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### SELECTION OF COMPARABLE ANATOMICAL LOCATIONS OF MUSCLE CROSS-SECTIONAL IMAGES IN THE OSTEOARTHRITIS INITIATIVE MRI DATA

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**Purpose:** Muscle forces and cross sectional areas (CSA) play an important role in the onset and progression of OA. The OA Initiative provides images of muscle CSAs of both limbs. These images are acquired starting 10 cm proximally of the distal epiphyseal line of the femur and cover 15 slices of 0.5 mm (7.5 cm) in proximal direction. The images therefore have a variable anatomical location with regard to the femur and thigh muscles in short and tall individuals, and this poses limits on the comparability between participants in cross sectional studies. The objectives were therefore to determine a) the location of the 15 slices in relation to the femur (%length) in persons with variable body height, b) which part of the femur (% length) is covered in all subjects, and c) whether the inter-subject variability of the location of these cross sectional images (versus the femoral length) can be effectively reduced, when accounting for differences in body height.

**Methods:** Clinical data, MR images of the thigh muscles, and full limb X-rays from 48 OA participants with calculated Kellgren Lawrence grade 3 were studied (OAI public data sets 0.2.2, 0.E.1, 1.E.1). The subjects were selected to cover the full body height distribution in men and women. In the women (n=24), the body height ranged from 151.1 to 180.2 cm, and in the men (n=24) from 162.8 to 188.8 cm. From the full-limb X-rays, the femoral length (distance of the knee joint space to the proximal end of the femoral head) was determined in vertical direction. The position of the epiphyseal line (in the femur) was measured in MRI scout views which were used to plan the thigh muscle MRI acquisitions.

**Results:** The femoral length (F) in the full-limb X-rays varied from 47.3 to 55.1 cm in men, and from 44.2 to 55.9 cm in women. The relationship between F and the body height (H) was similar in men and women (F=29.4% of H in women [min:27.5%, max:31.5%], and F=30.0% of H in men [min: 27.9%, max:33.8%]). Linear regression analysis provided the equations  $F=0.29 \times H \text{ mm} + 15.7 \text{ mm}$  for men ( $r^2=63\%$ ) and  $F=0.33 \times H \text{ mm} - 51.93 \text{ mm}$  for women ( $r^2=57\%$ ) as estimates of F. The epiphyseal line was clearly visible in 24 of the 48 MRI scout views; its relative position in the femur (from distal) was 6.0% in women (min:3.4%; max:8.5%), and 7.2% in men (min:5.5%, max:8.8%). The location was significantly different ( $p=0.03$ ) between sexes. From these data, it was derived that a region of 29.4% to 36.7% of the femoral length (from distal) was covered by the 15 axial MRI muscle slices in all men, and a region between 31.1% and 35.7% in all women, across the full range of body heights. Therefore a target slice located at 33% of F (from distal to proximal) was selected, so that all participants could be included in a measurement, independent of body height. This location corresponded to slice No7 (from distal to proximal) in a person of average height (=mean across the 48 subjects). When selecting slice No7 in every participant, its location varied between 30% and 37% of the femoral length (standard deviation [SD]=1.5%). When choosing the most appropriate slice after accounting for differences in body height (slice number 4 to 9), its location varied only between 32.5% and 33.5% (SD=0.3%).

**Conclusions:** Measurement of the femoral length and the epiphyseal line allows for the precise selection of comparable slices for measuring muscle CSAs in subjects with different heights. In cases where no full limb radiographs are available, the use of body height (H) as an estimate of femoral length (F) can reduce the variability of the slice location as expressed by the standard deviation by a factor of 5 compared with choosing the same slice across all subjects.

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### USING T2 PHANTOMS TO OBTAIN CONSISTENT T2 RELAXATION TIMES REGARDLESS OF PULSE SEQUENCE

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**Purpose:** T<sub>2</sub> relaxation times in articular cartilage have been correlated with variations in macromolecular concentration, collagen orientation and structure and tissue hydration. Each MRI system manufacturer has developed a different sequence for creating T<sub>2</sub> maps. In addition, these sequences are often a purchased option which not all clinical sites may have. The purpose of this paper is to show that by utilizing T<sub>2</sub> phantoms during the

imaging, it does not matter the exact pulse sequence used to calculate the T<sub>2</sub> map.

**Methods:** Seventy vials with varying concentrations of CuSO<sub>4</sub> were placed in a container and imaged in a GE Twin Speed HDx 1.5T magnet. The container was oriented with the vials standing vertically within the magnet. All images were in the coronal plane with a slice thickness of 3.5mm, matrix of 256×256 and FOV of 38cm (Figure 1).

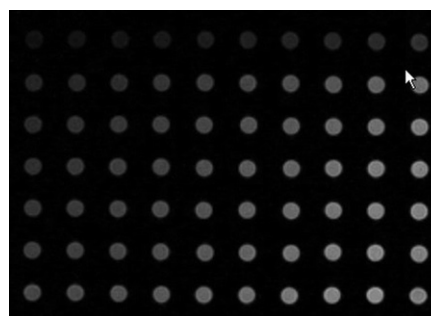


Figure 1. Coronal scan of the 70 vials illustrating the different T<sub>2</sub> relaxation times.

To obtain a "gold standard" for the T<sub>2</sub> relaxation times, 8 spin-echo sequences were collected with TR/TE = 1500ms/10, 20, 30, 40, 50, 60, 80 and 100ms. Four of the vials were used as the reference values to simulate having a four-vial phantom with known T<sub>2</sub> relaxation times. The T<sub>2</sub> relaxation times for these vials were approximately 39ms, 61ms, 120ms and 237ms. Several different T<sub>2</sub> mapping sequences were then obtained. T<sub>2</sub> maps were calculated from these sequences both with and without the use of the four known values. To map the calculated T<sub>2</sub> relaxation times using the four known values, piecewise linear interpolation was used.

**Results:** The raw T<sub>2</sub> relaxation times for each of the sequences are shown in Figure 2, and the corrected results are shown in Figure 3. The T<sub>2</sub> relaxation

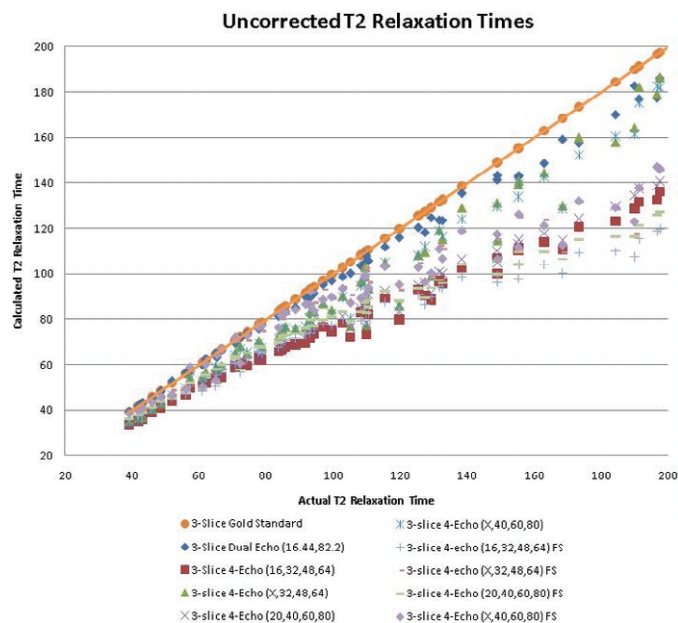


Figure 2. Uncorrected T<sub>2</sub> relaxation times plotted versus the actual T<sub>2</sub> relaxation time.

Table 1. Average percent error in calculated T<sub>2</sub> values

Sequence	Uncorrected		Corrected	
	<100ms	<200ms	<100ms	<200ms
Dual echo	-1.52%	-5.31%	0.6%	0.5%
4 echo A	-18.8%	-28.5%	6.7%	7.5%
3 echo A	-11.4%	-14.6%	9.5%	9.1%
4 echo B	-17.4%	-25.9%	6.7%	6.8%
3 echo B	-12.2%	-15.2%	10.5%	9.3%
4 echo A FS	-16.2%	-30.7%	10.2%	9.1%
3 echo A FS	-5.5%	-19.5%	16.5%	14.6%
4 echo B FS	-14.0%	-27.7%	9.4%	7.9%
3 echo B FS	-5.7%	-19.9%	14.6%	12.4%