

# Measurement of T<sub>1</sub> relaxation time in articular cartilage using SWIFT

M. J. Nissi<sup>1,2</sup>, L. J. Lehto<sup>3</sup>, C. A. Corum<sup>4</sup>, D. Idiyatullin<sup>4</sup>, O. H. Gröhn<sup>5</sup>, and M. T. Nieminen<sup>6,7</sup>

<sup>1</sup>Department of Physics, University of Kuopio, Kuopio, Finland, <sup>2</sup>Department of Clinical Radiology, Kuopio University Hospital, Kuopio, Finland, <sup>3</sup>Department of Biotechnology and Molecular Medicine, University of Kuopio, Kuopio, Finland, <sup>4</sup>CMRR, University of Minnesota, Minneapolis, MN, United States, <sup>5</sup>Department of Neurobiology, A.I. Virtanen Institute for Molecular Medicine, University of Kuopio, Kuopio, Finland, <sup>6</sup>Department of Medical Technology, University of Oulu, Oulu, Finland, <sup>7</sup>Department of Diagnostic Radiology, Oulu University Hospital, Oulu, Finland

## INTRODUCTION

A new imaging method, SWIFT was recently introduced [1]. SWIFT utilizes interleaved excitation and acquisition, enabling detection of signal from spins with extremely short T<sub>2</sub> relaxation times. Articular cartilage has T<sub>2</sub> relaxation times ranging from less than one millisecond up to around 80 ms, depending on proton pool and orientation [2,3]. These very short T<sub>2</sub> values, particularly in the deep tissue, can typically result in poor signal-to-noise ratios with conventional MRI, possibly hindering the diagnostic feasibility of these methods. The aims of this study were to 1) assess the feasibility of measuring T<sub>1</sub> relaxation time in articular cartilage using SWIFT and to 2) evaluate the performance of the SWIFT method for T<sub>1</sub> relaxation time measurement in articular cartilage.

## MATERIALS AND METHODS

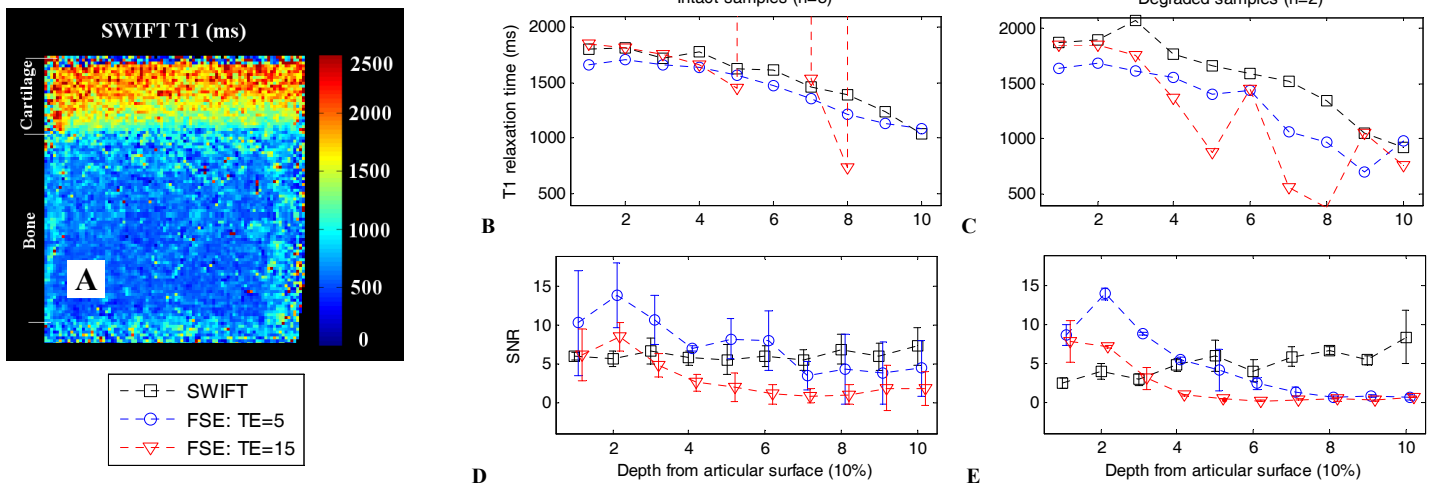
Cartilage-bone plugs from bovine patellae were prepared using core drill (n = 5, dia. = 8.5 mm). Two of the plugs were digested in 1mg/ml trypsin solution for 150 minutes at 37°C, while the rest of the samples were directly immersed in phosphate buffered saline (PBS) containing enzyme inhibitors. Prior to the measurements, all the samples were frozen in PBS containing enzyme inhibitors at -20° C. Prior to imaging the samples were thawed and placed inside a Teflon-test tube and immersed in fomblin. The imaging was conducted at room temperature at 9.4 T vertical magnet interfaced to a Varian DirectDrive console. The samples were positioned inside the tube so, that the samples were located approximately at the RF center of the coil (19 mm quadrature transceiver volume coil). The T<sub>1</sub> relaxation time of the samples was measured using SWIFT by varying the nominal flip angle (FA=3.0, 4.0, 5.6, 8.0, 12.0 and 20.0 degrees, 256 complex points, 62.5 kHz bandwidth, TR = 5.1 ms, 96 000 spokes and 3 averages, 25 mm<sup>3</sup> FOV). SWIFT images were reconstructed using custom-made LabView software, with an isotropic output resolution of 256 points. Subsequently the T<sub>1</sub> relaxation times were calculated in MATLAB using non-linear three-parameter fitting for saturation recovery and two-parameter fitting to the equation:

$$S = M_0 \frac{1 - \exp(-TR / T_1)}{1 - \exp(-TR / T_1) \cos(\theta)} \sin(\theta)$$

for SWIFT, where  $\theta$  is the nominal flip angle that was used [1]. Furthermore, T<sub>1</sub> relaxation time of the samples was measured with saturation recovery fast spin echo sequence (SR-FSE) (TR = 80, 160, 320, 640, 1280, 2560 and 5120 ms) using two different TEs (5 ms and 15 ms) (single 1 mm slice, 256 x 128 resolution, 19.2 x 19.2 mm FOV). Depth-wise T<sub>1</sub> relaxation time profiles for 1 mm columns were averaged from all T<sub>1</sub> maps and resampled for further evaluation. The SNRs were calculated for T<sub>1</sub> relaxation time profiles as ratios of mean to standard deviation and further adjusted by factor 1/(voxel volume \* sqrt(imaging time)). The imaging times were 11.5 minutes for each FSE and 166 minutes for SWIFT.

## RESULTS

T<sub>1</sub> mapping with SWIFT proved to be feasible using variable flip angles, and an example of T<sub>1</sub> relaxation time map is shown in Fig. 1A. The relaxation time values, as measured by SWIFT were comparable to those obtained using conventional FSE-based method (Fig. 1B and C). However, the T<sub>1</sub> relaxation time fits in the deep tissue were less reliable for FSE with long echo time, regardless of tissue status (Fig. 1B and C). The overall imaging time for SWIFT was longer in the current measurement setup, but data for more slices could be collected than could have been collected with FSE. The average volume and imaging time -adjusted depth-wise SNR profiles were better for SWIFT (Fig 1. D and E) in the deep part of the tissue.



**Figure 1.** Representative SWIFT T<sub>1</sub> relaxation time map (single reconstructed slice, thickness ~100  $\mu$ m) (A). Depth-wise average T<sub>1</sub> relaxation time profiles for SWIFT and both FSE methods for intact (B) and degraded cartilage (C). Depth-wise average volume and imaging time -adjusted SNR profiles for SWIFT and FSE in intact (D) and degraded cartilage (E).

## DISCUSSION

The results indicate that SWIFT can be used for the reliable measurement of T<sub>1</sub> relaxation time in articular cartilage. This is important as both pre- and post-contrast T<sub>1</sub> of cartilage is correlated with cartilage degeneration [4,5], and the dGEMRIC method has become a cornerstone of cartilage MRI. Furthermore, the SNR performance of SWIFT indicated it was better in the deep tissue compared to the conventional FSE measurement. More specifically, the adjusted SNR provided by SWIFT was approximately equal to that of FSE for superficial cartilage with relatively long T<sub>2</sub> relaxation times [6]. For deep cartilage with typically short T<sub>2</sub> relaxation times, the SNR provided by SWIFT was markedly better than that of FSE. As a result of the poor SNR, also the fitting of T<sub>1</sub> relaxation time in the deep tissue was unstable for FSE with an echo time of 15 ms, while FSE with an echo time of 5 ms produced acceptable results. The difference between the T<sub>1</sub> relaxation times as measured using SWIFT or FSE was very small, although statistical significance could not be tested due to the small number of samples measured so far. In the clinical setup, the possibility of reliably acquiring full three-dimensional T<sub>1</sub> data in reasonable time could alleviate the limitations related to anisotropic resolution, imaging only few sections and slice repositioning in follow-up studies.

## REFERENCES

- [1] Idiyatullin D et al. J Magn Reson 2006;181:342-349; [2] Zheng S et al. J Magn Reson 2009;198:188-196; [3] Reiter DA et al. Magn Reson Med 2009;61:803-809; [4] Berberat J et al. Magn Reson Imaging 2009;27:727-732; [5] Bashir A et al. Magn Reson Med 1999;41:857-865. [6] Xia Y et al. Magn Reson Med 2002;48:460-469.