

Development of in vivo multi-slice spiral T1rho mapping in cartilage at 3T and its application to osteoarthritis

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INTRODUCTION

The T_{1ρ} parameter describes spin-lattice relaxation in the rotating frame. It probes the slow motion interactions between motionally restricted water molecules and their local macromolecular environment. The extracellular matrix (ECM) in articular cartilage provides a motionally restricted environment to water molecules. Changes to the ECM, such as proteoglycan (PG) loss, therefore, may be reflected in measurements of T_{1ρ}(1). Since the loss of PG has been shown to be an initiating event in early stages of OA, T_{1ρ} mapping has been proposed as a promising diagnostic tool for the early detection of OA (2). However, the relationship between T_{1ρ} and the PG/collagen matrix, and whether T_{1ρ} can provide additional information to T₂ quantification remains controversial in the literature (3,4). We have previously developed a single-slice T_{1ρ}-weighted imaging method based on a spiral sequence (5). In this study, a multi-slice T_{1ρ} imaging technique was developed and patients with osteoarthritis were examined at 3T.

MATERIALS AND METHODS

The spin-lock sequence consists of a hard 90 degree pulse followed by a spin-lock pulse and a hard -90 degree pulse (Fig. 1). The phase of the second half of the spin-lock pulse was shifted 180° from the first half to reduce artifacts caused by B1 inhomogeneity (6). Magnetization stored along the z-axis is read out by a multi-slice spiral sequence. The spiral acquisition was placed as close together in time as possible followed by time for T1 recovery. A RF cycling technique was used in order to eliminate T1 recovery from slice to slice (7). The magnetization is inverted immediately after alternate T_{1ρ} preparation. The longitudinal magnetization at the time of acquisition (ta) can be described as: $M_z(ta) = M_z^{prep} e^{-ta/T1} + M_0 (1 - e^{-ta/T1})$ without inversion and $M_z(ta) = -M_z^{prep} e^{-ta/T1} - M_0 (1 - e^{-ta/T1})$ with inversion. Thus, the difference of these signals is proportional to $M_z(ta) = 2M_z^{prep} e^{-ta/T1}$ where M_z^{prep} is proportional to $\exp(-TSL/T1\rho)$. Data with varying TSLs were acquired, and a Levenberg-Marquardt mono-exponential fitting algorithm developed in C was used to reconstruct a pixel-by-pixel T_{1ρ} map. Cylindrical homogeneous agarose gel phantoms were used for sequence development and reproducibility studies. Nine volunteers (4 female and 5 male, ages 22-61, median=30) without OA symptoms and five patients (1 female and 4 male, ages 18-62, median=52) with OA symptoms and/or radiologic findings of cartilage degeneration were examined on a 3T GE Excite Signa MR scanner using a quadrature knee coil. Among them, four volunteers were scanned twice to study reproducibility. The acquisition parameters were: 14 interleaves/slice, 4,096 points/interleaf, FOV=15 or 16cm, effective in-plane resolution = 0.6 * 0.6 mm, slice thickness = 3mm, skip = 1mm, number of slice = 14-16, TR/TE = 2s/5.8ms, TSL=20/40/60/80 ms, spin lock frequency = 500 Hz, total acquisition time approximately 13 minutes. T_{1ρ}-weighted images with the shortest TSL were registered to high-resolution T₁-weighted SPGR images acquired in the same exam. The transformation matrix was applied to the reconstructed T_{1ρ} map. Cartilage was segmented semi-automatically based on high-resolution SPGR images using a software package based on IDL (Interactive Data Language) developed in-house. 3D cartilage contours were generated and overlaid to the registered T_{1ρ} map. Mean, standard deviation, and median T_{1ρ} values were calculated. A non-parametric rank test was used to compare T_{1ρ} values between controls and patients.

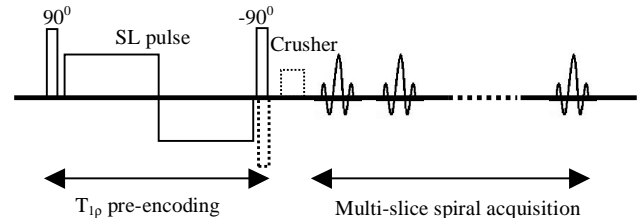


Fig. 1. The pulse sequence for spiral T_{1ρ}-weighted imaging

Fig. 2 shows T_{1ρ} values through the 18 slices of an agar phantom (concentration approximately 4%, g/ml) collected in a single multi-slice acquisition with a median of 54 ms. The T_{1ρ} values were consistent with those obtained with the single slice method and the variation from first slice to last was within 3.7%. The reproducibility (average coefficient of variation for median T_{1ρ}) was 1.46% for phantoms and 4.80% for volunteers. Table 1 shows the mean and standard deviation of median T_{1ρ} within femoral (trochlea) and patellar cartilage respectively for healthy volunteers and patients with OA. A significant difference was found in T_{1ρ} of femoral cartilage between controls and patients. Fig. 3 shows the T_{1ρ}-weighted images of a healthy volunteer. Fig. 4 shows T_{1ρ} maps for a healthy volunteer (a) and a patient with OA (b).

RESULTS

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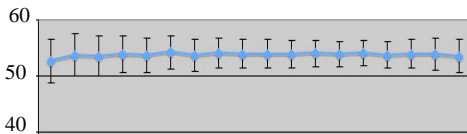


Fig. 2. T_{1ρ} through slices in an agar phantom

Table 1 Average±standard deviation of median T_{1ρ} within femoral and patellar cartilage

	Controls (n=9)	OA Patients (n=5)	P-value
Femoral	45.6±4.56	57.0±1.71	0.003
Patellar	44.1±4.46	47.8±7.68	0.43

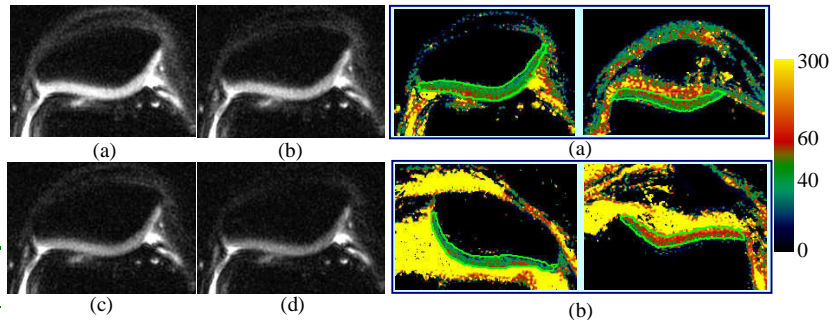


Fig. 3. T_{1ρ}-weighted images for a volunteer with TSL=20,40,60,80ms from (a) to (d).

Fig. 4. T_{1ρ} maps for a healthy control (a) and a patient with OA (b). Left: patellar cartilage; right: femoral cartilage.

CONCLUSIONS AND DISCUSSION

A robust in vivo multi-slice T_{1ρ} imaging method has been developed. Increased T_{1ρ} relaxation time in femoral cartilage indicated that T_{1ρ} may be a promising marker for OA detection. The non-significant differences between OA patients and controls in the patella are not unexpected since the patella is non weight-bearing, and the most pronounced changes in OA are found at the femoro-tibial joint. Spatial heterogeneity of T_{1ρ} within the cartilage has been observed and will be addressed in the future by generating z-score maps and line profiles of T_{1ρ}. A larger cohort of healthy volunteers and patients with different stages of OA will be studied in the future and changes of T_{1ρ} relaxation time in the longitudinal follow-up in patients with OA and volunteers will be analyzed.

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