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T₂ Relaxation Time Quantitation Differs Between Pulse Sequences in Articular Cartilage

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Abstract

Background—To compare T₂ relaxation time measurements between MR pulse sequences at 3 Tesla in agar phantoms and in vivo patellar, femoral, and tibial articular cartilage.

Methods—T₂ relaxation times were quantified in phantoms and knee articular cartilage of eight healthy individuals using a single echo spin echo (SE) as a reference standard and five other pulse sequences: multi-echo SE (MESE), fast SE (2D-FSE), magnetization-prepared spoiled gradient echo (3D-MAPSS), three-dimensional (3D) 3D-FSE with variable refocusing flip angle schedules (3D vfl-FSE), and quantitative double echo steady state (qDESS). Cartilage was manually segmented and average regional T₂ relaxation times were obtained for each sequence. A regression analysis was carried out between each sequence and the reference standard, and root-mean-square error (RMSE) was calculated.

Results—Phantom measurements from all sequences demonstrated strong fits ($R^2 > 0.8$; $P < 0.05$). For in vivo cartilage measurements, R^2 values, slope, and RMSE were: MESE: 0.25/0.42/5.0 ms, 2D-FSE: 0.64/1.31/9.3 ms, 3D-MAPSS: 0.51/0.66/3.8 ms, 3D vfl-FSE: 0.30/0.414.2 ms, qDESS: 0.60/0.90/4.6 ms.

Conclusion—2D-FSE, qDESS, and 3D-MAPSS demonstrated the best fits with SE measurements as well as the greatest dynamic ranges. The 3D-MAPSS, 3D vfl-FSE, and qDESS demonstrated the closest average measurements to SE. Discrepancies in T₂ relaxation time quantitation between sequences suggest that care should be taken when comparing results between studies.

Keywords

cartilage; magnetic resonance imaging; T₂ relaxation time mapping; pulse sequence

Osteoarthritis (OA) IS A degenerative joint disease that affects articular cartilage, subchondral bone, and other tissues predominantly in the hand, knee, and hip (1).

Approximately 20 million people in the United States live with OA, and this number is expected to increase due to an aging population and increasing rates of obesity (2,3).

Conventional MRI provides a noninvasive assessment of soft-tissue morphology and allows for detection of cartilage defects that are characteristic of OA (4). However, these morphological changes are preceded by degradation of the cartilage ultrastructure, including breakdown of the collagen matrix and loss of supporting proteoglycans (5). Detection of early osteoarthritic changes requires more advanced MR sequences that are sensitive to biochemical changes in cartilage (6,7).

Spin-spin or T_2 relaxation time mapping is one such technique that has successfully been used to track early osteoarthritic changes in patients (8–12). The biochemical information captured by T_2 relaxation is still under investigation. In articular cartilage, T_2 relaxation times increase with increases in free water content and mobility (13). A healthy, highly structured collagen matrix immobilizes water and keeps it bound to supporting macromolecules. This system breaks down with early OA, and T_2 relaxation time is thus believed to provide an indirect assessment of collagen content and orientation. Other evidence suggests that T_2 relaxation times increase with decreases in proteoglycan content within the matrix (14). Most importantly for OA research, T_2 relaxation times generally increase with biochemical degradation of cartilage. This phenomenon makes T_2 relaxation time mapping an effective tool for tracking changes over time within and between patient and control populations. For this reason it has been selected for use in large-scale clinical studies such as the Osteoarthritis Initiative (OAI) (15).

Compared with other quantitative imaging techniques, T_2 relaxation time mapping presents its own advantages and disadvantages. The primary advantage of T_2 relaxation time mapping is that it can be performed without the use of intravenous contrast agents or ionizing radiation, unlike other quantitative imaging sequences such as dGEMRIC (delayed gadolinium-enhanced MRI of cartilage) and CT (computed tomography) arthrography. The primary disadvantage associated with T_2 relaxation time mapping is its susceptibility to the magic angle effect, in which T_2 values may be artificially elevated in certain regions based upon the orientation of cartilage in relation to the main magnetic field (16). Regions susceptible to this effect, particularly along curved surfaces such as the femoral head and condyles, are assumed to have some influence from magic angle. However, the magic angle effect should not impact results tracking changes over time or between study populations, so long as subjects are positioned consistently within the magnet.

While T_2 relaxation time is meant to be an objective measure, several factors have been shown to influence T_2 quantitation. Significant differences in T_2 quantitation have been observed based on the selection of MR scanner (17), radiofrequency coil (18), and postprocessing fitting method (19). An additional potential source of variation in T_2 quantitation is the MR pulse sequence used (20). As with all other external factors affecting T_2 quantitation, the impact of pulse sequence selection must be understood for researchers and clinicians to interpret and compare results between studies.

Several MR pulse sequences have been developed for T_2 relaxation time quantitation. The most fundamental of these are stimulated echo acquisition mode (STEAM) spectroscopy (21) and single echo spin echo (SE). These sequences suffer from low signal-to-noise ratio (SNR) and long scan times, respectively, that prevent their use for clinical examination of cartilage ultrastructure. More advanced 2D approaches overcome these drawbacks and include multi-echo SE (MESE) and fast SE (FSE). 3D approaches are also currently available for T_2 relaxation time mapping. A magnetization-prepared angle-modulated partitioned k -space spoiled gradient echo sequence (3D-MAPSS) uses a nonselective T_2 magnetization preparation followed by a 3D spoiled gradient echo (SPGR) acquisition (22). Additionally, a 3D FSE sequence with variable refocusing flip angle schedules (3D vfl-FSE) uses a T_2 magnetization preparation followed by a pseudo steady-state 3D FSE acquisition (23). In addition to sequences that rely on acquiring multiple echo times to fit T_2 relaxation to an exponential decay, a 3D double-echo steady state (DESS) sequence has been modified for T_2 relaxation time quantitation, and is known as qDESS (24,25). Analysis of the variation in T_2 quantitation between all these sequences can provide a stronger basis for interpreting quantitative outcomes and can eventually allow for comparison of absolute and relative relaxation time differences across studies that use different pulse sequences for T_2 relaxation time mapping.

To date, variation in quantitative outcome from T_2 relaxation time mapping sequences has received limited attention, but previous reports suggest this variation is not trivial. The selection of a multi-slice versus a single-slice sequence has been shown to impact cartilage T_2 relaxation times by an average of 6–9% (26). Additionally, T_2 relaxation times have been shown to vary up to 42% between MESE and FSE sequences in agar phantoms (27). In vivo studies of cartilage have been limited to analysis of patellar cartilage in the axial plane, and differences of up to 48% between FSE and SE sequences have been reported (28,29). More recently, an average difference of 15% has been reported between 3D-MAPSS and SE within patellar cartilage (20).

An analysis of sequence-dependent variation within femoral and tibial cartilage is lacking. Previous reports use axial imaging and are therefore limited to analysis of patellar cartilage. Additionally, studies have compared only a few pulse sequences at a time, so a singular analysis of many sequences is lacking. The aim of the present study is to assess the differences in T_2 relaxation time quantitation between an array of MR pulse sequences in agar phantoms and in vivo patellar, femoral, and tibial articular cartilage and to compare these results with a SE reference standard.

MATERIALS AND METHODS

Phantoms and Volunteers

Imaging experiments were performed on an agar phantom with regions of varying relaxation time and on knees of healthy volunteers. All imaging was performed on a 3.0 Tesla (T) MRI scanner (MR 750, GE Healthcare, Milwaukee, WI) with a 16-channel receive-only coil (NeoCoil, Pewaukee, WI). The phantom was made in-house by immersing six cylindrical vials of agar gel into a larger container of water. A range of T_2 relaxation times similar to that of articular cartilage (~30–70 ms) was achieved amongst the vials by altering

concentration of scientific-grade (Bacto Laboratories, NSW, Australia) from 10 to 50 g/L (30,31). Full dissolution of agar into deionized water was achieved through intervals of heating and cooling with careful stirring, to avoid spillover and the formation of air bubbles (32). The T_1 relaxation time constant for the agar was measured to be 1050 ± 170 ms, similar to that of in vivo articular cartilage (33). In vivo images were obtained from healthy knees of eight volunteers (six males, two females; mean age, 24.4 ± 4.6 years; mean body mass index, 23.3 ± 4.2). The study was approved by the Institutional Review Board before scanning and informed consent was obtained from all participants.

Imaging Protocol

Phantoms were scanned with nine MR pulse sequences: single slice SE, STEAM spectroscopy (21), multislice SE, single slice MESE, multi-slice MESE, 2DFSE, 3D-MAPSS (22), 3D vfl-FSE (23), and qDESS (24). STEAM spectroscopy from a single voxel was acquired for each phantom. qDESS involved obtaining two sets of images: one set with a large spoiler gradient area ($135.62 \text{ ms} \cdot \text{mT/m}$) and small flip angle (18°) and another set with a small spoiler gradient area ($27.12 \text{ ms} \cdot \text{mT/m}$) and large flip angle (35°). All images were acquired in the sagittal plane with the following imaging parameters: FOV, $16 \times 16 \text{ cm}^2$; matrix, 128×128 ; bandwidth, $\pm 62.5 \text{ kHz}$, and slice thickness 3 mm. Additional parameters are outlined in Table 1.

Volunteers were scanned with the same sequences as the phantoms, excluding STEAM spectroscopy and single slice sequences. STEAM was not used in vivo due to SNR and partial volume limitations. Matrix size for in vivo images was 256×256 , and all other parameters were identical to those for the phantom experiments. The legs of volunteers were positioned neutrally.

Image Analysis

T_2 relaxation times were calculated pixel-by-pixel using packaged software (OsiriX DICOM Viewer, Pixmeo Sarl, Bern, Switzerland). For all sequences, except qDESS, relaxation times were calculated by mono-exponentially fitting to the equation: $S(t) = S_0 \cdot e^{(-t/T_2)}$. The signal in each of the four magnitude qDESS images is dependent on T_1 and T_2 relaxation, as well as the apparent diffusion coefficient (ADC). The Wu-Buxton signal model was used to generate a signal database containing signals based on a range of possible values of T_1 , T_2 , and ADC for the four magnitude images (34). For each voxel, this signal database was searched to match the observed signal magnitudes, thereby providing a corresponding estimation for T_1 , T_2 , and ADC (24).

Regions of interest (ROIs) were manually defined by one reader (SJM) for all images using the same packaged software. For phantom images, the slice captured by single-slice sequences in the mid-region of the phantom was used for analysis and identical square ROIs were placed in the center of each vial. Square ROIs were chosen to match the voxel selected for STEAM spectroscopy. For in vivo knee images, ROIs were drawn in both the medial and lateral compartments to include patellar, femoral, and tibial cartilage. The slices capturing the most central region of the medial and lateral femoral condyles were chosen for segmentation. Patellar cartilage was segmented to include equal lengths of superior and

inferior ROIs. Femoral cartilage was segmented into anterior, central, and posterior ROIs, with borders defined by the outer edges of the meniscus. Tibial cartilage was segmented to include equal lengths of anterior and posterior ROIs. Lastly, each ROI was divided in half to generate deep and superficial regions of equal thickness, as demonstrated in the lateral slice in Figure 1. Cartilage was included in a ROI only where its thickness spanned at least two full cartilage voxels, so as to exclude voxels in bordering tissues. In cases of slight movement of the knee between scans, images were manually registered using rigid transformations so that each sequence included pixels from the same physical location. A few cases of dramatic movement between scans necessitated the exclusion of some measurements. Within each ROI, T_2 relaxation times were averaged for each sequence.

Statistical Analysis

Single slice SE T_2 relaxation time measurements were used as the reference standard for phantom data. Measurements from each sequence were plotted against those from the SE reference standard. Linear regressions were performed on each of these plots to determine the regression line equations and coefficients of determination (R^2 values).

Similarly, multi-slice SE T_2 relaxation time measurements were used as the reference for in vivo data and regression analyses were performed for deep and superficial cartilage regions, as well as all regions. The slope of each regression line is used as an indicator of the dynamic range of T_2 relaxation times output by each sequence. For example, a steep slope indicates a large dynamic range while a shallow slope indicates a small dynamic range of T_2 relaxation time outputs from a sequence. The root-mean-square-error (RMSE), as a measure of similarity in T_2 quantitation to that of the SE pulse sequence, was calculated for each sequence. The percent difference between all sequences for all regional T_2 measurements

was also calculated using the equation: $Percent\ difference = \frac{\sum_1^n (\frac{comparison - reference}{reference} * 100)}{n}$, for n total regions. Finally, mean T_2 relaxation times for six ROIs were reported; they were deep and superficial regions of the medial central femur, medial posterior femur, and lateral posterior tibia. These regions were selected because they have shown early osteoarthritic changes and are thus most relevant in MR research on OA (35).

RESULTS

Phantom Studies

3D-MAPSS, 3D vfl-FSE, and qDESS each provided average T_2 measurements within 5% of SE measurements while other sequences demonstrated greater differences from SE. Measurements from STEAM spectroscopy were an average of 8% lower than those from SE. Measurements from both single and multislice MESE sequences were an average of 30% lower than those from SE, while 2D-FSE measurements were an average of 40% higher than those from SE. T_2 relaxation times of vials within the phantom ranged from 23 to 64 ms, as determined by the single slice SE reference standard (Fig. 2). The effect of a multi-slice acquisition on T_2 quantitation with the SE sequence appeared negligible (Fig. 3). Despite the observed variation in absolute T_2 values, the relationships between

measurements from each sequence with SE measurements allowed for high coefficients of determination ($R^2 > 0.8$; $P < 0.05$ for all sequences).

In Vivo Studies

There was greater variation in T_2 quantitation between pulse sequences in vivo, with average percent differences between any two sequences ranging from 0 to 38% (see Fig. 4). Standard deviations describing these differences ranged from 8 to 22%. 3D vfl-FSE and 3D-MAPSS showed the most agreement in T_2 quantitation, with an average difference of 0–1%. Measurements from the 2D-FSE sequence were 25–38% higher than those from all other sequences. This trend can be observed qualitatively in the T_2 relaxation time maps in Figure 5 as well as for specific regions of cartilage in Figure 6. RMSE for each sequence, as a measure of absolute difference from SE T_2 measurements, was as follows: MESE, 5.0 ms; 2D-FSE, 9.3 ms; 3D-MAPSS, 3.8 ms; 3D vfl-FSE, 4.2 ms; qDESS, 4.6 ms.

Regression analyses comparing in vivo SE T_2 measurements with those of all other sequences revealed 2D-FSE and qDESS to have the greatest coefficients of determination with SE measurements ($R^2 = 0.64$ and 0.60 , respectively) (Fig. 7c). These two sequences also demonstrated the steepest trendline slopes (1.31 and 0.90, respectively), while 3D vfl-FSE and MESE demonstrated the shallowest slopes (0.41 and 0.42, respectively). Steeper slopes and greater coefficients of determination were observed in superficial layers of cartilage, compared with deep, for all pulse sequences (Figs. 7a and 7b).

DISCUSSION

This study examined sequence-dependent variation in T_2 relaxation time quantitation in phantoms and in vivo knee cartilage using single echo SE as a reference standard. Variation between sequences was observed not just in terms of average T_2 quantitation, but also in terms of goodness of fit with SE measurements and dynamic range of T_2 relaxation times being output.

Data from phantom imaging largely agreed with data from in vivo imaging, but discrepancies were observed for T_2 measurements in deep regions of cartilage for all sequences. The slopes of trendlines for phantom measurements and superficial cartilage measurements were mostly comparable, suggesting the sequences perform similarly between phantoms and superficial regions of cartilage. However, trendline slopes and coefficients of determination were considerably reduced for T_2 measurements of deep regions of cartilage, likely due to SNR issues presented by in vivo imaging. Deep regions of cartilage typically have shorter T_2 relaxation times (36), causing reduced SNR particularly in later echoes. This can compromise signal measurements along the T_2 decay curve and introduce error in the relaxation time calculations. The effects should be least evident in the SE reference standard images, because each echo was obtained from a separate acquisition lasting over 6 min. This demonstrates one of the difficulties of in vivo T_2 quantitation. While pulse sequences with shorter scan times demonstrate relatively strong correlation with SE measurements in phantoms and superficial regions of cartilage with longer T_2 relaxation, they are not optimized to provide optimal SNR for T_2 quantitation in deep regions of cartilage.

Results from this study are supported by additional reports of variation between pulse sequences. The 3D-MAPSS sequence has previously been shown to yield T_2 measurements an average of 15% greater than SE measurements for in vivo cartilage imaging, although the current results suggest this discrepancy is not so large, with an average difference of 3% (20). Comparable quantitative results between 3D vfl-FSE and 3D-MAPSS have also been reported (23). Finally, qDESS has previously been shown to have an average error of 2% compared with SE in phantoms, which is in line with the present phantom results (24).

Consistently higher T_2 relaxation times were observed using the 2D-FSE sequence in phantom and in vivo articular cartilage imaging. RMSE results further support this conclusion that 2D-FSE yields T_2 relaxation times furthest from the SE reference standard. This is not the first study to report discrepancies in T_2 quantitation between these two sequences. 2DFSE has previously been reported to yield an average of 62% higher T_2 relaxation times compared with SE measurements (20). The magnitude of this disagreement certainly depends on the sequence parameters, but this general trend is supported by other studies of phantoms and in vivo cartilage (28,29). Moreover, reports of differences between these two sequences are not limited to studies of cartilage. 2D-FSE has been observed to yield higher T_2 relaxation time measurements in imaging of the prostate and the hippocampus (27,37,38). This phenomenon is typically attributed to the presence of stimulated echoes throughout the echo train that result from imperfect 180° refocusing pulses. Residual longitudinal magnetization between echoes results in partial T_1 -weighting, leading to an elevation in T_2 relaxation time estimation.

The average percent differences in T_2 relaxation time quantitation between all sequences in vivo provide a baseline understanding of the observed variation. T_2 outcomes between two sequences differed on average by as little as 0–1% (3D vfl-FSE and MAPSS), and as much as 27–38% (2D-FSE and qDESS), suggesting that it is critical to consider pulse sequence as a factor that affects T_2 relaxation time quantitation. It must be noted that the standard deviations exceed their corresponding average percentage differences in all comparisons except when 2D-FSE is involved. This observation suggests it would be difficult to apply one of these average percent differences to predict a regional T_2 outcome from one sequence based on the results of another. Additionally, the average percent differences in T_2 quantitation fail to capture the complexity of variation between sequences. On average, 3D vfl-FSE and MAPSS provide the nearest T_2 measurements to the reference standard, differing from SE by only 2 and 3%, respectively. However, this is partly a result of the tendency to overestimate T_2 at low T_2 relaxation times and underestimate T_2 at high T_2 relaxation times. As a result of the complexity of these relationships, the full extent of variation between pulse sequences cannot be simply described by average percent differences.

Other metrics used within this study provide additional ways to describe how T_2 quantitation varies between pulse sequences. The coefficient of determination (R-squared) characterizes the extent to which T_2 relaxation times from each pulse sequence replicate measurements by the SE sequence. Additionally, the dynamic range of T_2 values being output is represented by the slope of the regression line. This metric is of value because ultimately T_2 mapping is used to differentiate either between regions of cartilage or to detect

subtle changes over time. Having a greater dynamic range of T_2 values inherently provides a stronger ability to make such distinctions. 2D-FSE and qDESS measurements demonstrated the closest fit with SE measurements as well as the largest range of T_2 values. 3D vfl-FSE and MESE measurements did not fit as well with SE measurements, and they exhibited the smallest range in T_2 values. The decreased dynamic range of T_2 values from the MESE sequence has also been observed in prostate imaging (27).

This study was designed and optimized to provide an understanding of the differences in T_2 relaxation time quantitation between pulse sequences. To accomplish this, scan parameters were kept as consistent as possible between sequences so as not to impact the comparisons. Additionally, the regional segmentation is consistent with the methods used in much of the literature involving MRI of knee cartilage (39), making this analysis representative of the variation present in the literature.

This study also had several limitations that must be acknowledged. It is understood that some of the variation in T_2 relaxation time outcomes may have resulted from differences in SNR between sequences, particularly in deep regions of cartilage. This drawback was necessary to provide a more realistic understanding of current variation in T_2 quantitation because scan times are comparable to those of patient studies. More broadly, in addition to differences in SNR between pulse sequences, spatial resolution and the accuracy of the curve fit are very important to consider when reporting T_2 relaxation times. The changes in T_2 relaxation associated with disease will need to be of a greater magnitude than the variation introduced by these external factors when considering only absolute T_2 relaxation times. For clinical applications, quantitative T_2 techniques may need to analyze spatial variation of T_2 relaxation times, rather than just absolute values. An additional limitation to this study, all echoes for the MESE sequence were used for T_2 quantification to keep echo times similar between sequences. As the second and later echoes contain a stimulated echo contribution in addition to the spin echo component, this results in increased magnetization relative to the first echo and thus an overall increase in the calculated T_2 relaxation time (40). Some studies make up for this by excluding the first echo in the calculation for the best-fit T_2 (41,42). This limitation may have impacted the present results by artificially increasing T_2 results from MESE.

In conclusion, the variation in T_2 relaxation time quantitation between pulse sequences is highly complex. Pulse sequences demonstrate mean differences as large as 38% in T_2 relaxation time outcomes. More importantly, differences in T_2 quantitation between pulse sequences cannot simply be described by mean percentage differences. The sequences that demonstrated the greatest dynamic range of T_2 relaxation time measurements were, in decreasing order: 2DFSE, qDESS, and 3D-MAPSS. In the same order, these sequences also demonstrated the closest fits with the spin echo reference standard for in vivo T_2 relaxation time quantitation. Alternatively, sequences with the closest absolute T_2 relaxation time measurements to the reference standard, as measured by RMSE, were 3D-MAPSS, 3D vfl-FSE, and qDESS. This study highlights the importance of understanding the influence of pulse sequence on T_2 relaxation time outcomes and the importance of standardization of methodology within the field of musculoskeletal MRI.

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Figure 1. Patellar, femoral, and tibial cartilage were manually segmented into regions; each region was divided into a deep and superficial layer.

Figure 2.

T_2 relaxation time map of agar vials calculated from the single-slice SE sequence. T_2 relaxation times ranged from 23 to 64 ms. Square ROIs were chosen to be coincident with the voxels captured with STEAM spectroscopy. The two phantoms without ROIs were filled with water, as was the area surrounding the vials. [Color figure can be viewed in the online issue, which is available at wileyonlinelibrary.com.]

Figure 3.

Phantom experiment results. T_2 relaxation times calculated from each pulse sequence are plotted against those from the SE reference standard. Outcomes from each sequence demonstrate strong trendline fits with SE measurements ($R^2 > 0.8$; $P < 0.05$). [Color figure can be viewed in the online issue, which is available at wileyonlinelibrary.com.]

Reference Sequence	Comparison Sequence					
	SE	MESE	2D-FSE	MAPSS	3D vfl-FSE	qDESS
SE		-6±13%	25±14%	-3±11%	-2±13%	-9±11%
MESE	9±15%		35±22%	5±14%	6±15%	-2±15%
2D-FSE	-19±10%	-24±14%		-22±9%	-21±12%	-27±8%
MAPSS	4±12%	-3±13%	29±14%		1±9%	-6±11%
3D vfl-FSE	4±14%	-4±14%	28±19%	0±9%		-6±14%
qDESS	12±14%	4±17%	38±14%	8±13%	9±17%	

Percent difference = $\frac{\sum_1^n \left(\frac{\text{comparison} - \text{reference}}{\text{reference}} * 100 \right)}{n}$. All regional differences were averaged to determine the average percent difference in T₂ quantitation within each set of pulse sequences. [Color figure can be viewed in the online issue, which is available at wileyonlinelibrary.com.]

Figure 4.

Average percent differences and standard deviations between all T₂ relaxation time mapping sequences in vivo. Percent difference for each region across all volunteers was first

determined by the equation: Percent difference = $\frac{\sum_1^n \left(\frac{\text{comparison} - \text{reference}}{\text{reference}} * 100 \right)}{n}$. All regional differences were averaged to determine the average percent difference in T₂ quantitation within each set of pulse sequences. [Color figure can be viewed in the online issue, which is available at wileyonlinelibrary.com.]

Figure 5.

T₂ relaxation timemaps from each sequence overlaid onto the same morphological image of the knee. Color differences between pulse sequences illustrate absolute differences in quantitative outcomes. [Color figure can be viewed in the online issue, which is available at wileyonlinelibrary.com.]

Figure 6.

Mean T_2 measurements ($\pm$ standard error) across all volunteers from various regions of cartilage. These regions have been reported to be prone to degradation in early OA. (M.=medial, L.=lateral, (d)=deep, (s)=superficial). [Color figure can be viewed in the online issue, which is available at wileyonlinelibrary.com.]

Figure 7.

Regression analyses comparing in vivo T_2 measurements with those of other pulse sequences. Plotted data points are means from each segmented ROI. Deep (a) and superficial (b) cartilage are displayed separately and together (c). Trendline equations and coefficients of determination (R^2 values) are reported with each graph.

Table 1

Scan Parameters for Phantom and In Vivo Imaging

Sequence	TR/TE (ms)	Signal averages	Acceleration (phase $\times$ slice)	In vivo scan time (min)
SE	2500/10,14,19,26,36,50	0.5	1×1	$6:10 \times 6$
STEAM (phantom)	2500/14,19,26,36,50	8.0		
MESE	2500/11,14,22,28,42,56	1.0	1×1	$11:10 \times 2$
2D-FSE	2500/15,22,29,37,44,52	1.0	1×1	10:45
3D-MAPSS	4.1/10,13,16,26,39,48	1.0	2×2	16:15
3D vfl-FSE	2235/9,12,19,25,35,51	1.0	2×2	13:56
qDESS	26/9,43	1.0	1×1	$4:27 \times 2$