

# REPEATABILITY OF T1-QUANTIFICATION IN dGEMRIC FOR THREE DIFFERENT ACQUISITION TECHNIQUES: 2D-INVERSION RECOVERY, 3D-LOOK-LOCKER AND 3D-VARIABLE FLIP ANGLE

C. Siversson<sup>1</sup>, C-J. Tiderius<sup>2</sup>, P. Neuman<sup>2</sup>, L. Dahlberg<sup>2</sup>, and J. Svensson<sup>1</sup>

<sup>1</sup>Department of Radiation Physics, Lund University, Malmö, Sweden, <sup>2</sup>Department of Orthopaedics, Lund University, Malmö, Sweden

## Introduction

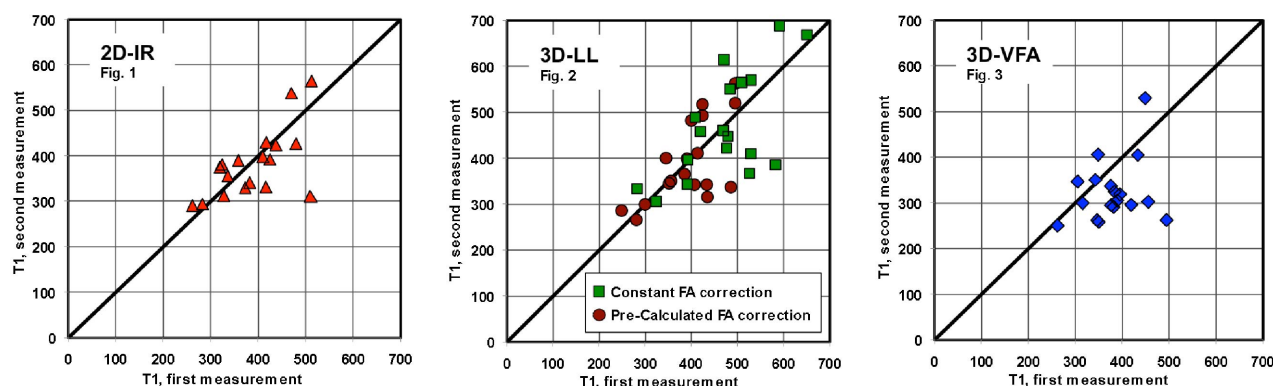
Delayed Gadolinium enhanced MRI of cartilage (dGEMRIC) is a technique for molecular imaging of the proteoglycan level in cartilage using quantitative T1 measurements [1]. Until now there have been no studies of the repeatability of such T1 quantifications for 3D-dGEMRIC. The aim of this work is thus to measure this repeatability in vivo for two successive measurements and for three different dGEMRIC techniques, 2D-Inversion Recovery (2D-IR), 3D-Look Locker (3D-LL) and 3D-Variable Flip Angle (3D-VFA).

## Methods

dGEMRIC measurements were performed twice on the same knee, with two weeks separation, on a total of 9 subjects having various degree of osteoarthritis (OA). Data acquisitions for 2D-IR (FOV = 12\*12 cm, Matrix = 256\*256, TR=2000 ms, 6 TI from 50 - 1600 ms), 3D-LL (FOV = 16\*16 cm, Matrix = 256\*256, 30 slices, TR 2500 ms, FA = 6°, 12 contrasts) and 3D-VFA (FOV = 16\*16 cm, Matrix = 256\*256, 30 slices, TR 40 ms, FA = 4.8° and 23.9°) were performed consecutively (90-110 minutes after contrast injection). T1 was calculated in central parts of the lateral and the medial femoral weight-bearing cartilage for each method at each measurement occasion. For 3D the T1 quantification was performed in off-center slices (ROIs drawn in slices 6-10, and 22-24 for the respective subjects). 3D-LL was further evaluated using both standard constant FA correction [2] and pre-calculated FA correction [3]. The constant FA correction was performed using the nominal FA from the sequence parameters in combination with equation 1. The pre-calculated FA correction was also performed using equation 1, but with the FA retrieved from an FA slice profile previously measured using a set of gel-phantoms, as described by Siversson et al [3]. The 3D-VFA measurement was evaluated as previously described by Mamisch et al [4]. All imaging was performed on a Siemens Magnetom Sonata 1.5 T scanner equipped with a CP Extremity coil.

## Results

All corresponding first and second T1 measurements are plotted for each method in figures 1-3. As can be seen, the 3D-LL sequence with constant FA correction shows a larger dynamic range of its measured T1s, which is an error introduced due to the method not taking the slice dependent FA variation into account. In order to compare the repeatability of each method, regardless of the T1 dynamics, the relative deviation (D, eq.2) between the temporal measurements was calculated for each quantification method and averaged for all subjects (table 1).



<b>Table 1.</b>	<b>2D-IR</b>	<b>3D-LL Const. FA corr.</b>	<b>3D-LL Pre-calc. FA corr.</b>	<b>3D-VFA</b>
Average D	12%	14%	13%	21%

$$\text{Eq 1. } \frac{1}{T_1} = \frac{1}{T_1^*} + \frac{\ln(\cos(\alpha))}{\tau} \quad \text{Eq 2. } D = \frac{2(T1_{first} - T1_{last})}{T1_{first} + T1_{last}}$$

## Discussion and conclusions

The use of a 2D-IR sequence for T1 quantification is generally considered to be a very stable method, and serves as the gold standard in this study. However, in repeated dGEMRIC measurements, variations to some degree are expected, due to the complexity of both the biological and technical processes behind the measurement. Thus, the measured 2D-IR average relative deviation (table 1) is likely the lowest achievable of any dGEMRIC measurement method. The 2D-IR and 3D-LL sequences are shown to perform roughly equally well, thus verifying the stability of the 3D-LL sequence for dGEMRIC. The larger dynamic range of the T1s measured using 3D-LL with constant FA correction does not affect the repeatability considerably, as long as the positioning of each subject is essentially equal for the successive measurements. With 3D-VFA however there is a considerably larger average relative deviation than with the other sequences. It is not likely to assume that this is due to slice dependent FA variations, since those should cancel out, similar to the case with 3D-LL with constant FA correction. Instead this is likely an effect of 3D-VFA being noise sensitive, which might improve if more than two FAs are used for T1 calculation.

## References

1. Bashir et al, MRM, 41:857-865 (1999)
2. Kimelman et al, Inv. Radiol. 41:198-203 (2006)
3. Siversson et al, ISMRM No.5289 (2008)
4. Mamisch et al, MRM 60:768-773 (2008)