values, obtained with the three different scanners (NMR spectrometer at Pavia University, Siemens Aera and General Electric Signa MRI scanners in our Hospital), and between CPMG and SE values, obtained respectively with the NMR spectrometer and with the MRI scanners: the expected linear dependence of relaxation times with temperature is observed considering the experimental errors (± 3% for T_1 and ± 10% for T_2, limits of agreement, Fig.3). The correspondence between CPMG (NMR spectrometer) and SE (MRI scanners) values suggests that MRI scanners use a sequence similar to the CPMG one. Agreement is not found if system response curves are not sampled properly, especially for T_1 estimation methods.

Estimation methods are MRI diagnostic scanner-independent, but not sequence-independent: as can be seen in NMR spectrometer results, IR underestimated (15%) values determined with SR.

Gnuplot analysis helped in highlighting estimated relaxation times errors, of which all information are lost in mapping procedure: analysis methods as those proposed by Kellman et al. in 2013 [7], i.e. the creation and measurements of standard deviation maps associated to parametric maps, should be considered.

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