Rapid T1 and T2 mapping of the hip articular cartilage with radial MR fingerprinting

Martijn A Cloos[1], Leeor Alon[1], Christian Geppert[2], Daniel K Sodickson[1], and Riccardo Lattanzi[1]

[1]*Center for Biomedical Imaging, Department of Radiology, New York University School of Medicine, New York, NY, United States,* [2]*Siemens AG Healthcare, Erlangen, Germany*

TARGET AUDIENCE: Clinicians and researchers interested in Magnetic Resonance (MR) fingerprinting and MR-based biochemical assessment of articular cartilage.

PURPOSE: Since morphologic MRI cannot accurately diagnose early cartilage damage, various MR-based techniques have been proposed to detect deterioration of cartilage biochemical components. T_2 mapping detects changes in collagen structure and water content[1], whereas T_1 mapping in the presence of gadolinium (i.e., dGEMRIC), is sensitive to the earliest cartilage deterioration that occurs at the molecular level with loss of proteoglycans (PG)[2,3]. Ex-vivo results[4] have shown that T_1, without gadolinium, correlates with PG concentration and cartilage hydration, and that its combination with T_2 can improve cartilage biochemical characterization. However, spatial resolution requirements for the hip cartilage have prevented effective implementation of multiparametric approaches in-vivo, due to scan time limitations with standard parameter mapping techniques. In this project, we describe and validate a novel technique, based on the principles of MR Fingerprinting[5], to enable rapid, in-vivo simultaneous mapping of T_1 and T_2 in the hip cartilage.

METHODS: The new fingerprinting sequence designed to rapidly acquire 6 radially placed slices. Although crosstalk between slices will void the quantitative values at the intersection, the radial sections provide a near optimal sampling of the cartilage. To sequence consisted of 4 segments each containing 120 excitations spaced 6.8ms apart. The first and third segments contain RF spoiled gradient echoes that predominantly encode RF-field distribution (B_1^+) and T_1, whereas the other segments also add a T_2 relaxation component (no RF spoiling). Collectively, these 480 snapshots capture a distinct signal evolution (fingerprint) that simultaneously identifies B_1^+ and tissue properties. To increase T_1 accuracy a strategically chosen delay was inserted between each segment. When interleaving 6 slices each delay can be used to image a radial section (**Fig. 2**), thus eliminating any dead time in the protocol. An in-plane radial sampling strategy (not to be confused with the radial slice planning just described) was selected using golden angle increments between snapshots to promote incoherence between undersampling artifacts. The underlying tissue properties were retrieved by identifying the dictionary element that best correlates with a compressed fingerprint (compression strategy described elsewhere[6]). The matching algorithm was implemented in MatLab (The MathWorks, Inc., Natick, Massachusetts, United States) augmented with C++ code.

To validate the accuracy of the proposed approach, phantom measurements were performed. The phantom consisted of 7 test tubes (2.5cm diameter), filled with distilled water doped with different concentrations of Manganese Chloride. The matrix size was 480x480, with an in-plane resolution of 0.6x0.6 mm^2, TR/TE = 6.6/3.1 ms, 5.0 mm slice thickness. Single spin echo experiments were performed to obtain a gold standard T1 map (TI = {25, 50, 100, 200, 400, 800, 1600, 3200, 6400} ms) and T2 map (TE = {12, 24, 36, 48, 60, 72, 84, 96, 144, 192, 278, 384} ms). In both cases a repetition time of 6.5s was selected to minimize saturation effects. An in-house image processing software was used to extract the T1 and T2 from the DICOM images[8].

The hip of a healthy volunteer was scanned on a 3 T MR system (MAGNETOM Skyra, Siemens). Since detecting hip cartilage pathology is inherently difficult with conventional imaging planes, we used six equally spaced radially prescribed imaging planes (Fig. 2 c,d), which provide a true cross section of the cartilage and labrum[6]. Each shot in the MR fingerprinting time series was acquired using 25 radial spokes, with TR/TE = 6.8/3.2 ms, matrix size = 264x264, 0.8x0.8 mm^2 in-plane spatial resolution, 4.0 mm slice thickness. The total scan time for all 6 slices combined was 8 minutes. In addition to T_1 and T_2 maps, a proton-density (PD) weighted image was reconstructed for each slice. In addition, to more closely approximate contrast used for morphological assessment all 480 shots were added to produce an approximately PD weighted image. The study was approved by our institutional review board (IRB), and written informed consent was obtained prior to the examination.

RESULTS: Phantom validation (**Fig. 1**) showed good agreement between our technique and the gold standard for the T_1 (~ 900-1200 ms) and T_2 (~ 20-60 ms) ranges of interest for articular cartilage at 3 T. **Fig. 3** shows the reconstructed parameter maps and proton-density weighted image for the six radial section.

DISCUSSION: A previously described rapid 2D T_1 mapping technique reported a scan time of 1:40 min per radial hip section[9]. Our method allowed reconstruction of T_1 and T_2 maps as well as a PD weighted image with similar spatial resolution (0.8x08 vs. 0.6x0.6 mm^2 in-plane) in a scan time of 1:20 min per slice. Although our radial k-space sampling scheme allows spatial resolution to be increased without lengthening the acquisition, signal-to-noise ratio (SNR) is currently a limiting factor that will need to be addressed in future work. Due to a relatively low SNR in select areas of the fingerprint, the T1 values fluctuate substantially around expected value. This in combination with some residual interactions between slices may explain the slight variations in the T_1 and T_2 values among slices (not observed in the phantom measurements). We plan to improve these results by tailoring delay times to maximize the sensitivity in the parameter ranges relevant to cartilage assessment. MRI of the hip joint is particularly challenging due to the relatively thin layer of cartilage and to the deep anatomical location of the hip. The multiparametric mapping technique presented here can be applied directly to other joints, such as the knee, where the cartilage is thicker and local RECEIVE coils can provide an SNR boost. By enabling a fast comprehensive morphological and biochemical preoperative assessment, we hope to improve assessment and staging of cartilage damage, predict risk for progression, and impact patient management decisions.

REFERENCES: [1] A Watanabe et al. JMRI 2007; 26(1) p. 165. [2] A Bashir et al. MRM 1996; 36(5) p. 665. [3] R Lattanzi et al. OAC 2012; 20(10) p. 1127. [4] PC Lin et al. JMR 2009; 201(1) p. 61. [5] D Ma et al. Nature 2013; 495 p. 187. [6] M Cloos, ISMRM 2015 submitted. [7] CN Petchprapa et al. Radiographics 2013; 33(3) p. E97. [8] http://www.cai2r.net/resources/software/firevoxel. [9] R Lattanzi et al. OAC 2014; 22(3) p. 447.

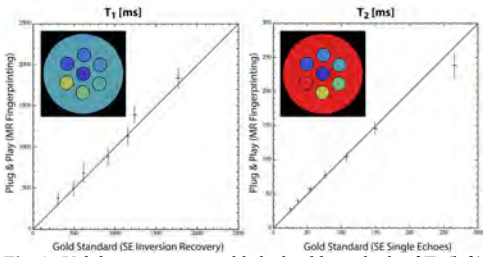

Fig. 1. Validation against established gold standards of T_1 (left) and T_2 (right) values obtained with the proposed MR fingerprinting technique. Each datapoint shows average and standard deviation of T_1 and T_2 in a different phantom compartment.

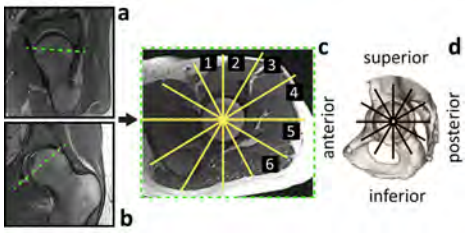

Fig. 2. A radial scout (c) was obtained from true axial (a) and coronal views (b) of the hip. MR fingerprints were acquired for six radial sections, equally spaced around the acetabular opening (c,d).

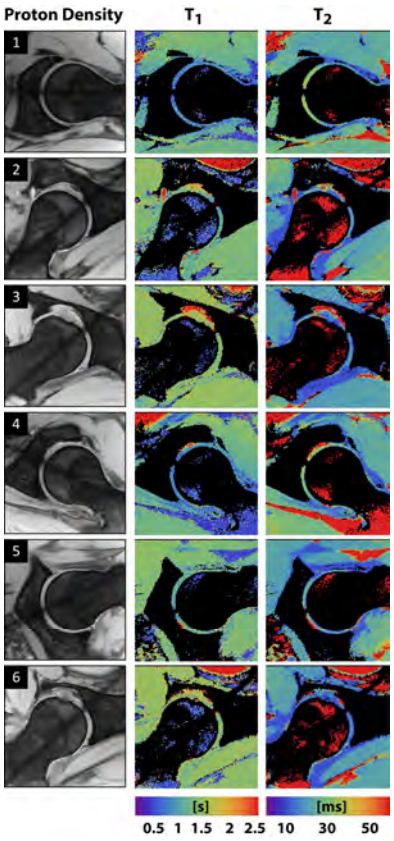

Fig. 3. Reconstructed PD images, T_1 maps and T_2 maps of the hip for the six radial sections in Fig. 2. Total acquisition time was ~8 minutes.