Technical feasibility of two-component T2* mapping on cartilages in human knee with 54-TE acquisitions

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INTRODUCTION

Disruption of well-organized collagen fibers in articular cartilages in human knee is an early sign of developing osteoarthritis (1). Short component of T_2* relaxation has the potential to detect collagen fiber disruptions (2-4). Two-component T_2* mapping has capability to show variations of the short-T_2* relaxation by separating it from the long-T_2* component. It has been demonstrated that, at the level of region of interest (ROI), two-component T_2* mapping is technically feasible on human on clinical 3T MRI scanner (4). However, two-component T_2* mapping at pixel level is still challenging due to limited signal-to-noise ratio (SNR) available in clinical setting. A large number of TE acquisitions is here proposed to improve performance of the two-component T_2* mapping at pixel level.

METHODS AND EXPERIMENTS

Methods. To acquire T_2*-weighted images on cartilages in the knee at a large number of echo times (TEs), an ultrashort echo time (UTE) pulse sequence was modified to allow for acquiring images at multiple TEs per a sequence run. Multiple sequence runs were used to complete the acquisitions of required T_2*-weighted images. ***Experiments.*** Three healthy adult subjects were scanned on a clinical 3T scanner (Magnetom Trio Tim, Siemens Medical Solutions, Erlangen, Germany) with an 8-channel knee coil (Invivo Inc., Gainesville, FL), under an approved IRB protocol. A customer-developed UTE sequence, AWSOS (5), was used for data acquisition with parameters of TR/θ = 100-120ms/30º, 54 TEs between 0.66-90ms (Fig. 1), 6 TEs per a RF excitation, 60 slices of thickness 2mm, FOV=140mm, matrix size=256, in-plane resolution=0.55mm, in-plane spirals=24, and spiral readout Ts=11.70ms. The acquisition time per a sequence run was 2min 24sec. The total acquisition time (TA) for 9 sequence runs, which produced 54-TE images, was 22min. ***T_2* mapping.*** Two-component T_2* mapping was performed on a pixel-by-pixel basis in cartilage regions. An automatic, NNLS-based, iterative algorithm was used for the FID curve fitting at individual pixels. Averaging over a region of 3×3 pixels was performed on the two-component T_2* maps but not on the single-component T_2* maps.

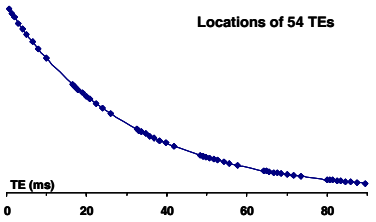

Fig. 1. Location of the 54 TEs.

RESULTS AND DISCUSSION

Figure 2 illustrates the UTE image of cartilages at patellar, femoral and tibial regions of interest, and the maps of short- and long-T_2* relaxation time (T2*short, T2*long) and component intensity fraction (a21, a22), along with the map of single-component T_2* relaxation time. Figure 3 shows quantification of the mapping regions shown in Figure 2 via mean and standard deviation (SD). On the maps are cartilage layers visible from superficial to deep regions more clearly on the two-component maps than on the single-component map. The mean values of the two-component T_2* relaxation in the cartilage regions are consistent with what was measured before at ROI-level (4). These results have demonstrated the technical feasibility of two-component T_2* mapping on knee cartilages at pixel level via a large number of TE acquisitions (54 TEs). The total data acquisition time was 22 min in this study, which can be shortened to ~18 min by further optimizing acquisition parameters such as the number of TEs per a sequence run and the TR.

REFERENCES: [1] Blumenkrantz G, *et al*. Eur Cell Mater 2007; 13:75-86. [2] Lattanzio PJ, *et al*. MRM 2000; 44:840-851. [3] Williams A, *et al*. OC 2010; 18:539-46. [4] Qian, *et al*. MRM. 2012 (Epub, early view). [5] Qian Y, *et al*. MRM 2008; 60:135-145.

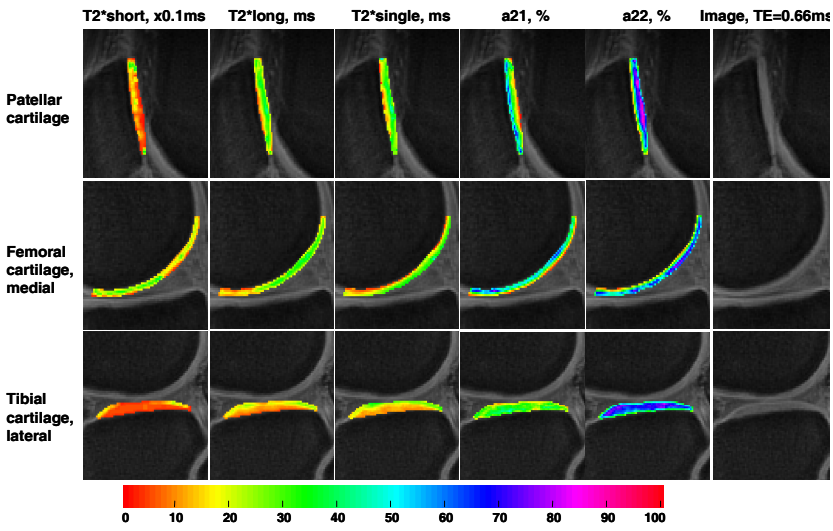

Fig. 2. Maps of short- and long-T_2* relaxation time and intensity fraction, as well as single-component T_2* time, in cartilage regions of interest of a healthy subject.

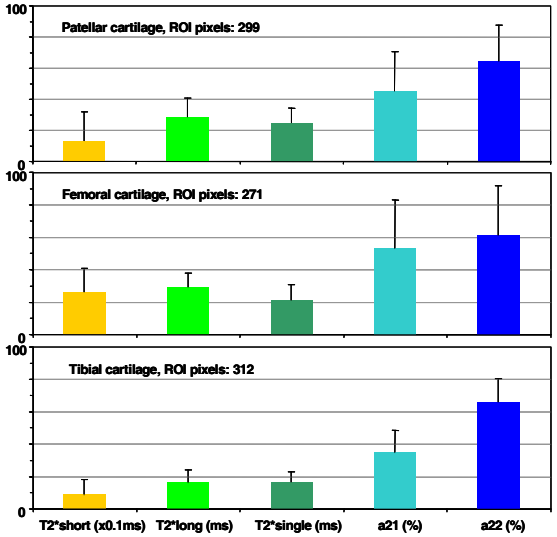

Fig. 3. Mean (color bar) ± SD (error bar) of short-/long-T2* relaxation time and intensity fraction in the regions in Fig. 2.