Derivation and validation of simple equations to predict total muscle mass from simple anthropometric and demographic data[1–3]

Yasmin Y Al-Gindan, Catherine Hankey, Lindsay Govan, Dympna Gallagher, Steven B Heymsfield, and Michael EJ Lean

ABSTRACT

Background: Muscle mass reflects and influences health status. Its reliable estimation would be of value for epidemiology.

Objective: The aim of the study was to derive and validate anthropometric prediction equations to quantify whole-body skeletal muscle mass (SM) in adults.

Design: The derivation sample included 423 subjects (227 women) aged 18–81 y with a body mass index (BMI; in kg/m^2) of 15.9–40.8. The validation sample included 197 subjects (105 women) aged 19–83 y with a BMI of 15.7–36.4. Both samples were of mixed ethnic/racial groups. All underwent whole-body magnetic resonance imaging to quantify SM (dependent variable for multiple regressions) and anthropometric variables (independent variables).

Results: Two prediction equations with high practicality and optimal derivation correlations with SM were further investigated to assess agreement and bias by using Bland-Altman plots and validated in separate data sets. Including race as a variable increased R^2 by only 0.1% in men and by 8% in women. For men: SM (kg) = 39.5 + 0.665 body weight (BW; kg) − 0.185 waist circumference (cm) − 0.418 hip circumference (cm) − 0.08 age (y) (derivation: R^2 = 0.76, SEE = 2.7 kg; validation: R^2 = 0.79, SEE = 2.7 kg). Bland-Altman plots showed moderate agreement in both derivation and validation analyses. For women: SM (kg) = 2.89 + 0.255 BW (kg) − 0.175 hip circumference (cm) − 0.038 age (y) + 0.118 height (cm) (derivation: R^2 = 0.58, SEE = 2.2 kg; validation: R^2 = 0.59, SEE = 2.1 kg). Bland-Altman plots had a negative slope, indicating a tendency to overestimate SM among women with smaller muscle mass and to underestimate SM among those with larger muscle mass.

Conclusions: Anthropometry predicts SM better in men than in women. Equations that include hip circumference showed agreement between methods, with predictive power similar to that of BMI to predict fat mass, with the potential for applications in groups, as well as epidemiology and survey settings. *Am J Clin Nutr* 2014;100:1041–51.

INTRODUCTION

In addition to its obvious roles in posture control and capacity for movement, skeletal muscle has important metabolic functions that influence health and well-being. Variations in muscle mass and its functional capacity thus affect physical security and metabolic factors related to cardiovascular disease risk (1). Skeletal muscle mass (SM)[4] can vary for several reasons. It usually reaches a peak in early adult life, with differences between individuals of presumed genetic origin as well as training effects, and declines with advancing age (2). Reductions in SM, with loss of physical and metabolic functions, occur through local injury, denervation, systemic disease, and chronic inflammation and as a result of aging combined with a sedentary lifestyle.

Despite widespread recognition that low SM and strength, or "sarcopenia," has major clinical and epidemiologic importance, its diagnosis, and thus research into its clinical and public health consequences, is hampered by the lack of any agreed-upon simple method to assess SM (3, 4). Both muscle mass and strength are 2 important aspects of sarcopenia (5, 6), but these components need to be measured or estimated reliably and unified in agreed-upon criteria, maintaining both sensitivity and practicality.

Total body mass and its major constituents (total body fat, whole-body SM, etc) can be measured accurately by modern imaging methods and then correlated with height, weight, and circumferences for field use. Anthropometric measurements have many advantages (eg, simple, quick, safe, noninvasive, cheap, need only low skill levels, give immediate results), provided they are shown to be sensitive and specific predictors (7). We previously developed anthropometric prediction equations for total body fat content, which were found to depend strongly on waist circumference (8); this work gave rise to key diagnostic criteria for metabolic syndrome (9). Agreement on a method to quantify muscle mass, in addition to muscle strength, would be a step toward better identification of sarcopenia, at least at a population level. Our systematic review (10) identified only one published anthropometric method to estimate whole-body muscle mass as measured by MRI (11). The authors developed 2 equations that were both cross-validated by the same investigators in a separate

[1] From the Department of Human Nutrition (YYA-G, CH, and MEJL) and the Institute of Health and Well Being (LG), College of Medical, Veterinary, and Life Sciences, School of Medicine, University of Glasgow, Glasgow, United Kingdom; the Institute of Human Nutrition, Columbia University, New York, NY (DG); and Pennington Biomedical Research Center, Baton Rouge, LA (SBH).

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[3] Address correspondence to MEJ Lean, Human Nutrition, New Lister Building, Room 2.19, 10-16 Alexander Parade, University of Glasgow, Glasgow G31 2ER, United Kingdom. E-mail: mike.lean@glasgow.ac.uk.

[4] Abbreviations used: BW, body weight; PI, prediction interval; SM, skeletal muscle mass.

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subject group from the same population. One used height, sex, race, limb circumferences (arm, thigh, and calf), and skinfold thicknesses. The need for skinfold thickness measurement limits practical application. The second equation used more widely available, simpler anthropometric variables, as follows: SM (kg) = 0.244 × body weight (BW; kg) + 7.80 × height (m) − 0.098 × age (y) + 6.6 × sex + race − 3.3. High correlations (R^2 = 0.86, $P < 0.0001$, SEE = 2.8 kg) were seen in the derivation study in nonobese subjects and in their validation among obese subjects (R^2 = 0.79, $P < 0.0001$, SEE = 3.0 kg) (11). However, the term for race is specific to US categories, and these strong correlations may have exaggerated the predictive value for individuals because the equations included the wide ranges afforded by combining the sexes.

The aim of the present study was to derive, and to evaluate for possible use in clinical and/or epidemiologic settings, prediction equations for whole-body SM estimation by using simple anthropometric variables and whole-body MRI as the reference method. We validated the derived prediction equations as well as the previously published whole-body SM prediction equation of Lee et al (11) in an independently measured sample.

SUBJECTS AND METHODS

Data included in the derivation and validation studies were collected from adult subjects in whom the same measurements had been made by different investigators in studies conducted at New York Obesity Nutrition Research Center's Body Composition Unit, St Luke-Roosevelt Hospital, New York. For both anthropometric and MRI measurements, readers were blinded. Race-ethnicity was determined by self-report and included declaration of race-ethnicity for parents and grandparents. Variables were created for 4 race-ethnicity categories: white, African American, Hispanic, and Asian. All studies obtained written informed consent and were approved by the institutional review board of St Luke's-Roosevelt Hospital (12–14).

Subjects

Derivation study sample

A total of 423 subjects (227 women) aged 18–81 y with a BMI (in kg/m^2) of 15.9–40.8 participated in several related studies between 2000 and 2004 (12). Subjects were classified as having no known or diagnosed diabetes, cancer, heart disease, or any health conditions that would affect body composition or fat distribution; they were ambulatory, weight-stable (<2 kg weight change in previous 6 mo) adults who underwent testing that included a whole-body MRI scan. Four subjects were excluded from this sample because of technically poor or incomplete MRI scans.

Validation study sample

Data sets from 2 previous studies (13, 14) were combined, giving a total of 197 subjects (105 women, 92 men). Subjects were recruited [study 1: 2001–2004 (13); study 2: 2011 (14)] through advertisements in local newspapers, the Internet, and on flyers posted in the local community. A BMI upper limit of 37 was set to accommodate the MRI scanner capacity limitations. Participants were required to be ambulatory nonsmokers, free of medical conditions or metabolic characteristics (abnormal thyroid or cortisol concentrations) that could affect the variables under investigation, weight stable (<2 kg change within past 6 mo), and not regularly engaging in vigorous exercise. The subjects varied in age (18–83 y) and BMI (15.7–36.4) (**Table 1**). This final sample, carefully checked to ensure that there was no duplication of subjects between the derivation and validation samples or between the 2 validation samples, was used in validating our derived equations and those of Lee et al (11).

Methods

MRI

All data were collected in the same laboratory by an analysis team (n = 3) for derivation and validation samples. For the 2011 study, a single MRI analyst performed the measurements; therefore, the MRI methods used are identical for both studies. Total-body skeletal muscle volume was measured by using whole-body multislice MRI. Subjects were placed on a 1.5-T scanner (6X Horizon; General Electric) platform with their arms extended above their heads. Images were created by using a T1-weighted spin-echo sequence with a 210-ms repetition time and an echo time of 17 ms. The intervertebral space between the fourth and fifth lumbar vertebrae (L4–L5) was set as the point of origin for all scans. Transverse images (10-mm slice thickness) were then obtained across the entire body, with between-slice gaps of 40 mm. Each whole-body scan thus included ~30–40 cross-sectional images. Images were by analyzed by using Sliceomatic software (TomoVision, Inc) for segmentation and calculation of cross-sectional tissue areas. Total-body skeletal muscle volume estimates were converted to mass by using an assumed density of 1.04 kg/L for skeletal muscle. The technical error for repeated readings of the same adult whole-body scans by the same analyst of MRI-derived skeletal muscle volume is small, with CVs considered to be similar to that of computed tomography scanning at 1.4% (15). The intraclass correlation coefficient between analyses for total-body MRI-derived skeletal muscle from the same adult subjects was 0.99. For the validation samples, the technical error for 3 repeated readings of the same scan by the same observer for the MRI-derived SM was 1.9% (16).

Anthropometric measurements

Three technicians were trained in the body composition laboratory, and they obtained all of the anthropometric data. BW was measured to the nearest 0.1 kg by using a balance beam scale (Weight Tronix) with the subject wearing a hospital gown. A wall-mounted stadiometer (Holtain) was used to measure standing height to the nearest 0.1 cm. Anthropometric circumferences were obtained by using a heavy-duty inelastic plastic-fiber tape measure (Gulick II Tape Measure; Fischer Scientific): the waist was measured midpoint between the lowest rib and the upper border of the iliac crest (17); hips were measured at the level of the pubic symphysis and the greatest gluteal protuberance; the midarm was measured at the midpoint between the lateral tip of the acromion and the most distal point on the olecranon; the midthigh was measured at the midpoint between the inguinal crease and the proximal border of the patella; and the calf was measured at the maximum girth.

TABLE 1
Subject characteristics and variables used in this study for derivation and validation studies[1]

	Derivation sample		Validation sample	
	Men (n = 196)	Women (n = 227)	Men (n = 92)	Women (n = 105)
Age (y)	39.2 ± 13.9[2]	44.4 ± 16.2	43.3 ± 15.9	44.1 ± 16.4
BW (kg)	79.8 ± 12.7	67.1 ± 15.1	77.4 ± 14.1	66.3 ± 10.7
Height (cm)	176.0 ± 6.8	162.0 ± 7.2	174.5 ± 7.3	162.2 ± 5.9
BMI (kg/m^2)	25.4 ± 3.7	25.6 ± 5.5	25.4 ± 4.0	25.2 ± 4.1
MRI (kg)				
SM	31.8 ± 5.5	19.7 ± 3.4	28.8 ± 5.8	20.0 ± 3.4
Fat	18.4 ± 7.9	25.6 ± 12.4	—	—
Hip circumference (cm)	99.7 ± 7.5	101.2 ± 11.9	97.5 ± 7.9	99.6 ± 8.5
Waist circumference (cm)	87.6 ± 10.7	80.1 ± 13.4	88.3 ± 12.1	82.0 ± 11.1
White (%)	41.4	42.9	36.6	33.6
African American (%)	29	31.9	26.9	36.4
Hispanic (%)	15	14.5	16.1	14.5
Asian (%)	14.5	11.1	20.4	15.5

[1] BW, body weight; SM, skeletal muscle mass; —, MRI fat mass not measured in validation studies.
[2] Mean ± SD (all such values).

Statistical analyses

All statistical analyses were carried out by using Minitab 15.1.30.0 (Minitab Inc). Data sets had all previously been checked and cleaned for errors of data entry but were explored to confirm that all data ranges were plausible. Multiple linear regressions generated equations separately for men and women to predict whole-body SM measured by MRI. The following 8 anthropometric variables were considered of interest, on the grounds of practicality for routine clinical and epidemiologic work: age, weight, height, and hip, waist, thigh, arm, and calf circumferences. Forward and backward stepwise regression analysis was performed (α to enter 0.15, α to remove 0.15) by using the 8 variables. Analyses were carried out by using 4 sets of variables: age, BW, height, hip, and waist; age, BW, height, hip, waist, and midthigh; age, BW, height, hip, waist, midthigh, and midarm; and age, BW, height, hip, waist, midthigh, midarm, and midcalf. The highest R^2 value of each set of stepwise regression was used for further investigation. Bland-Altman plots were used to explore distributions of errors (18). The best of the equations obtained from the derivation sample were then applied in a separate validation sample for external validation. Bland-Altman plots were also created in the validation sample by using the predicted SM values and observed values of whole-body SM from MRI to determine levels of agreement between predicted and true MRI estimates of whole-body SM. To investigate the effect of adding the variable "race" (as applied in mixed US populations) to the equation, we used the derivation study sample, with the addition of the variable (race) to our best-derived equations for both men and women. Given that we have a categorical value (race), an ANCOVA general linear model was used. To compare between models we used CVs. The CV was calculated as the ratio of the SEE to the mean of the dependent variable (%).

RESULTS

Subject characteristics, including MRI and anthropometric data and the percentage of each racial group, are shown in Table 1.

Derivation study

Linear regressions of each variable against MRI whole-body SM are shown in **Table 2**. The correlations of single variables with MRI SM were stronger for men than for women for almost all variables, except for height and waist. BW was the variable with the highest correlation with MRI SM (R^2 = 0.54 and 0.39) for men and women, respectively.

Stepwise regressions of all variable combinations had greater correlations for men than for women (R^2 = 0.76 and 0.58, respectively). The single best equation for both men and women was used for further analysis on the basis of correlation strengths (**Table 3**) for further evaluation. In men, midarm circumference was a stronger predictor than in women and the opposite was true for midthigh circumference. Height was a stronger predictor for women than for men. All of the most powerful prediction equations included hip circumference as a significant independent variable.

TABLE 2
Explained variance (R^2) in MRI whole-body skeletal muscle mass from linear regressions in the derivation study

	R^2	
Variable	Men	Women
	%	
Age	5.2	1.9
Body weight	53.9	38.8
Height	22.3	30.4
BMI	31.4	18.8
Race[1]	15.7	15.3
Waist circumference	11.6	16.7
Hip circumference	27.9	22.6
Midarm circumference	51.6	25.1
Midthigh circumference	36.9	27.7
Midcalf circumference	44.5	13.2

[1] Race included 4 categories as defined among the US population: white, African American, Asian, and Hispanic.

TABLE 3
Prediction equations derived from stepwise regression analyses to estimate whole-body SM as measured by using MRI[1]

	Prediction equations	R^2	
		No race	Including race
		%	
Men			
PE1m[2]	MRI (SM) = 39.5 + 0.665 BW (kg) − 0.185 waist (cm) − 0.418 hip (cm) − 0.0805 age (y)	76	77.1[3]
PE2m	MRI (SM) = 38.4 + 0.581 BW (kg) − 0.194 waist (cm) − 0.387 hip (cm) − 0.0738 age (y) − 0.0222 Ht (cm) + 0.279 midarm (cm)	75.8	76.2
PE3m	MRI (SM) = 5.4 + 0.355 BW (kg) − 0.406 hip (cm) − 0.108 age (y) + 0.0998 Ht (cm) + 0.410 midarm (cm) + 0.299 midcalf (cm)	75.6	76.0
PE4m	MRI (SM) = 40.0 + 0.710 BW (kg) − 0.394 hip (cm) − 0.294 waist (cm)	73.0	74.1
Women			
PE1w[4]	MRI (SM) = 2.89 + 0.255 BW (kg) − 0.175 hip (cm) − 0.0384 age (y) + 0.118 Ht (cm)	58	61.5[5]
PE2w	MRI (SM) = −1.51 + 0.219 BW (kg) − 0.217 hip (cm) − 0.0252 age (y) + 0.136 Ht (cm) + 0.133 midthigh (cm)	57.5	60.0
PE3w	MRI (SM) = −4.33 + 0.214 BW (kg) − 0.231 hip (cm) + 0.153 Ht (cm) + 0.148 midthigh (cm)	56.3	58.0

[1] BW, body weight; Ht, height; PE1m, prediction equation 1 for men; PE2m, prediction equation 2 for men; PE3m, prediction equation 3 for men; PE4m, prediction equation 4 for men; PE1w, prediction equation 1 for women; PE2w, prediction equation 2 for women; PE3w, prediction equation 3 for women; SM, skeletal muscle mass.

[2] Prediction equation chosen for further analysis.

[3] Prediction equation: MRI = 38.809 + 0.62855 BW (kg) − 0.17843 waist (cm) − 0.38782 hip (cm) − 0.08351 age (y) − 1.13176 (Asian) + 0.56004 (African American) + 0.21902 (Hispanic) − 0.3527 (white).

[4] Prediction equation chosen for further analysis.

[5] Prediction equation: MRI = 3.995 + 0.22249 BW (kg) − 0.15890 hip (cm) − 0.045317 age (y) + 0.11523 Ht (cm) − 0.79309 (Asian) + 1.34820 (African American) − 0.50311 (Hispanic) + 0.052003 (white).

Equation for men

In the derivation analysis (**Figure 1**A), agreement between methods was assessed in relation to MRI-measured compared with predicted estimates, with a strong correlation (R^2 = 0.76, SEE = 2.7 kg, CV = 8%) and a significant slope ($P < 0.001$) (for values of 25 and 35 kg, CVs were 11% and 8%, respectively). The addition of the race (Figure 1C) variable with the use of the ANCOVA general linear model did not add advantage to the equation in terms of agreement or correlation: R^2 increased by only 1.2%, both the SEE and CV remained the same, and there was a significant slope.

Distributions of errors were evaluated from Bland-Altman plots (Figure 1, B and D), and there was a significant negative relation ($P = 0.001$). The width of the 95% prediction intervals (PIs; Figure 1B) was 10.3 kg (95% PI: −4.2, 6.1) for a fitted value of 25 kg and was 10.3 kg (95% PI: −5.6, 4.7) for a fitted value of 35 kg.

Validation of our derived equation for men (Figure 1E) had higher correlation (R^2 = 0.79, SEE = 2.7 kg, CV = 9%) and significant slopes ($P < 0.001$) compared with the derivation analysis; the addition of race (Figure 1G) did not increase the value of the equation. Bland-Altman plots (Figure 1, F and H) were better compared with the derivation analysis with no relation between mean and difference (P = 0.285 and 0.289, respectively). Significant constant bias was observed for equations without and with race (limits: 7.1, −3.7, and 6.7, −4.1, respectively). The 1-sample t test was significant ($P = 0.000$), with limits of agreement calculated by using SDs. By using the same data used to validate the Lee et al (11) equation (Figure 1, I and J), correlations were lower (R^2 = 0.75) and SEE was higher at 2.9 kg and the CV remained the same, with a significant slope ($P < 0.001$). A Bland-Altman plot had a clear negative relation ($P < 0.001$), indicating an overestimation for those in the lower range of muscle mass and an underestimation for those with larger values of muscle mass.

Equation for women

In general, women (**Figure 2**, A and C) had lower correlations and SEEs than did men. In the derivation analysis, R^2 was 0.58 (SEE = 2.2 kg, CV = 11%) and there was a significant slope ($P < 0.001$; for values of 15 and 25 kg, CVs were 15% and 9%, respectively). Adding race to the equation increased R^2 to 0.61 and the SEE and CV decreased by 0.1 kg and 1%, respectively, with significant slopes ($P < 0.001$). Bland-Altman plots (Figure 2, B and D) had negative relations ($P < 0.001$) for the equations with and without race. For women with SM in the lower range, the prediction equations tended to overestimate SM, whereas they underestimated SM for women in the higher range. For example, the prediction equation for an average woman whose total muscle mass is 15 kg overestimated by 8 kg (95% PI: −2.5, 5.5 kg), whereas for an average woman whose total muscle mass is 25 kg it underestimates by 8 kg (95% PI: −5.5, 2.5 kg).

As in men, higher R^2 values for equations both with and without race (Figure 2, E and G) were seen after validation (R^2 = 0.67 and 0.59, respectively), whereas the SEE decreased to 2.1 kg and the CV remained the same (11%, 10%) in both equations (significant slopes were still observed; $P < 0.01$) in Bland-Altman plots (Figure 2, F and H). In women, validation analysis had a clear negative relation ($P = 0.000$; for values of 15 and 25 kg, CVs were 15% and 9%, respectively). Validation with the Lee et al (11) equation (Figure 2I), with the use of the same validation sample we used in our equations, had lower correlations than our equation with race and higher correlation than our equation without race (R^2 = 0.63). Nevertheless, our validation analysis of Lee et al's equation showed SEE and CV values that

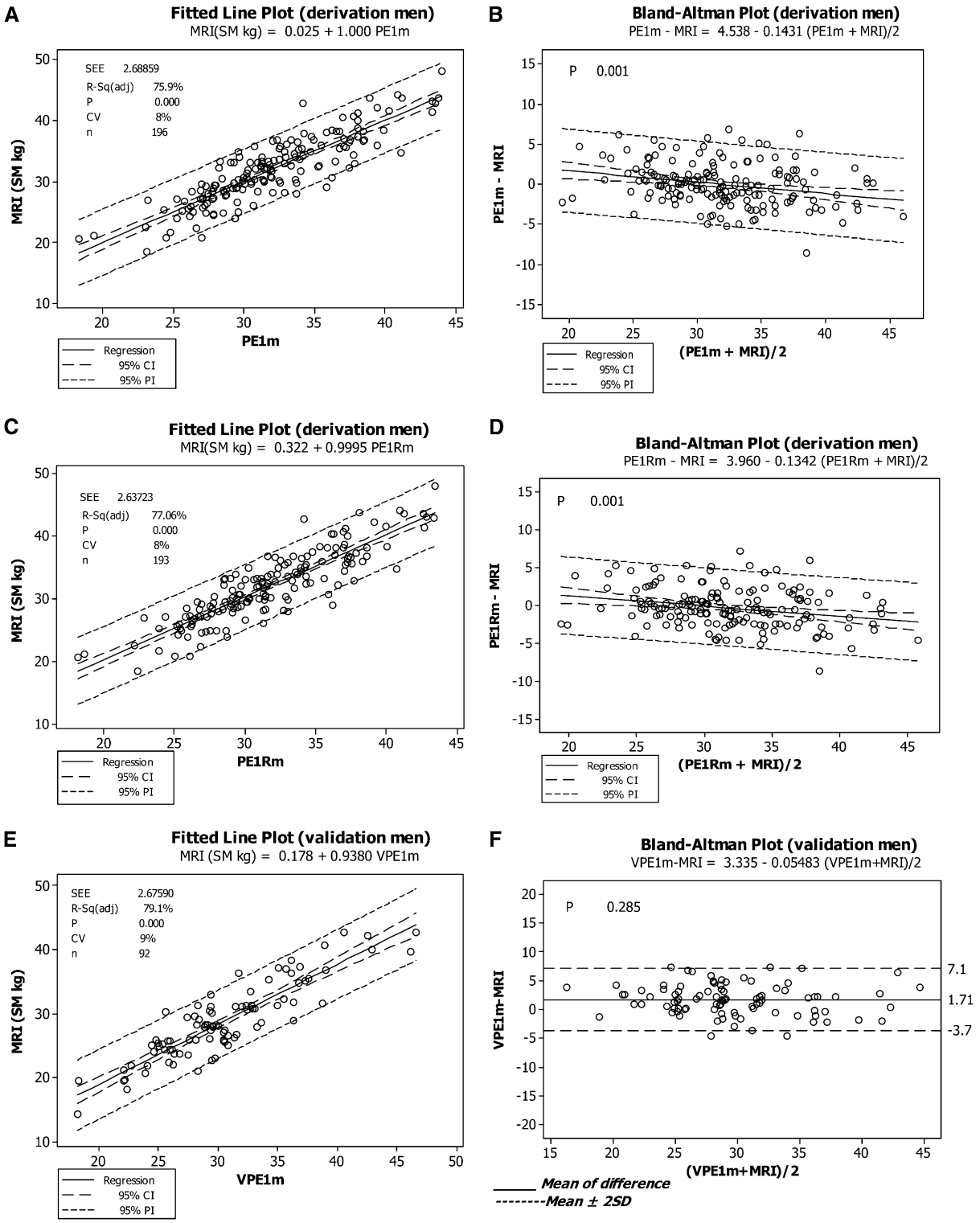

FIGURE 1. Men: Panels A, C, E, G, and I show scatterplots of MRI-measured SM values (*y*-axis) against estimated SM values from PEs, whereas panels B, D, F, H, and J show Bland-Altman plots of difference between predicted and MRI-measured SM values (*y*-axis) against their mean (*x*-axis). Plots A and B and C and D represent results from the derivation of our PE without race (PE1m) and with race (PE1Rm), respectively. Plots E and F and G and H represent results from the validation of our equation without race (VPE1m) and with race (VPE1Rm), respectively. Plots I and J represent the validation of Lee et al's equation (11) (VPELm). For the plots with no significant slope, Bland-Altman plots show the mean difference with limits of agreement around the mean difference as a test for bias (mean difference significantly different from 0) with the use of the 1-sample *t* test. For the plots with a significant slope, Bland-Altman plots show the PI around the regression line. *P* values represent a test of significance of the slope. PE, prediction equation; PI, prediction interval; SM, skeletal muscle mass; VPE, validation of prediction equation.

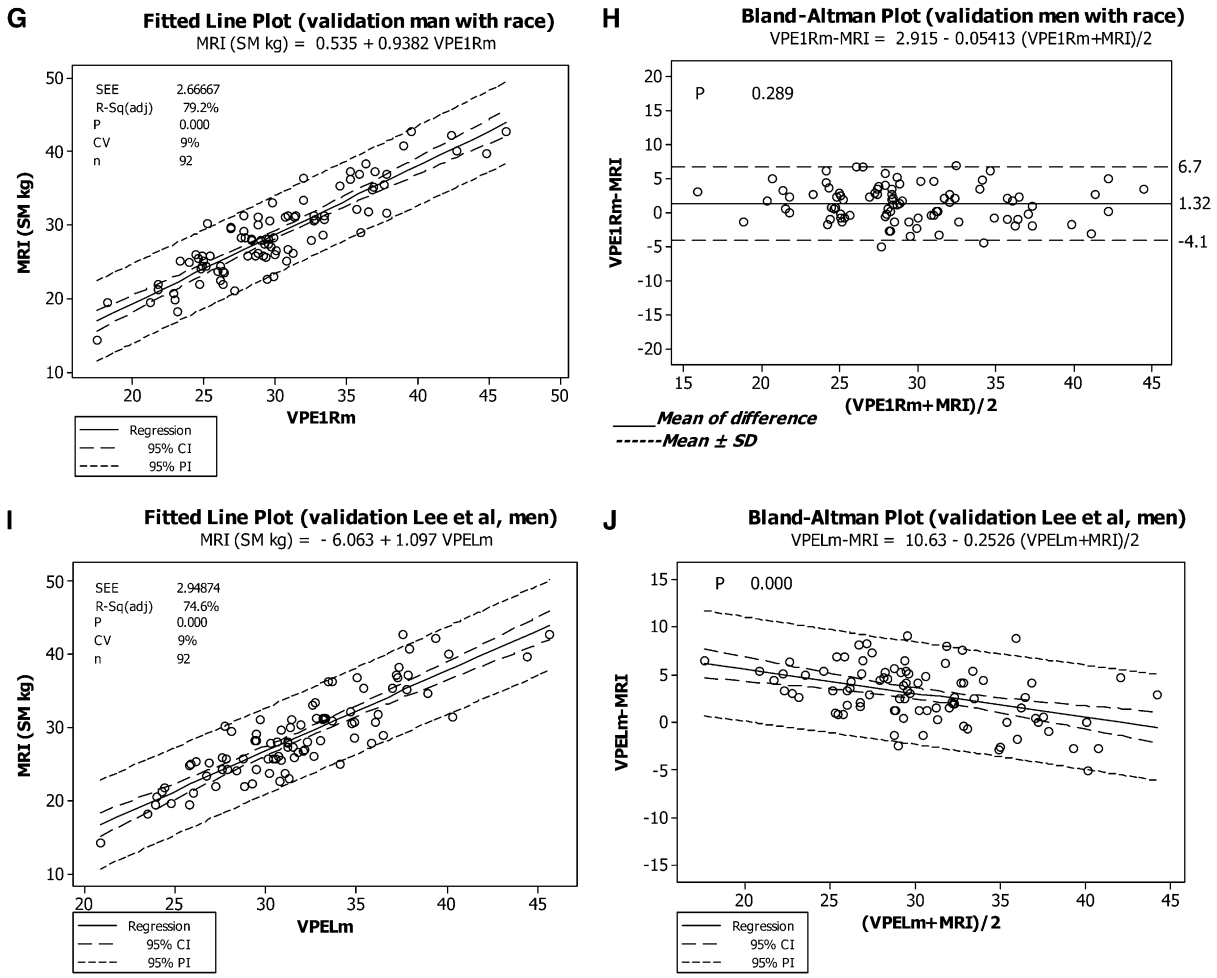

FIGURE 1. Continued.

were almost the same (SEEs: 2.1, 1.9, and 2.2 kg; CVs: 10%, 10%, and 11%; significant slope $P < 0.001$) and our equations with and without race, respectively. However, there was no negative relation in the Bland-Altman plot (Figure 2J) ($P = 0.236$), and mean difference was 2.6 kg in the validation of Lee et al's equation (95% limits of agreement: 7.2, −2). The 1-sample *t* test was significant, with limits of agreement calculated by using SDs.

To improve the agreement between our predictions and the MRI measurements for women we performed 2 forms of calibration. First, as suggested by Bland-Altman (18), logarithmic transformations of both the predicted measure and MRI measure were plotted in the Bland-Altman plot (data not shown). However, this did not account for the negative relation between the mean and difference in the Bland-Altman plot. Second, we performed a calibration of our equations. This involved regressing the predicted values against the MRI values and adjusting the new equation to remove the negative relation seen in the Bland-Altman plots for the derivation analysis. The calibration was successful in the Bland-Altman plot for the derivation analysis in which the negative relation between the mean and difference of the measures no longer existed. However, the use of the calibrated equation did not account for the negative relation in the Bland-Altman plot for the validation data set. Therefore, for women with SM in the lower part of the range, the prediction equations tend to overestimate SM by 8 kg on average, whereas they underestimate SM for women at the higher end of the range by 8 kg on average.

Combining men and women, the Lee et al (11) equation (Figure 2K) increased the R^2 to 0.85 (SEE = 2.6 kg). Bland-Altman plots (Figure 2L) did not have a significant slope ($P = 0.229$), although there was evidence of slight bias (mean difference: 2.77; 95% limits of agreement: 8, −2.4).

DISCUSSION

The aim of this study was to develop and validate simple equations for the estimation of SM that are sufficiently practical for use in epidemiologic settings. Although computed tomography scanning was used in the past (19), MRI is now established as the preferred reference method to measure SM (20). Dual-energy X-ray absorptiometry scanning has been used as a screening tool for low muscle mass (21). However, it is a relatively expensive method, only an indirect estimate of MRI measurement, and impractical for whole-body muscle mass estimation for large-scale health surveys or routine clinical work.

Because whole-body MRI is time-consuming and expensive, a number of studies have focused on single limbs and produced anthropometric prediction equations for regional muscle volumes on the basis of single MRI slices of limb-muscle areas (22–24).

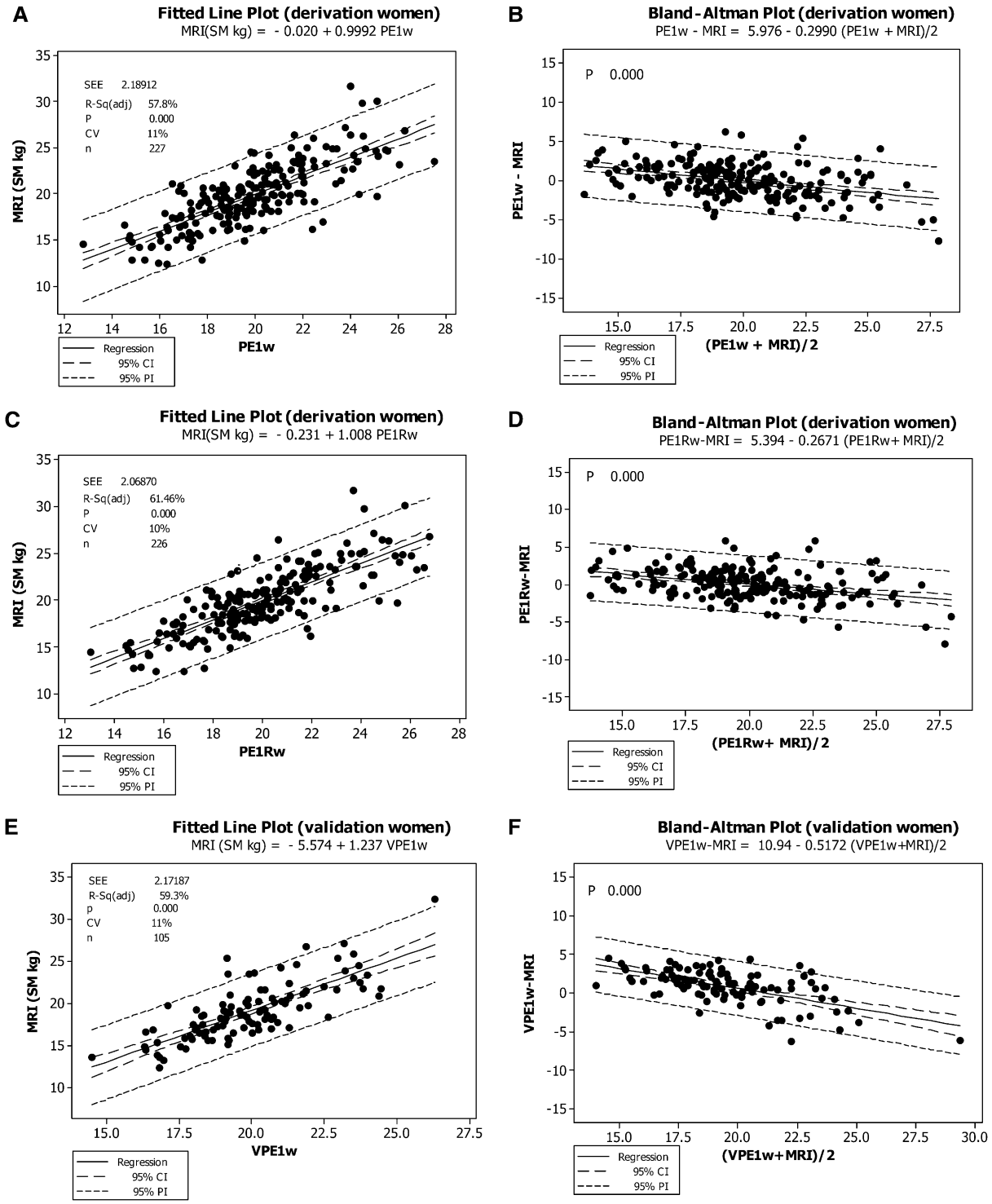

FIGURE 2. Women: Panels A, C, E, G, I, and K show scatterplots of MRI-measured SM values (*y*-axis) against estimated SM values from prediction equations, whereas panels B, D, F, H, J, and L show Bland-Altman plots of difference between predicted and MRI-measured SM values (*y*-axis) against their mean (*x*-axis). Plots A and B and C and D represent results from the derivation of our PE without race (PE1w) and with race (PE1Rw), respectively. Plots E and F and G and H represent results from the validation of our equation without race (VPE1w) and with race (VPE1Rw), respectively. Plots I and J represent validation of Lee et al's equation (11) for women (VPELw), and plots K and L represent validation of Lee et al's equation for men and women combined (VPELm+w). For the plots with no significant slope, Bland-Altman plots show the mean difference with limits of agreement around the mean difference as a test for bias (mean difference significantly different from 0) with the use of the 1-sample *t* test. For the plots with a significant slope, Bland-Altman plots show the PI around the regression line. *P* values represent a test of significance of the slope. PE, prediction equation; PI, prediction interval; SM, skeletal muscle mass; VPE, validation of prediction equation.

Although single-slice–based estimates may relate to physical function and possibly identify malnutrition, regional muscle masses have not been established to relate in a direct way to whole-body muscle mass. Lee et al (25) compared MRI-measured regional and whole-body muscle mass and found that skeletal muscle values obtained from a single scan of the thigh

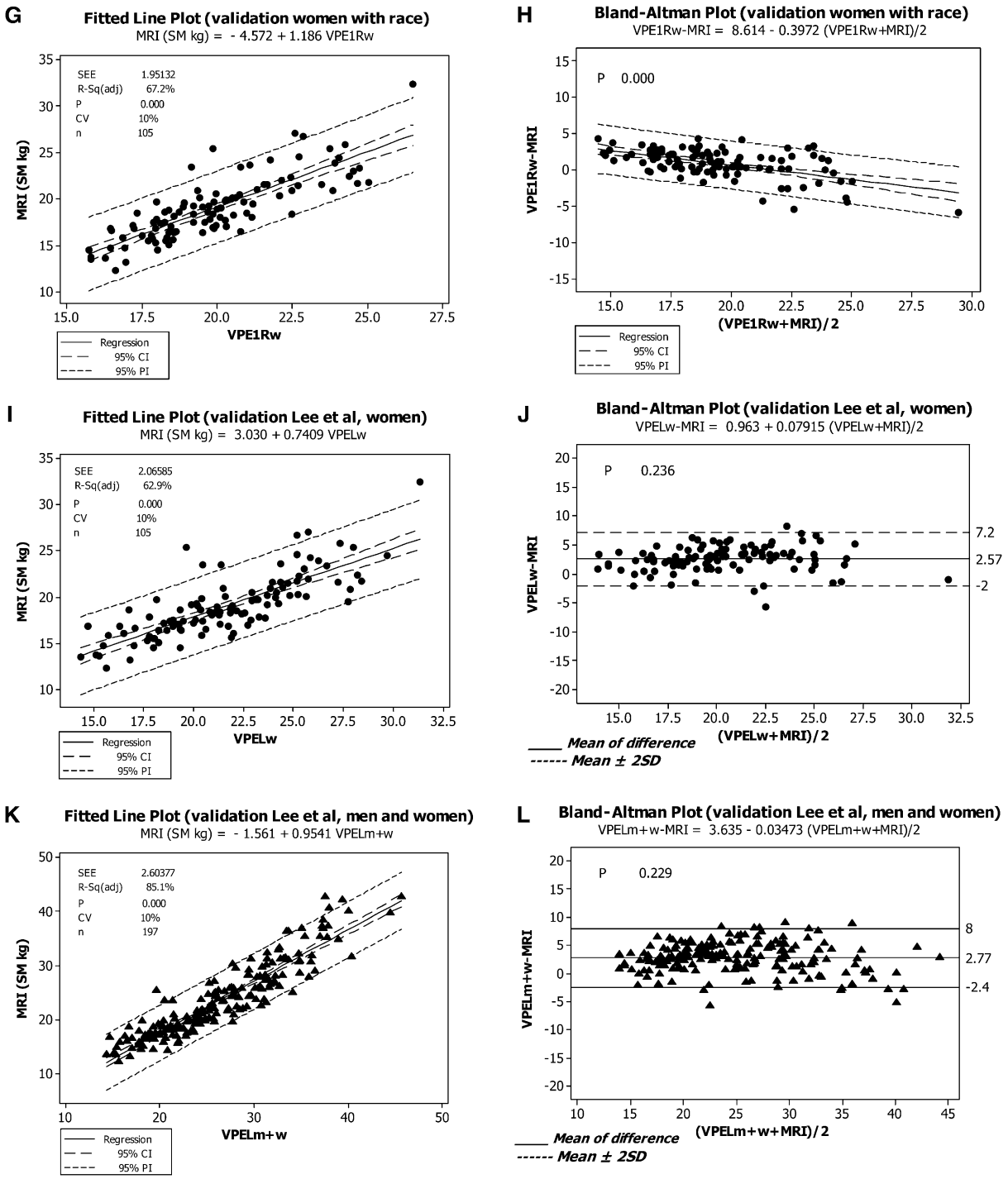

FIGURE 2. Continued.

region were a reasonably good indicator of whole-body muscle mass (R^2 = 0.77, 0.79; SEE = 7.4%, 5.4%) in men and women, respectively. The use of 7 consecutive images of the thigh region was only marginally better (R^2 = 0.84, 0.90; SEE = 5.4%, 5.1%), respectively. No existing study provides a method to convert limb SM to whole-body SM, although one study had correlations between regional and whole-body SM by using MRI measurements (25). In attempts to improve the prediction of regional muscle mass, several studies have adjusted limb circumferences with the overlying skinfold thickness (11, 22, 26, 27). The incorporation of skinfold thickness appears to improve estimation of regional muscle mass—for example, in the context of malnutrition—and thus potentially the prediction of whole-body muscle mass. However, skinfold-thickness measurement takes time, requires training, and may introduce high individual variability (28, 29). Skinfold thickness measurements are not made routinely in most population health surveys.

We explored the potential to use the type of anthropometric measurements made routinely in large-scale health surveys to

predict SM as measured by MRI. There appears to have been only one published study in which this was attempted (11). Our validation of Lee et al's equation concurs with the original publication, which showed $R^2 = 0.75$ (SEE = 2.3) in men and $R^2 = 0.63$ (SEE = 2.2) in women ($R^2 = 0.86$ and SEE = 2.8 kg for both men and women). Combining men and women, as Lee et al (11) did, will increase the number of adults studied and the range in body composition. This increased the R^2 to 0.85 but without improving the prediction of individual SM, as shown by the errors on Bland-Altman plots (Figure 2, K and L). The SD of 3.4 kg indicates the spread of measurements of SM for women, which is less than that for men at 5.5 kg (Table 1). The combined group (Figures 1I and Figure 2, I and K) SD was 8.9 kg. The relative proportion of variation (ie, the R^2 value) explained by the prediction equation was greater for men (0.75) and the combined group (0.85) than for women (0.63). This does not necessarily mean that the prediction equation was less accurate for women than for men; it may simply reflect that the relative amount of variation that could be explained in women was less.

The validations of our new equation gave higher R^2 and SEE values for men compared with our validation of the Lee et al equation (11). On the other hand, in women, our validation of Lee et al's equation (**Table 4**) gave higher R^2 and SEE values than did our new equation. Our new equations included only anthropometric variables, whereas Lee et al (11) used race as a variable. Incorporating a term for race increased R^2 of our validations by only 0.1% in men and by 7.9% in women, indicating that most of the variance associated with race was accounted for by simple anthropometric measurements, especially in men. Attributing race to individuals in mixed populations can be potentially difficult and misleading, so there is a practical advantage for equations that do not require this term.

Our equations all used simple measurements, which can be made quickly with modest training in epidemiologic settings. Indeed, these measurements are already being made routinely in most national population health surveys. A consistent finding in the equations (Table 4) we examined is that the prediction of SM was substantially less accurate for women than for men. This was also the case for the published equations to predict lean body mass (30) and SM (11). This sex difference probably reflects the much smaller muscle mass of women and a greater range of variability in other tissues, particularly fat mass. Ross et al (30) found that BW and hip circumferences contributed strongly to predictions of MRI whole-body–measured lean tissue in obese android women. In men, a combination of thigh and waist circumferences and BW gave the strongest prediction. Among our derived equations from stepwise regression, those with the highest correlations with SM ($R^2 = 0.73$–0.76 for men and $R^2 = 0.54$–0.58 for women) all included hip circumference as a variable. This finding supports previous reports suggesting that variance in hip circumference may reflect differences in muscle mass (31, 32), thereby explaining some of the health associations of "waist:hip ratio." Waist:hip ratio is not a useful indicator of total body fat or fat distribution (33, 34), but it does predict type 2 diabetes, insulin resistance, and coronary artery disease in cross-sectional studies (35). The explanation may, therefore, be that reduced SM through illness or inactivity (eg, in persons who develop type 2 diabetes) results in a lower hip circumference and thus a greater waist:hip ratio, rather than a greater body fat content with increased waist circumference.

The present study allows a degree of confidence that is greater for men than for women for the estimation of total body muscle mass from simple measures that can be collected in analysis surveys (Table 4). Our equations had moderate to high correlations with MRI-measured whole-body SM and moderate SEEs and CVs. However, there are limitations to the study. From our published systematic review (10), SEEs were within the ranges seen in other SM anthropometric prediction studies, but we found few studies that used simple anthropometric measurements to estimate total body muscle mass using whole-body MRI as the reference method, which limited our capacity to compare equations. In general, our equation seemed to be more sensitive in men, and the Lee et al equation (11) was more sensitive for women. There is a significant negative relation between the mean difference and the average value in the Bland-Altman plots in women. The negative relation crosses over the zero line, meaning that the mean difference will be pulled more toward zero (ie, lower values are positive whereas upper values are

TABLE 4
Derivation and validation analysis summary of present prediction equations and summary of validation of Lee et al (11) prediction equations for men and women separately and combined[1]

	Men				Women			
Equation	R^2	SEE	CV for mean	Difference[2]	R^2	SEE	CV for mean	Difference[2]
		kg	%	*kg*		*kg*	%	*kg*
Derivation								
Prediction equation 1	0.76	2.7	8	NA	0.58	2.2	11	NA
Prediction equation 1 with race	0.77	2.6	8	NA	0.61	2.1	10	NA
Validation								
Prediction equation 1	0.79	2.7	9	1.7 ± 2.7	0.59	2.2	11	NA
Prediction equation 1 with race	0.79	2.7	9	1.3 ± 2.7	0.67	2.0	10	NA
Prediction equation of Lee et al (11)	0.75	2.9	9	NA	0.63	2.1	10	2.6 ± 2.3
Prediction equation of Lee et al (11), men + women	0.85	2.6	10			2.8 ± 2.6		

[1] R^2 is the correlation evaluating the variability explained by the model; SEE measures how different the actual value is from the prediction line, sum of square error; CV is the ratio of the SEE to the mean of the dependent variable and measures the relative closeness of the prediction to the actual value. NA, not applicable.

[2] Mean (±SD) difference between SM values as predicted by using the equation and observed MRI values for skeletal muscle mass ± SD; equations with slope (significant relation between mean and difference) were not applicable.

negative), suggesting a better agreement than actually exists. The samples for derivation and validation studies were drawn in different years—2000–2004 for the derivation study subjects and 2001–2011 for the validation study subjects—which give some confidence for the validity of the equations when applied in other groups. However, wider application must be made with caution, because subject numbers are always restricted in studies that use whole-body MRI, and our population samples were also of mixed racial types in North America. Confirmation is needed that our prediction equations do not give rise to systematic errors if applied to groups of subjects with restricted ranges of ages or BMIs or of a single racial type. In particular, it is possible that the different body compositions of some Asian and Pacific Islander groups will demand specific prediction equations for muscle mass, as they do for body fat (36, 37). The difference in R^2 from adding ethnicity to our prediction equations was minimal, so for general use in mixed populations, in which an individual's ethnicity is often mixed and hard to verify, we favor the use of a simpler equation without ethnicity. Our samples included few subjects who were obese or severely obese, in particular elderly obese among whom relative paucity of muscle (sarcopenic obesity) is an emerging health concern (38). Data to confirm anthropometric estimation of muscle mass in obese and elderly groups are therefore needed. It will also be valuable to establish the effects of factors such as illness and weight change on the reliability of anthropometric SM estimation in longitudinal studies. Finally, although our equations have been validated and appear to offer value for epidemiology and in groups, their predictive power is insufficient for clinical use or among individuals. The R^2 values for predicting muscle mass in this study are similar to those models that use BMI to predict fat mass (39).

In conclusion, anthropometric prediction equations for whole-body muscle mass were derived and externally validated by using separate populations. Predictions had greater predictive power and less error for men than for women. Predictive equations with the greatest R^2 all included hip circumference, which emerged as a consistent predictor of SM. Two equations (including for men, body weight, waist, hip, and age, and for women, body weight, hip, age, and height) were identified as offering high practicality. They lack predictive power for use in individuals or for clinical purposes but have sufficient accuracy for use to estimate SM in groups and for research and survey purposes within mixed populations, without the need to adjust for race.

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