Quantitative Characterization of Meniscal Pathology: UTE MRI versus Long T2 Techniques

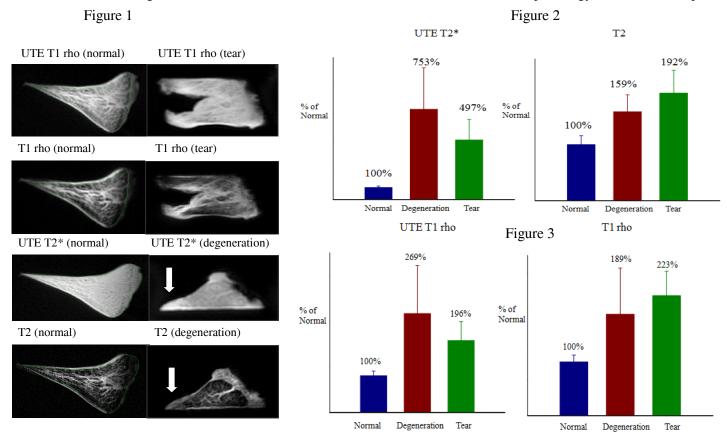
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Purpose: To determine if quantitative MR values for normal and pathologic menisci correlate with structural and biochemical alteration. Evaluate T1 rho and UTE T1 rho for proteoglycan evaluation and T2 and UTE T2* for collagen assessment.

<u>Methods</u>: Ten cadaveric meniscus samples (normal=6, degeneration=2, tear=2) were imaged with 3.0T MRI (Figure 1). T1 rho, UTE T1 rho, T2, and UTE T2* values were obtained by manual placement of regions of interest (ROI) focally at the site of morphologic pathology and compared to normal. Mixed-effects linear regression was used to determine variations in values as a function of morphology. Groups were analyzed utilizing ANOVA one-way analysis of variance.

Results: UTE T2*, T2, UTE T1 rho, and T1 rho values for pathologic menisci were higher than normal. UTE T2* values for tear (10.5±3.6), degeneration (15.9ms±7.3), and normal (2.6ms±0.2) were compared to T2 values for tear (37.9ms±8.0), degeneration (31.4ms±6.0), and normal (19.7ms±3.1) (Figure 2). UTE T1 rho values for tear (15.8ms±4.1), degeneration (21.7ms±10.5), and normal (8.0ms±1.0) were compared to T1 rho values for tear (33.7ms±6.9), degeneration (28.5ms±13), and normal (15.1ms±1.9) (Figure 3). UTE T2* values were more sensitive in identification of pathology than T2 values (p=0.03).



<u>Discussion</u>: UTE T2* allows improved quantification of short T2 structures, such as menisci, compared to T2 values, reflecting improved detection of collagen disorganization in meniscal pathology.² Increased UTE T1 rho and T1 rho values in pathologic menisci correlate with proteoglycan degradation. UTE pulse sequences demonstrate improved visualization and quantification of subtle meniscal degeneration compared to traditional sequences.

<u>Conclusion</u>: Quantitative MR values correlate with structural and biochemical meniscal alterations, providing additional insight into meniscal pathology that may not be unmasked on standard sequences, and which may aid in early diagnosis and quantifying treatment outcomes.³

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