$T_1\rho$ in articular cartilage and the loss of proteoglycans

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Introduction

Relaxation time in the rotating frame ($T_1\rho$) has been reported to be a sensitive marker of the loss of proteoglycans in articular cartilage (1-3). Changes of $T_1\rho$ were observed in cartilage plugs chemically or enzymatically depleted of proteoglycans but not in collagenase-treated tissue (2). On the other hand, Menezes et al. (4) found no correlation between the cartilage $T_1\rho$ and proteoglycan concentration. In addition, it was reported that the dominant $T_1\rho$ and T_2 relaxation mechanism at $B_0 \leq 3T$ is dipolar interaction due to slow anisotropic motion of the water molecules in the collagen matrix (5). The contradictory reports regarding $T_1\rho$ as a possible marker for the proteoglycan loss prompted us to compare $T_1\rho$ maps of cartilage-bone specimens, obtained from patients undergoing total joint replacement, with proteoglycan-specific histologic staining of the corresponding slices with Safranin-O.

Specimens and instrumentation

Eight human cartilage-bone specimens were harvested from femoral condyles obtained during replacement surgery. Some of the specimens showed no macroscopically visible signs of damage on the cartilage surface, others showed clear signs of mechanical overuse. Because of the age of the patients undergoing surgery and the fact that degeneration does not occur uniformly across the joint surface, various stages of degenerative changes were found in all the specimens. MR images were obtained on a 3 Tesla Bruker MEDSPEC scanner equipped with a microimaging gradient set. For measuring T_2 relaxation times, twelve echoes were collected in the multiple echo protocol with the echo times ranging from 6.2 ms to 74.4 ms. The $T_1\rho$-weighted images were measured using a magnetization preparation spin locking pulse sequence (6), followed by a gradient echo sequence. The $T_1\rho$ relaxation maps were calculated from series of six images measured as a function of the spin-locking time varied in the range from 6 ms to 80 ms. The amplitude of the spin-locking field, $\gamma B_1/2\pi$ was 1000 Hz.

Results

Fig. 1 shows the$T_1\rho$ and T_2 relaxation maps and the corresponding histological slices of two cartilage specimens. The color scales of the respective relaxation maps were adjusted optimally for each parameter. In the upper specimen, the central deep region of cartilage containing high amount of proteoglycans (purple on histology, long thick arrow) corresponds to the regions of short T_2 and $T_1\rho$ values, 23 ± 4 ms and 47 ± 8 ms, respectively. The eroded superficial part of cartilage (long thin arrow) shows long T_2 and $T_1\rho$ values, 57 ± 9 ms and 103 ± 17 ms. Even longer T_2 and $T_1\rho$ values are found in the proteoglycan-depleted superficial region (short thick arrow), 76 ± 8 ms and 115 ± 16 ms, respectively. In contrast, the deep region of cartilage near the bone on the left hand side of the specimen (short thin arrow in histology) with lowered proteoglycans shows a low $T_1\rho$ value (24 ± 5 ms).

In the lower specimen, no correlation is seen between histology and relaxation times. The central region of the cartilage layer rich in proteoglycans (long thick arrow in the histological preparation) has intermediate T_2 and $T_1\rho$ values (36 ± 8 ms and 58 ± 4 ms, respectively). The region with depleted proteoglycans (short thick arrow) has unusually short T_2 and $T_1\rho$ relaxation times (26 ± 3 ms and 41 ± 7 ms, respectively). These relaxation times are much shorter than the values in the intermediate region (long thin arrow) which has high concentration of proteoglycans in histology (41 ± 8 ms and 65 ± 3 ms, respectively).

Discussion

In general, visual appearance of T_2 and $T_1\rho$ relaxation maps is similar. In the upper specimen, most regions with depleted proteoglycans show elevated relaxation times. However, $T_1\rho$ and T_2 are known to be longer in the transitional than in the deep cartilage zone. If considering also the magic angle effect, it is difficult to decide which factor, either orientation of the collagen fibers or concentration of proteoglycans, is responsible for the changes in $T_1\rho$ and T_2. In the lower specimen, no correlation of $T_1\rho$ with the amount of proteoglycans is observed. We conclude that $T_1\rho$ seems to be sensitive on more progressive stages of cartilage degeneration characterized by corrupted cartilage microstructure.

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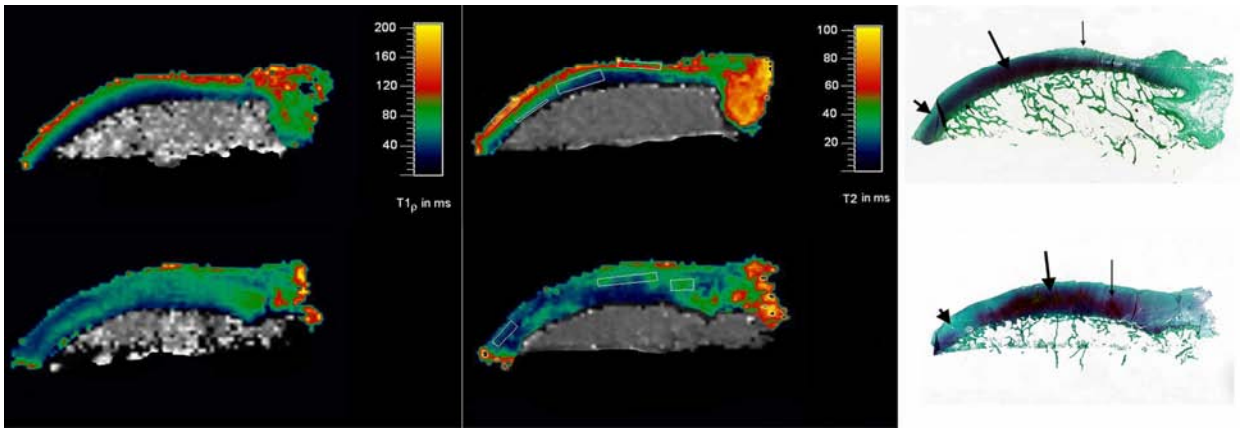

Fig. 1. $T_1\rho$ map (left column), T_2 map (middle column) and histology preparations (right column) of two articular cartilage specimens. Relaxation times given in the text are mean values calculated for the marked ROIs.

References

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