Comparison of Quantitative T_2 Mapping Techniques for Articular Cartilage

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Introduction: T_2 relaxation time mapping of free water content and mobility in articular cartilage provides an indirect assessment of collagen content and orientation [1]. Biochemical changes are characteristic of the early stages of osteoarthritis (OA), and T_2 mapping is increasingly used in both clinical and research settings. New MR pulse sequences, including 3D approaches, provide more advanced and faster methods for T_2 quantitation, but may introduce a bias in T_2 measurements. Previous studies comparing several T_2 quantification methods reported differences up to 42% in agar phantoms [2] and 63% for *in vivo* knee cartilage [3]. Analysis of current T_2 mapping techniques provides a basis for interpreting absolute and relative relaxation time differences across studies using different MR sequences and allows researchers and clinicians to better interpret their results. To date, relevant studies only compare a couple T_2 mapping techniques and are primarily limited to analysis of patellar cartilage. The present study analyzes quantitative outcomes from six MR sequences for *in vivo* T_2 mapping of patellar, femoral, and tibial cartilage. Single echo spin echo is used as a reference standard to judge the agreement and utility of all other techniques.

Methods: ***Acquisition:*** All imaging experiments were performed on a GE MR 750 3.0T MRI scanner (GE Healthcare, Milwaukee, WI) with a 16-channel coil (NeoCoil, Pewaukee, WI). First, 6 agar phantoms of variable T_2 were imaged with unsuppressed stimulated echo acquisition mode (STEAM) spectroscopy and single echo spin echo (SE) to characterize the baseline error in T_2. Next, *in vivo* images were obtained from knees of 8 healthy volunteers (6M, 2F, age 24.4±4.6years, BMI 23.3±4.2). Sequences tested include: SE, multi-echo spin echo (MESE), 2D-fast spin echo (2D-FSE), 3D spoiled gradient recalled-based acquisition (3D-MAPSS) [4], 3D-fast spin echo with variable flip angle (3D-FSE), and quantitative double-echo steady state (qDESS) [5]. All images were acquired in the sagittal plane with constant imaging parameters: FOV: 16x16cm^2, matrix: 256x256, BW: ±62.5kHz, and slice thickness 3mm. Additional imaging parameters are outlined in Table 1. ***Analysis:*** T_2 relaxation times were calculated using a mono-exponential fit in OsiriX and averaged within 26 regions of interest for each knee, corresponding to superficial and deep layers of cartilage in the medial and lateral patella, femur, and tibia as indicated in Figure 1. Error from SE measurements, as measured by root mean square error (RMSE) was calculated for each technique.

Sequence	TR/TE (ms)	Signal Ave.	Scan time (min)
STEAM	2500/14,19,26,36,50		
SE	2500/10,14,19,26,36,50	0.5	6:10 x 6
MESE	2500/11,14,22,28,42,56	1.0	11:10 x 2
2D-FSE	2500/15,22,29,37,44,52	1.0	10:45
3D-MAPSS	4.1/10,13,16,26,39,48	1.0	16:15
3D-FSE	2235/9,12,19,25,35,51	1.0	13:56
qDESS	26/9,43	1.0	4:27 x2

Table 1. T_2 mapping scan parameters.

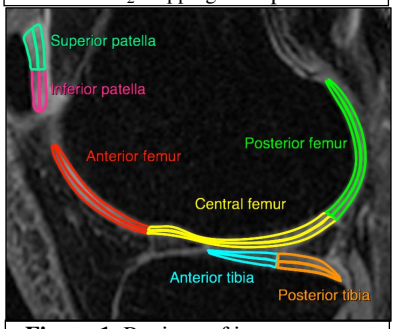

Figure 1. Regions of interest.

Results: ***Phantoms:*** The 6 agar phantoms ranged in T_2 from 22–56ms, as calculated from STEAM spectroscopy. SE measurements overestimated these values by 9.3±2.3%. ***In vivo:*** Individual measurements from SE are plotted against those from each technique in Figure 2, and corresponding R^2 values are reported. RMSE for each technique was as follows – MESE: 5.0ms, 2D-FSE: 9.3ms, 3D-MAPSS: 3.8ms, 3D-FSE: 4.2ms, qDESS: 4.6ms. Regional analysis of T_2 variation from all sequences reveals that patellar cartilage RMSE (4.9ms) is lower than that of tibial (5.6ms) and femoral (5.7ms) cartilage RMSE.

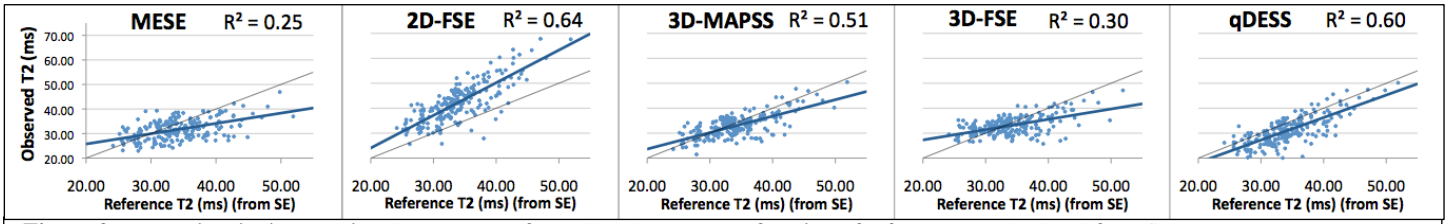

Figure 2. Data points indicate regional T_2 averages from all volunteers as a function of reference T_2 calculated from SE measurements.

Discussion: Figure 2 demonstrates that some sequences have a consistent bias from SE T_2 measurements (ie: 2D-FSE, qDESS) while others overestimate in lower T_2 regions and underestimate at higher T_2 regions (ie: MESE, 3D-FSE). The agreement of each technique with SE is not necessarily indicative of its correlation with SE measurements, as evidenced by the minimal error of 3D-MAPSS (RMSE = 3.8) but greater correlation observed with 2D-FSE and qDESS sequences (R^2 = 0.64, 0.60, respectively). Amongst all sequences, greatest agreement was observed in patellar cartilage. Previous studies of T_2 differences between sequences focus primarily on patellar cartilage imaged in the axial plane, and thus likely underestimate the variation occurring in femoral and tibial cartilage. T_2 quantitation of cartilage is meant to track changes in T_2 associated with OA, so some applications of these techniques may benefit from a steeper sloped regression line in Figure 2, rather than more accurate T_2 measurements.

Conclusion: There is an appreciable amount of variation in quantitative results amongst the sequences currently available for *in vivo* T_2 mapping. The regional analysis above is consistent with much of the literature involving MRI of knee cartilage [6], so the results are likely representative of the discrepancies in absolute and relative relaxation times reported in OA research. An important question this study highlights is whether accurate measurement of T_2 or a general ability to quantitatively distinguish between regions with different biochemistry is more important. Further study of these variations, especially in patient populations, will be necessary to fully understand how best to interpret quantitative MR results and ultimately how best to track OA in its earliest stages.

References: [1] David-Vaudey et al. (2004) Magn Reson Imaging 22(5):673-82 [2] Liney et al. (1996) J Magn Reson Imaging 6(4):603-7 [3] Pai et al. (2008) Magn Reson Imaging 26(9):1215-20 [4] Li et al. (2008) Magn Reson Med 59(2):298-307 [5] Staroswiecki et al. (2012) Magn Reson Med 67(4): 1086-96 [6] Eckstein et al. (2006) Osteoarthritis Cartilage 14(10):974-83 **Acknowledgements:** NIH EB002524, AR062068, and CA159992, Arthritis Foundation, and GE Healthcare.