

# Sodium Relaxation Times in the Knee Joint In Vivo at 7T

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## Introduction

Sodium concentration correlates directly with the concentration of proteoglycans (PG) in cartilage, the loss of which is an early signature of osteoarthritis (OA). Quantitative sodium MRI is a promising technique for assessing the degeneration of articular cartilage in patients with OA [1]. Sodium relaxation times can also provide information on the degradation of cartilage: it has been shown *ex vivo* that T1 and T2\*<sup>long</sup> are longer and T2\*<sup>short</sup> shorter when the PG concentration decreases [2]. In the present study, the average relaxation times of the  $^{23}\text{Na}^+$  ions were measured *in vivo* at 7T in 4 different regions of the cartilage in the knee joint. T1, T2\*<sup>short</sup> and T2\*<sup>long</sup> relaxation maps were also calculated. These relaxation times and maps can further be used in the correction factors applied for calculating sodium concentration maps [3] as well as information complementary to quantitative sodium MRI in the quest for detecting early OA.

## Materials and Methods

All sodium images were acquired on a 7T whole-body Siemens scanner using a single tuned quadrature birdcage RF knee coil (Rapid MR International), tuned to 78.6 MHz. The data were acquired with a 3D UTE radial sequence written with SequenceTree [4] and compiled with Siemens IDEAS VB15A. Acquisition parameters were: 3500 projections, RF pulse duration 0.5 ms, FOV 200×200×200 mm<sup>3</sup>. 8 healthy volunteers (4 females, 4 males) were scanned (average age: 30.1±5.1 years). Calibration phantoms consisting of a tube of PBS (154 mM of NaCl) and 5 tubes of Agar 4% with [NaCl] = 100, 150, 200, 250, 300 mM were placed within the FOV, their relaxation times were also measured and they can later be used for  $^{23}\text{Na}$  maps calculations. For T1 measurements, 5 acquisitions were obtained with a FA = 90°, TE = 0.4 ms and TR = 30, 60, 100, 150, 250 ms. For T2\* measurements, 9 acquisitions were obtained with FA = 70°, TR = 70 ms and TE = 0.4, 0.8, 1.2, 1.8, 3, 5, 10, 25, 40 ms. Total time of acquisition was 1h15min. Images were reconstructed offline in Matlab with a Non-Uniform Fast Fourier Transform (NUFFT) algorithm [5]. Here, kmax = 17 (unit:1/FOV) and images have an Nyquist resolution of 5.9 mm. As a regridding algorithm is included in the NUFFT method, the images were reconstructed as 80×80×80 matrices and the nominal resolution (pixel size) is 2.5 mm. The acquisition time used in the reconstruction algorithm is 1.6 ms. The T1 data was fitted with a monoexponential function, T2\* data was better fitted with a biexponential function.

## Results

Average sodium relaxation times and their parts of the signal in % (for T2\*<sup>short</sup> and T2\*<sup>long</sup>) are given in Table 1 (abbreviations: F: femur, T: tibia, PAT: patellar, MED: FT medial, LAT: FT lateral, CON: F condyle). On average in cartilage, T1 = 20.4±2.9 ms, T2\*<sup>short</sup> = 0.8±0.3 ms and T2\*<sup>long</sup> = 14.6±1.6 ms. The cartilage regions have similar T1 and slightly different T2\*<sup>short</sup> and T2\*<sup>long</sup>, with significantly different % of signal (PAT and CON T2\*<sup>short</sup> represents >40% of the signal but only 20% for MED and LAT). A significant difference in T1 in cartilage, blood and muscle between male and female has also been noticed (P<0.05). No significant difference was observed for T2\*. Fig. 1 shows an example of spatial distribution of relaxation times within the cartilage.

## Discussion

The point spread function (PSF) of the 3D sequence was calculated for a weighted average T2\* ~ 11 ms (30% of T2\*<sup>short</sup> ~ 1 ms and 70% of T2\*<sup>long</sup> ~ 15 ms for cartilage *in vivo*). The full width at half maximum (FWHM) of the PSF is 3.7 pixels. This means that these images are quite blurred and that partial volume effect affects the accuracy of the relaxation times measurements (mainly due to the presence of synovial fluid around the cartilage). No satisfactory explanation was found to interpret the large difference in % of the signal from T2\*<sup>short</sup> and T2\*<sup>long</sup> components in the different regions of cartilage, but it can be assumed that they are very dependent on the density of collagen fibers, their orientation distribution and the presence of different amounts of fluids within the measurement ROIs.

## Conclusion

This preliminary work shows the feasibility of sodium T1 and T2\* measurements in the articular cartilage *in vivo* at 7T in a reasonable time (~35 min for each relaxation time) and the calculation of relaxation maps. Relaxation measurements could be useful as a complement to the sodium concentration maps for assessing early OA in patients as T2\* and T1 are expected to change with cartilage depletion. We also report differences in T1 and T2\* relaxation between different cartilage regions and in T1 relaxation between males and females. Future improvements of these studies may include fluid suppression for reducing partial volume effects and a systematic study of OA patients.

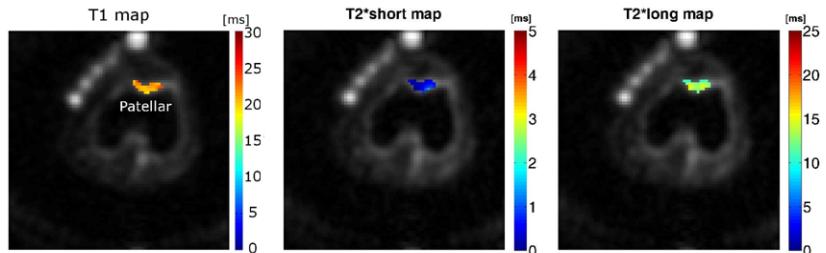
## References

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**Table 1.** Sodium relaxation times in ms (see text for abbreviations).

	T1	T2* <sup>short</sup>	% Signal	T2* <sup>long</sup>	% Signal
<b>Gels 4%</b>	24 ± 3	1.9 ± 0.3	47 ± 2	12.4 ± 0.7	53 ± 2
<b>PBS</b>	43 ± 5	-	-	24.7 ± 7.3	100
<b>Cart PAT</b>	18 ± 3	0.4 ± 0.2	47 ± 9	12.5 ± 1.4	53 ± 9
<b>Cart MED</b>	22 ± 5	0.7 ± 0.3	21 ± 4	14.1 ± 1.4	79 ± 4
<b>Cart LAT</b>	20 ± 4	1.1 ± 0.4	22 ± 4	15.6 ± 1.2	78 ± 4
<b>Cart CON</b>	21 ± 5	0.8 ± 0.4	40 ± 9	16.1 ± 3.1	60 ± 4
<b>Muscle</b>	29 ± 3	1.3 ± 0.2	52 ± 4	16.6 ± 3.7	48 ± 4
<b>Blood</b>	41 ± 6	1.6 ± 0.6	20 ± 4	18.8 ± 2.8	80 ± 4



**Figure 1.** Sodium T1, T2\*<sup>short</sup> and T2\*<sup>long</sup> maps in patellar cartilage *in vivo* at 7T.