



Deep learning–based fully automated body composition analysis of thigh CT: comparison with DXA measurement

Hye Jin Yoo^{1,2} · Young Jae Kim³ · Hyunsook Hong⁴ · Sung Hwan Hong^{1,2} · Hee Dong Chae^{1,2} · Ja-Young Choi^{1,2} 

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Abstract

Objectives To compare volumetric CT with DL-based fully automated segmentation and dual-energy X-ray absorptiometry (DXA) in the measurement of thigh tissue composition.

Methods This prospective study was performed from January 2019 to December 2020. The participants underwent DXA to determine the body composition of the whole body and thigh. CT was performed in the thigh region; the images were automatically segmented into three muscle groups and adipose tissue by custom-developed DL-based automated segmentation software. Subsequently, the program reported the tissue composition of the thigh. The correlation and agreement between variables measured by DXA and CT were assessed. Then, CT thigh tissue volume prediction equations based on DXA-derived thigh tissue mass were developed using a general linear model.

Results In total, 100 patients (mean age, 44.9 years; 60 women) were evaluated. There was a strong correlation between the CT and DXA measurements ($R = 0.813\text{--}0.98$, $p < 0.001$). There was no significant difference in total soft tissue mass between DXA and CT measurement ($p = 0.183$). However, DXA overestimated thigh lean (muscle) mass and underestimated thigh total fat mass ($p < 0.001$). The DXA-derived lean mass was an average of 10% higher than the CT-derived lean mass and 47% higher than the CT-derived lean muscle mass. The DXA-derived total fat mass was approximately 20% lower than the CT-derived total fat mass. The predicted CT tissue volume using DXA-derived data was highly correlated with actual CT-measured tissue volume in the validation group ($R^2 = 0.96\text{--}0.97$, $p < 0.001$).

Conclusions Volumetric CT measurements with DL-based fully automated segmentation are a rapid and more accurate method for measuring thigh tissue composition.

Key Points

- There was a positive correlation between CT and DXA measurements in both the whole body and thigh.
- DXA overestimated thigh lean mass by 10%, lean muscle mass by 47%, but underestimated total fat mass by 20% compared to the CT method.
- The equations for predicting CT volume (cm^3) were developed using DXA data (g), age, height (cm), and body weight (kg) and good model performance was proven in the validation study.

Keywords Sarcopenia · Body composition · Absorptiometry, photon · Deep learning · Image segmentation

Abbreviations

DL Deep learning
DXA Dual-energy X-ray absorptiometry

Introduction

Skeletal muscle plays an important role in physical activity as well as protein metabolism and glucose regulation [1, 2]. In

✉ Ja-Young Choi
drchoi01@gmail.com

¹ Department of Radiology, Seoul National University Hospital, Seoul, South Korea

² Department of Radiology, Seoul National University College of Medicine, 103 Daehak-ro, Jongno-gu, Seoul 110-799, South Korea

³ Department of Biomedical Engineering, Gachon University, Gil Medical Center, Incheon, South Korea

⁴ Medical Research Collaborating Center, Seoul National University Hospital, Seoul, South Korea

the past decade, the importance of muscle mass has been emphasized, and significant loss of skeletal muscle mass and function, i.e., sarcopenia, has become an important issue in clinical research [2–4]. Recently, concerns about thigh muscle mass and strength have also increased because a reduction in thigh muscle strength is known to be associated with knee pain and functional impairments [5, 6]. Thigh muscle strength is a potential risk factor for knee osteoarthritis [7–9] and may also be implicated in the risk of knee replacement [10]. Accordingly, there is increasing interest in quantifying skeletal muscle mass and size [2–4, 11, 12].

There are several imaging techniques used to measure muscle mass, including magnetic resonance imaging (MRI), computed tomography (CT), ultrasonography, bioelectrical impedance analysis (BIA), and dual-energy X-ray absorptiometry (DXA) [3, 4]. Among them, DXA has been popular for the measurement of body composition because it is relatively simple, affordable, and easily accessible and requires minimal radiation exposure. However, DXA utilizes two-dimensional projection and provides inaccurate or imprecise measures of appendicular tissue composition [3, 12]. MRI and CT have been considered the gold standard for quantifying and comparing skeletal muscle mass. However, their application is limited in clinical research because of their high cost, limited accessibility, high-dose radiation exposure (CT), and time-consuming segmentation process [3, 12, 13]. To date, CT-derived muscle measurements have only been performed on a single slice [11, 14–16] or a few representative slice images [11, 17–19] to reduce the scan time, radiation dose, and time for manual segmentation of individual muscles. Image segmentation of individual muscles is time-consuming and labor-intensive, severely limiting the application of CT in quantifying skeletal muscle mass [20, 21].

With great advances in CT technology, CT has become faster and provides lower radiation exposure and higher spatial resolution. Moreover, in recent years, an automated segmentation method of individual muscles based on deep learning (DL) that provides reproducible and accurate muscle quantification has been successfully developed. CT can also provide more detailed anatomical analysis and information about muscle quality. To our knowledge, no study has directly compared DXA estimations of total thigh muscle mass with CT measurements obtained from an entire thigh muscle instead of a few representative axial images.

Thus, the aim of our study was to compare three-dimensional (3D) volumetric CT with DL-based fully automated segmentation and DXA in the measurement of thigh tissue composition.

Materials and methods

This prospective study was approved by the Institutional Review Board of our center and has therefore been performed

in accordance with the ethical standards laid down in the 1964 Declaration of Helsinki and its later amendments. Written informed consent was obtained from all subjects before inclusion in the study.

Study population

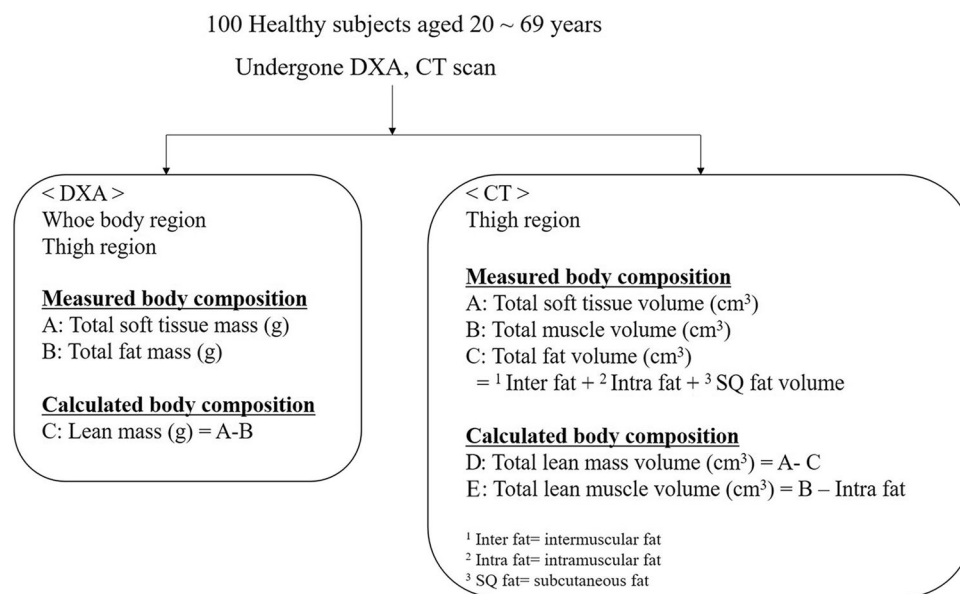
The study was designed to include a total of 100 healthy adults aged 20–69 years from January 2019 to December 2020. A total of 100 healthy adults (40 men and 60 women) were finally recruited through advertisements in the hospital. All participants were healthy, not known to suffer from any trauma around the knee joints or any infectious or rheumatoid disease. Participants were excluded if they were pregnant or if they had undergone hip or knee replacement surgery (Fig. 1). Body weight and standing height were measured, then body mass index (BMI) was calculated by dividing the participant's body mass in kilograms by their height-squared in meters.

Dual-energy X-ray absorptiometry

A whole-body dual-energy x-ray (DXA) (Lunar Prodigy Advance; GE Healthcare) scan was performed by a trained radiologic technician to measure total body composition and bone mineral density. Because whole-body scans can be used to divide the body into bone, fat, and lean compartments, lean or fat-free soft tissue can be calculated by DXA software [17, 22]. Whole-body scans were manually analyzed according to examiner-defined regions of interest (ROIs), including the trunk, arm, total leg, and thigh (Fig. 2). The ROI for the thigh was defined as the region from the ischial tuberosity to the proximal margin of the patella (Fig. 2). In whole-body and thigh ROIs, fat mass, fat-free lean mass, total tissue mass, and percent fat (%fat) were estimated using the Lunar Prodigy whole body and regional analysis modes (enCORE™ Software Platform, GE Healthcare).

Computed tomography scan

All computed tomography (CT) examinations were performed with a dual-layer spectral detector CT system (IQon Spectral CT; Philips Healthcare) in our institution. CT images were obtained with the following acquisition parameters: tube voltages of 120 kVp, reference tube current-time product of 140–150 mAs; effective rotation time of 0.4 s; collimation of 64×0.625 mm; pitch of 0.391; field of view (FOV) of $320 \sim 400 \times 320 \sim 400$ mm; reconstruction slice thickness of 2.0 mm; and no gap. Patients were scanned in the supine position from the anterior superior iliac spine to the knee joint.

Fig. 1 Flow diagram of the study population

CT measurement of body composition

A DL-based automated thigh segmentation software was developed in our institution for analysis of tissue composition from axial CT images of the thigh (Fig. 3). In the learning model, the conventional U-net architecture was modified to fit denoising purpose by reducing the number of convolution filters and applying batch-normalization (BN) to prevent overfitting while improving training stability [11, 12]. For all scans, axial CT images from the ischial tuberosity to the proximal margin of the patella were selected in exactly the same way as the DXA section, as far as possible, for comparison with DXA thigh ROIs. Then, the left and right sides of the thighs were separated and treated as two thigh volumes for analysis. All thigh CT images were automatically segmented into three muscle groups (extensor, flexor, and adductor group) and adipose tissue (subcutaneous, intramuscular, and intermuscular fat) by the custom-developed segmentation algorithms. Throughout this work, soft tissues were classified according to the previously used thresholds in Hounsfield units (HU): −29 to +150 HU for muscles and −190 to −30 HU for adipose tissue [23, 24]. The average segmentation time per participant was 2 min on a GPU-equipped Windows workstation (Intel (R) Core i7-8700 CPU @ 3.20 GHz, Memory 32.0 GB, GPU: NVIDIA GeForce GTX 1060 6 GB, OS: Windows 10). Subsequently, a DL-based automated muscle segmentation program reported total soft tissue volume, muscle volume per muscle group, subcutaneous and intermuscular fat volume, and intramuscular fat volume per muscle group [25, 26]. The lean mass was obtained by subtracting subcutaneous/intermuscular fat from total soft tissue volume, and the lean muscle volume was obtained by subtracting intramuscular fat from muscle volume. Skeletal

muscle and adipose tissue volume estimates were converted to mass by assuming a density of 1.04 kg/L for skeletal muscle and 0.92 kg/L for adipose tissue [11, 27]. The development of DL-based automated thigh segmentation software and the analysis of body composition were conducted by a technical expert (Y.J.K.) under supervision of radiologists (H.J.Y. and J.Y.C.).

Model for predicting CT volume (cm³) using DXA mass (g)

Total thigh lean muscle volume (cm³) prediction equations based on DXA-derived lean mass (g) were developed by using general linear regression model analysis of the right thighs [28]. Then, the prediction models were validated using left thigh data.

Statistical analysis

Statistical analysis was performed by one of the radiologist (H.J.Y.) using SPSS (version 22; SPSS) and R (version 4.0.3, <https://www.r-project.org/>). Data are reported as the means and standard deviations. Variables were compared between men and women by independent-sample t-tests. Pearson's correlation was used to determine the relationships between variables measured by DXA and CT. Bland–Altman analysis was used to assess the agreement between the two methods of tissue composition estimation, and the 95% limits of agreement between the two methods were obtained. A two-tailed *p* value < 0.05 was considered statistically significant.

In the second phase of the study, CT thigh soft tissue volume (cm³) prediction equations based on DXA-derived right thigh tissue mass (g) were developed by using a general linear

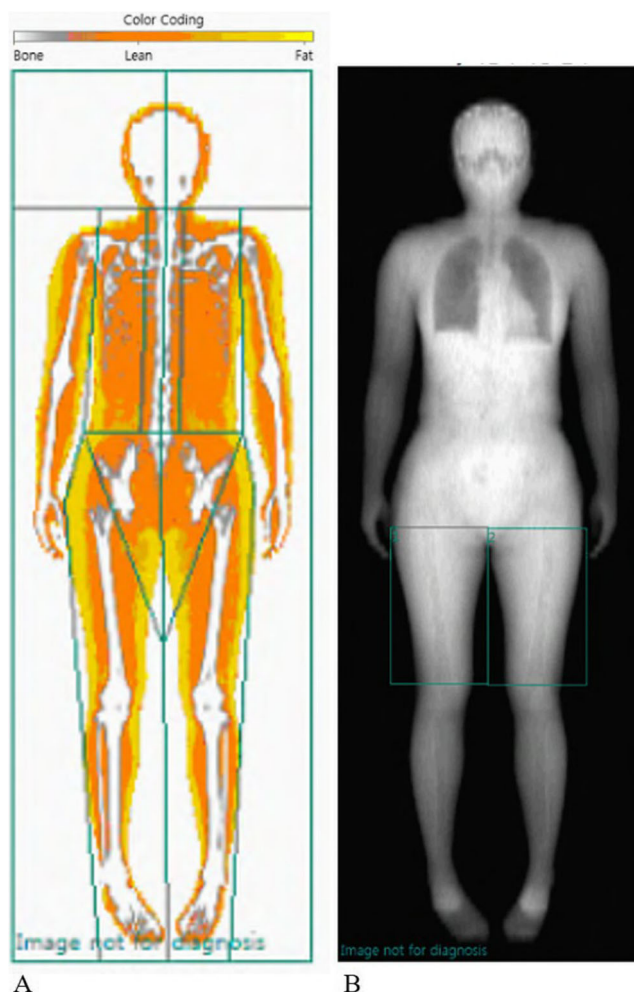
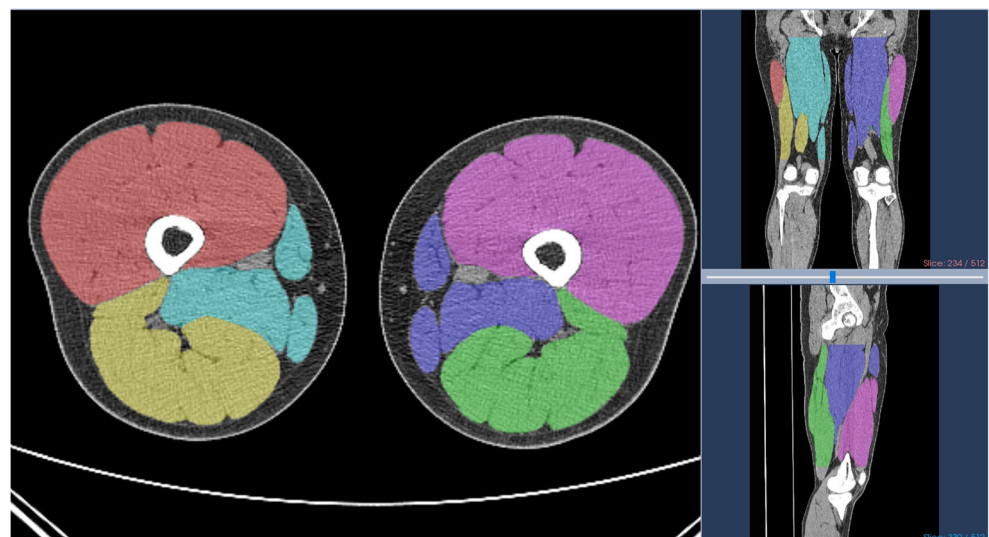


Fig. 2 DXA scan in the whole body and thigh. **A.** Whole-body scans were manually analyzed according to examiner-defined regions of interest (ROIs), including the trunk, arm, total leg and thigh. Body composition (fat, lean tissue mass and bone mineral content) was automatically calculated by DXA software. **B.** The ROI for the thigh was defined as the region from the ischial tuberosity to the proximal margin of the patella

Fig. 3 A fully automated CT image segmentation using custom-developed deep learning-based software. Thigh CT images were automatically segmented into three muscle groups, i.e., extensor, flexor and adductor groups, and adipose tissue



model [28]. Potential independent variables included DXA-measured tissue mass (g), age, body weight, height, and sex. Predictors were chosen by applying backward elimination based on the Akaike information criterion (AIC). The performance of the prediction model was assessed in terms of R^2 , calibration slope, and calibration-in-the-large. R^2 indicates the proportion of variation in total thigh soft tissue volume explained by the predictors, while calibration slope and calibration-in-the-large reflect the degree of agreement between observed and predicted values. Good calibration is achieved when the calibration-in-the-large is close to 0 and the calibration slope is close to 1. In addition, optimism-corrected performance measures were estimated based on 1000 bootstrap samples. To adjust the final prediction model for overfitting, the original coefficients were multiplied by a global shrinkage factor, the calibration slopes in the resamples were averaged, and the intercept was re-estimated accordingly. The final prediction model was validated using the left side data, and model performance was assessed using R^2 , calibration slope, calibration-in-the-large, and the Bland–Altman limit of agreement and its 95% confidence intervals [29].

Results

Table 1 describes the characteristics of the study population. The mean age and BMI were 44.87 years (range 22–68 years) and $24.05 \text{ kg}\cdot\text{m}^{-2}$ (range $18.2\text{--}36.5 \text{ kg}\cdot\text{m}^{-2}$), respectively.

The soft tissue estimates derived from DXA and CT are summarized in Table 2. There was no significant difference in total soft tissue mass between DXA and CT measurement ($p = 0.183$). However, the DXA-derived thigh lean mass was greater than the CT-derived thigh lean mass

Table 1 Characteristics of the study participants

	Whole group (<i>n</i> = 100)	Men (<i>n</i> = 40)	Women (<i>n</i> = 60)	<i>p</i> value
Age (years)	44.87 (± 12.84)	41.45 (± 12.55)	47.15 (± 12.62)	0.029
Height (cm)	164.66 (± 8.71)	172.8 (± 5.75)	159.2 (± 5.46)	< 0.001
Weight (kg)	65.58 (± 13.49)	76.15 (± 13.48)	58.53 (± 7.67)	< 0.001
BMI	24.05 (± 3.60)	25.42 (± 3.80)	23.14 (± 3.18)	0.02

Data were reported as the means and standard deviations

($p < 0.001$) and thigh lean muscle mass ($p < 0.001$), which means DXA overestimated thigh lean (muscle) mass. In contrast, the DXA-derived thigh total fat mass was significantly less than the CT-derived thigh total fat mass ($p < 0.001$), reflecting underestimation of total fat mass by DXA.

With both measurement methods, the total soft tissue, lean and lean muscle masses of the thigh were found to be significantly greater in men than in women ($p < 0.01$, all). Women had a significantly higher total fat mass of the thigh ($p < 0.05$). The subgroup analysis of the three muscle compartments showed similar differences in total soft tissue and lean mass between men and women, but there was no significant difference in intramuscular fat mass by sex. There was no significant difference in DXA estimates based on whole-body scans with regard to sex.

Correlation between DXA and CT measurements

There was a positive correlation between CT and DXA measurements in both the whole body and thigh (Table 2). The

DXA-derived total soft tissue mass of the thigh was highly correlated with the CT-derived total soft tissue mass (correlation coefficient value (R) = 0.909, $p < 0.001$ for the whole body and $R = 0.973$, $p < 0.001$ for the thigh). In addition, a strong relationship was found between CT measurements of lean muscle/total fat masses and DXA estimates of lean/total fat masses (R ranging from 0.813 ~ 0.981, $p < 0.001$, Table 2). Figure 4 shows the relationship between DXA and CT measurements.

Agreement between DXA and CT measurements

Figure 5 shows Bland–Altman plots for DXA- and CT-derived data for total soft tissue, lean (muscle) mass, and total fat mass. The Bland–Altman analysis indicated proportional bias, especially in the comparisons of lean and total fat mass. There was a tendency for the mean of the differences between the methods to increase with increasing lean mass ($R = 0.431$, $p < 0.01$) and lean muscle ($R = 0.721$, $p < 0.01$) and decrease with increasing total fat mass ($R = -0.548$, $p < 0.01$) [11]. The Bland–Altman plot also illustrates that DXA overestimated lean mass and lean muscle mass and underestimated total fat

Table 2 Comparison of DXA and three-dimensional CT using deep learning-based automated image segmentation technique for measuring tissue composition

	DXA (g)		CT (g) (thigh)				<i>p</i> value ^c	Pearson's coefficients (<i>R</i>)	
	Whole body	Thigh	Total	Extensor	Flexor	Adductor		Whole body DXA vs CT	Thigh DXA vs CT
Total soft tissue	63101.46 (± 3037.41)	5750.47 (± 1418.92)	5782.34 (± 1306.86)	1419.67 (± 454.53)	587.55 (± 170.64)	845.19 (± 263.92)	0.183	0.909	0.973
Lean mass ^a	42328.84 (± 9579.61)	4084.63 (± 1150.40)	3710.38 (± 1034.04)	NA	NA	NA	< 0.001	0.964	0.967
Lean muscle	NA	NA	2787.34 (± 870.14)	1393.47 (± 451.23)	573.35 (± 167.48)	826.63 (± 257.83)	< 0.001 ^d	0.956	0.963
Total fat ^b	20772.61 (± 6357.37)	1665.82 (± 636.96)	2071.96 (± 721.69)	23.25 (± 27.11)	12.60 (± 13.67)	16.48 (± 11.87)	< 0.001	0.813	0.981

Lean Mass^a (CT) = total soft tissue mass – total fat mass measured by CT

Total fat mass^b of thigh region measured by CT = subcutaneous fat + inter-/intramuscular fat

Fat^b of extensor, flexor or adductor compartment measured by CT = intramuscular fat

p value^c = *p* value in the comparison of means between DXA-derived and CT-derived thigh body composition

p value^d = *p* value in the comparison of means between DXA-derived thigh lean mass and CT-derived lean muscle mass

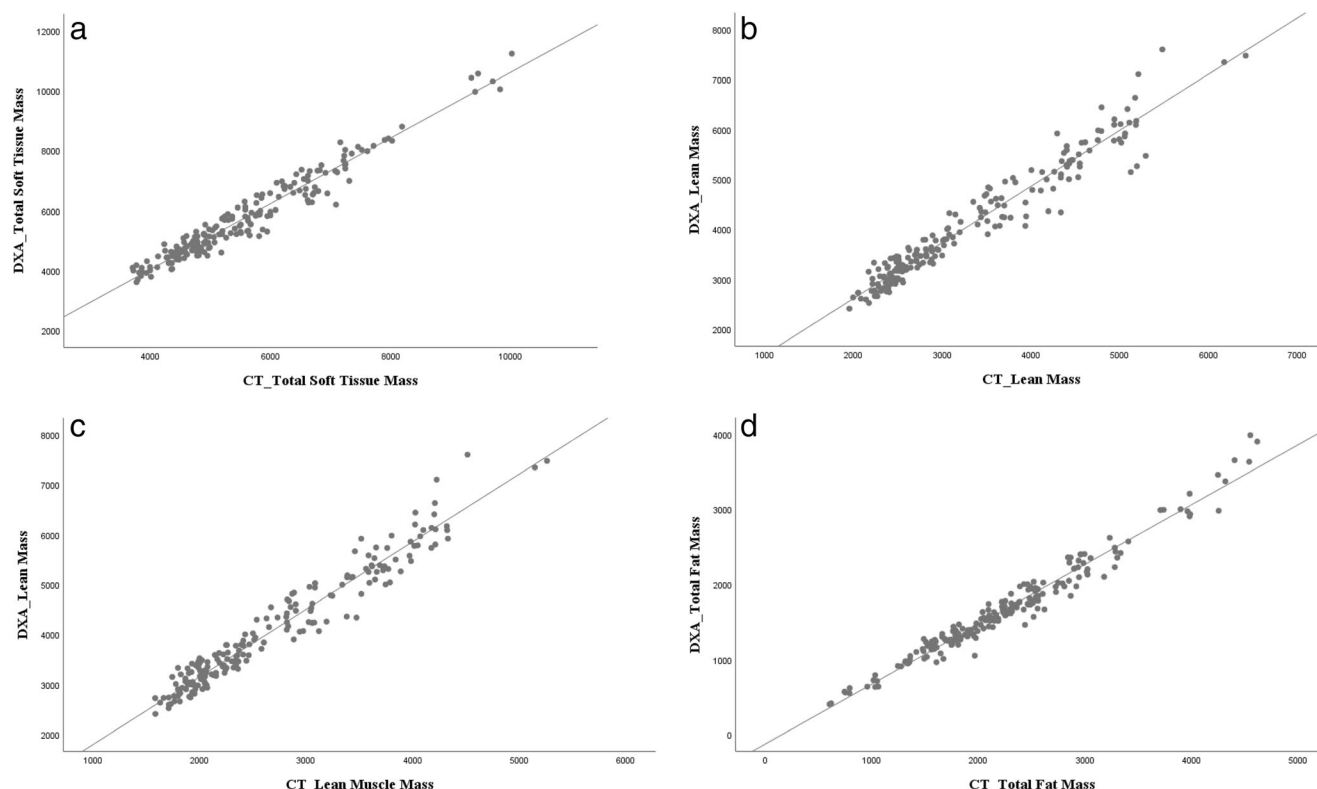


Fig. 4 Correlation between DXA and CT measurements. **a** The relationship between thigh total soft tissue mass derived by DXA and CT. **b** The relationship between thigh lean mass as measured by DXA

and CT. **c** The relationship between thigh lean mass as measured by DXA and lean muscle mass measured by CT. **d** The relationship between thigh total fat mass as measured by DXA and CT

mass (Fig. 5) [11, 30]. Logarithmic transformation was used to remove the effect of differences increasing with the magnitude of tissue composition (Fig. 6) [31]. The DXA-derived lean mass was an average of 10% (95% limit of agreement (LOA); 2~23%) higher than the CT-derived lean mass and 47% (95% LOA; 28~69%) higher than the CT-derived lean muscle mass. The DXA-derived total fat mass was an average of 20% (95% LAO; -31~-8%) lower than the CT-derived total fat mass.

Model for predicting CT volume (cm³) using DXA mass (g)

DXA-derived lean mass was the strongest predictor ($p < 0.001$) of CT lean muscle volume in the thigh region, explaining 37.3% of the variance in actual CT-measured lean muscle volume. Sex and height were the second and third strongest predictors, explaining an additional 26.9% and 19.3% of the variance in actual CT-measured lean muscle volume, respectively. Body weight and age contributed to the developed model by 13.5% and 2.6%, respectively. The final prediction equations for other CT measurements using DXA data (g), age, height (cm), and body weight (kg) were as follows:

$$\begin{aligned} \text{Predicted CT total tissue volume (cm}^3\text{)} &= 2,263.8961 + 0.6766 \times \text{DXA total tissue mass (g)} - 8.2471 \\ &\quad \times \text{Age} - 12.2029 \times \text{height (cm)} \\ &\quad + 25.0973 \times \text{weight (kg)} \\ &\quad (\text{for females, } -2,714.9335 + 18.0664 \times \text{height (cm)} \text{ should be added}) \end{aligned} \quad (1)$$

$$\begin{aligned} \text{Predicted CT lean muscle volume (cm}^3\text{)} &= 2,312.2226 \\ &\quad + 0.6910 \times \text{DXA lean mass (g)} - 2.3900 \times \text{Age} - 4.8467 \\ &\quad \times \text{weight (kg)} - 11.1755 \times \text{height (cm)} \\ &\quad (\text{for females, } -2,081.2443 - 0.1426 \times \text{DXA lean mas (g)} \\ &\quad + 14.0133 \times \text{height (cm)} \text{ should be added}) \end{aligned} \quad (2)$$

$$\begin{aligned} \text{Predicted CT total fat volume (cm}^3\text{)} &= 856.5714 + 1.0995 \\ &\quad \times \text{DXA total fat mass (g)} + 4.3606 \\ &\quad \times \text{weight (kg)} - 4.9144 \times \text{height (cm)} \\ &\quad (\text{for females, } -2050.7046 + 13.5700 \\ &\quad \times \text{height (cm)} \text{ should be added}) \end{aligned} \quad (3)$$

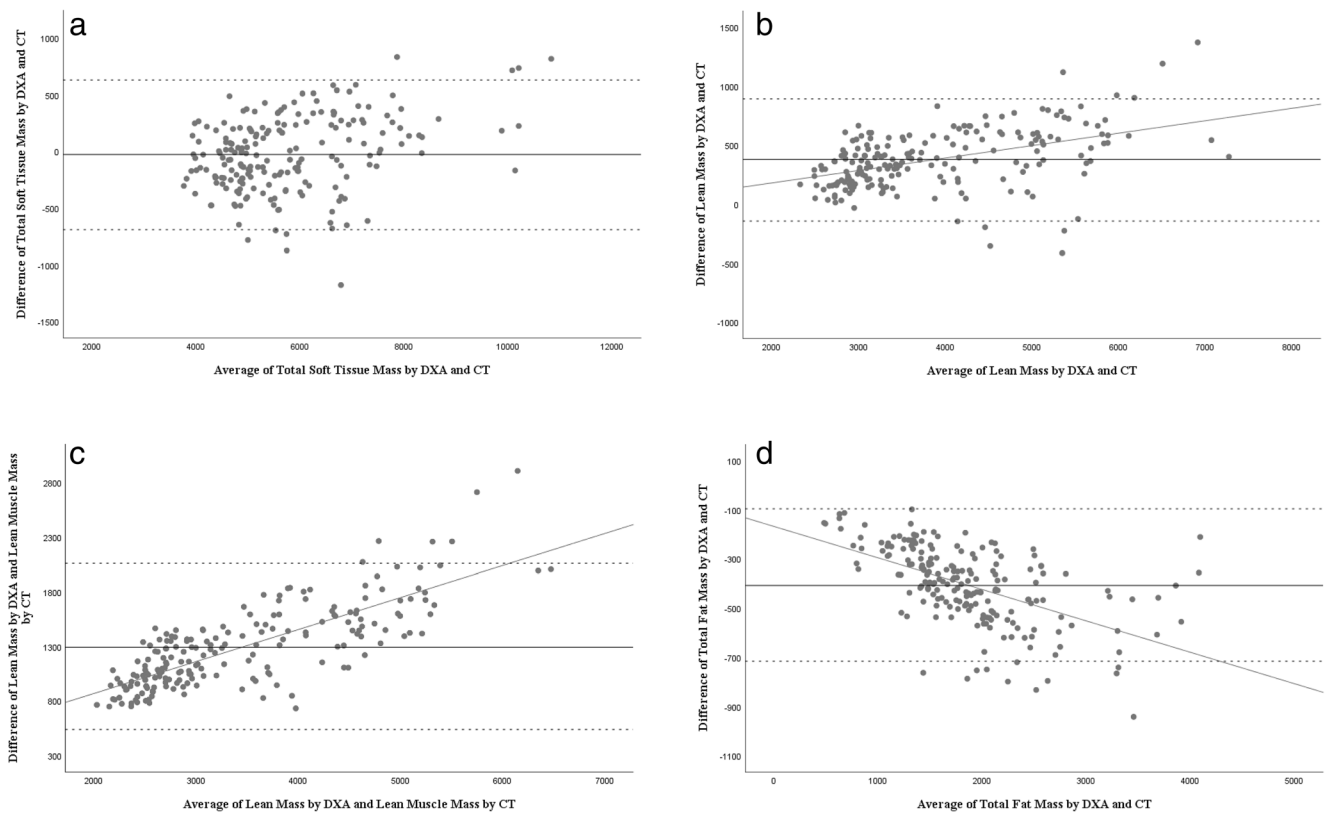


Fig. 5 Agreement between DXA and CT measurements. Bland-Altman analysis of thigh tissues: the difference between the CT and DXA values is plotted against the mean of these values. The solid line represents the average difference between the methods (bias); the dotted lines represent

the 95% CIs (limits of agreement) for the bias. **a** Total soft tissue mass. **b** Lean mass. **c** Lean mass by DXA vs. lean muscle mass by CT. **d** Total fat mass

When the final prediction model was validated using the left thigh data, R^2 for total tissue volume, lean muscle, or total fat volumes was high (0.96–0.97), and good calibration was achieved (Table 3). The Bland–Altman limit of agreement and its 95% confidence intervals were also provided in Table 3.

Discussion

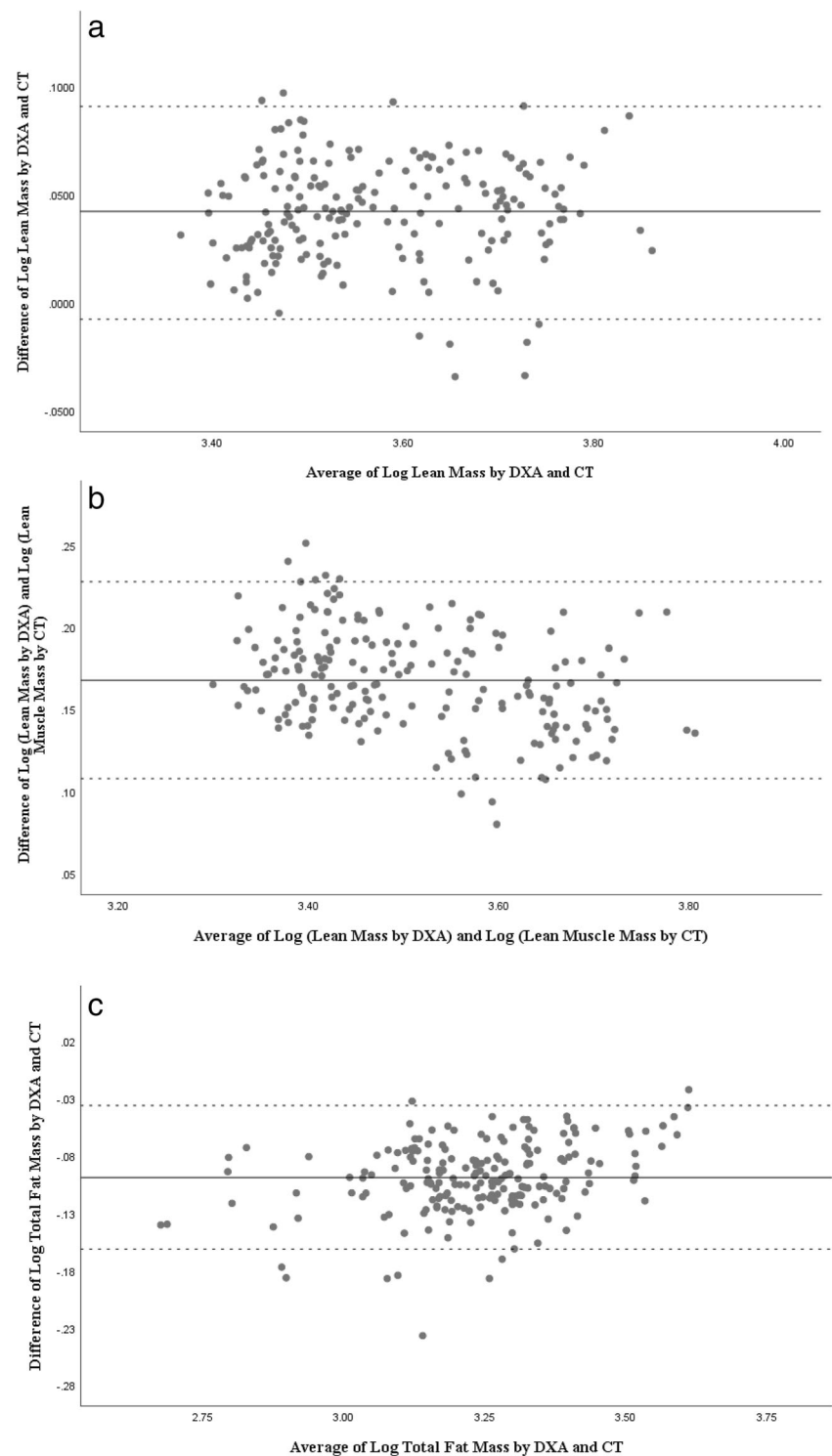
We found that 3D volumetric CT measurements with DL-based fully automated thigh segmentation are a rapid and promising method for assessing thigh tissue composition. The volumetric CT measurements with DL-based fully automated segmentation were well correlated with measurements obtained with the DXA method, which is the most popular method for measuring body tissue composition. However, thigh lean mass derived from DXA consistently overestimates not only CT-derived lean muscle mass but also CT-derived lean mass. Additionally, DXA-derived thigh total fat mass was consistently less than CT-derived thigh total fat mass.

Systematic differences between DXA and CT measures of skeletal muscle and fat mass have been reported [11, 14, 25]. These reports explained that differences in instrumentation

between the two methods may contribute to discrepancies between the measurements. DXA can discriminate body composition into three components: fat, lean tissue mass, and bone mineral content. Therefore, all nonfat and nonbone tissues are included in the DXA lean tissue mass estimates [25]. In contrast, all soft tissues other than skeletal muscle, such as skin, vascular structures, fascia, are excluded in CT lean muscle mass measurements. In our results, nonfat, nonskeletal muscle soft tissues constituted 19% of the lean soft tissue mass measured by CT; this estimate was obtained by subtracting the total fat volume from the total soft tissue volume. Furthermore, CT-derived adipose tissue in the subcutaneous and inter/intramuscular fat layers consists of 80% fat and 20% lean components (water, proteins, and minerals) [25]. The significant lean component in adipose tissue might contribute to the systematic discrepancies in total fat mass between the CT and DXA methods [11].

CT is regarded as a standard tool for body composition measurement but is considered a suboptimal method for clinical use due to radiation exposure and time-consuming image segmentation. However, recent advances in CT technology enable lower radiation exposure by applying various iterative reconstruction and DL-based denoising techniques [32, 33].

Fig. 6 Bland-Altman plots of log-transformed variables: the difference between the log-transformed CT and DXA values is plotted against the mean of these values. The solid line represents the average difference between the methods (bias); the dotted lines represent the 95% CIs (limits of agreement) for the bias. **a** Lean mass. **b** Lean mass by DXA vs. lean muscle mass by CT. **c** Total fat mass



Additionally, CT has become faster so that whole body volumetric data can be acquired within seconds, while MRI has a longer scan time and can only obtain several representative slices. Manual segmentation of volumetric CT images was a rate-limiting step in CT measurements in the past, but we found that the DL-based fully automated segmentation technique successfully and dramatically shortens the time for

image segmentation and analysis. It took only 2 min for all postprocessing, including image segmentation and measurement of body tissue composition from the volumetric CT data of the thigh.

Other advantages of volumetric CT measurements with DL-based fully automated image segmentation are that spatially resolved distribution of muscle and fat tissue can be

Table 3 Validation of final prediction model for CT volume (cm³) using the left thigh data

CT volume (cm ³)	Statistics
CT total soft tissue (cm ³)	R^2 Calibration-in-the-large [95% CI ^a] Calibration slope [95% CI] Mean difference between predicted and actual values [95% CI] 95% limit of agreement (LOA ^b)
CT lean muscle (cm ³)	R^2 Calibration-in-the-large [95% CI] Calibration slope [95% CI] Mean difference between predicted and actual values [95% CI] 95% limit of agreement (LOA ^b)
CT total fat (cm ³)	R^2 Calibration-in-the-large [95% CI] Calibration slope [95% CI] Mean difference between predicted and actual values [95% CI] 95% limit of agreement (LOA ^b)

^a CI is confidence interval^b Limit of agreement = mean difference between predicted and actual values ± 1.96 * standard deviation

obtained and that the technique can be applied to individual muscles or functional muscle groups. Recently, several studies have shown that knee extensor muscle weakness increases the risk of knee osteoarthritis [9, 34], and the knee extensor muscles seem to be more affected by aging than other muscles of the thigh [30]. This implies that it may be important to measure muscle size and the degree of intramuscular fatty infiltration in individual muscles or functional muscle groups. Our results demonstrated that skeletal muscles and intra- and intermuscular fat volumes could be easily and rapidly estimated by CT using DL-based segmentation techniques not only in the whole thigh region but also in individual muscle groups. Furthermore, our technique can be applied to any kind of opportunistic CT (abdominal, lower extremity, or PET-CT) so that the clinical impact of sarcopenia can be assessed in various diseases, including musculoskeletal or cardiovascular diseases and cancer, as an independent risk factor for numerous adverse outcomes [3].

As shown in our study, there was good overall correlation between DXA- and CT-derived measurements of thigh lean muscle mass, but DXA does not provide accurate skeletal muscle mass estimates. However, the prediction equations developed in our study make it possible to convert DXA-derived lean mass to the more accurate CT-derived skeletal muscle volume with high estimation accuracy ($R^2 = 0.96\text{--}0.97$). It implies that extra CT scanning (i.e., extra radiation exposure, time, or cost) is not needed to obtain the exact skeletal muscle mass because the presence of sarcopenia could be determined by prediction equations for CT measurements using DXA data.

Several limitations in our study need to be considered. First, the research data were collected from a single institute. Second, our work included only healthy people, so the segmentation method used in the present study was not proven to be suitable for patients with markedly severe fat infiltration. Further work should be performed to evaluate whether our DL-based segmentation method and prediction equation can be successfully applied in patient groups with variable muscle atrophy. Third, estimation of body composition has been shown to vary by DXA scanner manufacturer, model, and software, so our results may not be generalizable to all DXA scanners [16]. Last, this study was prospectively performed in the limited study population, so it was impossible to get the data sets (both CT and DXA of the thigh) in the daily clinical setting for external validation. However, the DL-based CT measurement and the prediction equations were validated using the left thigh data and high correlation and good calibration were proven.

To our knowledge, this is the first study to investigate the accuracy of DXA tissue composition measurement compared to volumetric CT measurement using DL-based segmentation for the entire thigh.

In conclusion, there was a good overall correlation between DXA and volumetric CT measurements using DL-based fully automated segmentation in the thigh region. However, there was a systemic discrepancy between the two methods: overestimation of lean mass and underestimation of fat mass. 3D volumetric CT measurements using DL-based fully automated segmentation are a rapid and more accurate method for measuring body tissue composition, including skeletal muscle mass.

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Declarations

Guarantor The scientific guarantor of this publication is Ja-Young Choi M.D., Ph.D.

Conflict of interest The authors of this manuscript declare no relationships with any companies, whose products or services may be related to the subject matter of the article.

Statistics and biometry One of the authors has significant statistical expertise.

Informed consent Written informed consent was obtained from all subjects (patients) in this study.

Ethical approval Institutional Review Board approval was obtained.

Methodology

- prospective
- pobservational
- pperformed at one institution

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