

Multi-Component T2 Analysis of Cartilage Degradation Model Using mcDESPOT at 3.0T

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Introduction: Water signal within articular cartilage is generally considered to consist of two components: 1) water tightly bound to macromolecules such as collagen and proteoglycan termed W_m and 2) bulk water loosely bound to the proteoglycan matrix termed W_b (1, 2). The multiple water components are effectively averaged when performing mono-component T2 mapping. Thus, mono-component T2 cartilage analysis is nonspecific and is influenced by multiple factors including hydration, macromolecular content, and tissue anisotropy with comparable T2 changes detected in disparate settings (3-5). Multi-component Driven Equilibrium Single Pulse Observation of T1 and T2 (mcDESPOT) is a technique that can evaluate two-component relaxometry using steady-state MRI (6, 7). mcDESPOT is a clinically feasible imaging method that can perform multi-component T2 mapping of the articular cartilage of the human knee joint at 3.0T in 20 minutes (8). This study was performed to determine whether mcDESPOT could provide improved specificity for evaluating cartilage matrix changes in an ex-vivo bovine cartilage degradation model.

Methods: A fresh bovine patella specimen was excised from a skeletally mature cow from a local farm store. The patella specimen were placed in a custom-built container filled with saline solution and imaged on a 3.0T scanner (Discovery MR750, GE Healthcare; Waukesha, WI) using a single-channel wrist coil (Mayo Clinic, Rochester, MN) both prior to and immediately following enzymatic degradation. During enzymatic degradation, a transverse cut was made through the cartilage and bone separating the patellar specimen into superior and inferior halves which allowed one portion of the cartilage to be immersed in 25 mg/ml of trypsin solution and the other portion to be immersed within saline solution for 24 hours. Spoiled gradient echo (SPGR) scans were acquired with TR/TE=5.5/2.6ms over a range of flip angles ($\alpha=3, 4, 5, 6, 7, 9, 13, 18^\circ$). Two fully-balanced steady-state free precession (bSSFP) scans with RF phase cycling on and off were acquired with TR/TE=7.1/3.6ms over a range of flip angles ($\alpha=2, 5, 10, 15, 20, 30, 40, 50^\circ$). An additional inversion recovery IR-SPGR scan with TR/TE=5.5/2.6ms, TI=450ms, and $\alpha=5^\circ$ was also acquired. All scans were performed in the sagittal plane covering the entire patellar specimen using a 14 cm field of view, 288 x 288 matrix, 3mm slice thickness, and one excitation with a total scan time of 25 minutes. Water fraction and T2 relaxation time maps for the W_m and W_b components were reconstructed in MATLAB using an mcDESPOT model (6,7). The mean value and standard deviation averaged across all slices of the superficial and deep halves of the control and degraded cartilage subsections of the patellar specimen before and after enzymatic degradation were measured and compared.

Results: Table 1 shows the mean water fraction and T2 relaxation time for the W_m and W_b components of the control and degraded cartilage subsections, with maps from a single sagittal slice through the patellar specimen illustrated in Figure 1. The values obtained before enzymatic degradation were nearly identical to those of the control subsection after degradation and are thus not shown. The water fraction of the W_m component was 21% lower in the superficial than deep cartilage for the control subsection and 45% lower for the degraded subsection. The T2 relaxation time of the W_m component was 40% higher in the superficial than deep cartilage for the control subsection and 145% higher for the degraded subsection. The T2 relaxation time of the W_b component was 21% higher in the superficial than deep cartilage for the control subsection and 55% higher for the degraded subsection.

Discussion: The W_m component measured using mcDESPOT is felt to represent mainly water component that is tightly bound to proteoglycan since the collagen-associated water component cannot be directly detected as its T2 relaxation time of 2.2ms is shorter to the repetition time of this sequence (1). Depth-dependent variations in multi-component T2 parameters were noted in the control cartilage subsection with lower water fraction of the W_m component and higher T2 relaxation time of the W_m and W_b components within superficial cartilage which was similar to the depth-dependent variations reported in human patella cartilage in-vivo (8). Trypsin degradation leads to proteoglycan loss in superficial cartilage exposed to the enzyme without disruption of the collagen fiber network. The decreased water fraction of the W_m component in superficial cartilage after trypsin degradation is likely due to a decrease in proteoglycan content. The increase in T2 relaxation time of the W_m and W_b components in superficial cartilage after trypsin degradation is consistent with the fact that while trypsin cleaves the core and link proteins of proteoglycan, it does not insure the complete removal of proteoglycan fragments from the cartilage matrix. Water tightly and loosely bound to proteoglycan fragments would be expected to have longer T2 relaxation times than water bound to the intact macromolecule. Similar changes in multi-component T2 parameters with trypsin degradation in ex-vivo bovine cartilage samples have been reported in studies using NMR spectroscopy with single slice analysis and long scan times (1, 2). Our study confirms the ability of multi-component T2 mapping to provide improved specificity for evaluating cartilage matrix changes using an mcDESPOT technique that can be performed on the human knee joint in a clinically feasible scan time (8). We are currently performing additional ex-vivo experiments using a larger number of patellar specimens, different enzymatic degradation models, and histologic correlation to better understand the factors responsible for changes in multi-component T2 parameters with cartilage degeneration.

References: (1) Reiter D. MRM, 2010. (2) Reiter D. NMR Biomed, 2011. (3) Smith H. JMIRI, 2001. (4) Mosher T. Radiology, 2005. (5) Lin P. MRM, 2009. (6) Deoni S. JMIRI, 2009. (7) Deoni S. MRM, 2008. (8) Liu F, ISMRM abstract #4365, 2012.

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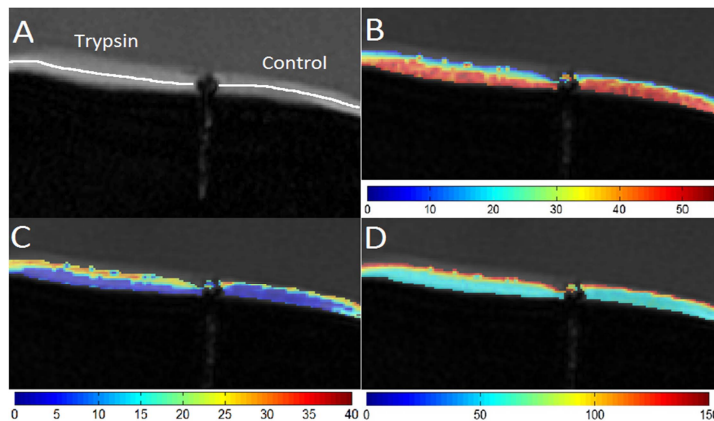


Figure 1: (A) IDEAL-SPGR source image (white line denotes superficial (top) and deep (bottom) halves of cartilage), (B) water fraction map for the W_m component, (C) T2 relaxation time map for the W_m component, and (D) T2 relaxation time map for the W_b component of an ex-vivo bovine patella specimen following trypsin degradation.

Table 1: Multi-Component T2 relaxation time and water fraction analysis for ex-vivo bovine patellar cartilage at 3.0T.

Multi-Component T2 Analysis	Fraction of W_m (%)		T2 of W_m (ms)		T2 of W_b (ms)	
	Superficial	Deep	Superficial	Deep	Superficial	Deep
Control	31.8±12.7	40.0±14.4	15.0±9.3	10.7±8.8	90.4±34.1	74.5±32.2
Trypsin	23.7±11.0	42.7±10.3	22.6±8.0	9.2±8.7	103.0±30.7	66.3±24.5