Carcass and primal cut composition of different pig genetic lines by dual-energy X-ray absorptiometry (DEXA)

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Introduction

Dissection has been and often still is used as a reference method for evaluating pig carcass composition or specific cuts. However, this approach is very time-consuming, costly and subject to biases associated with the dexterity and fatigue of the butchers. Dual energy X-ray absorptiometry (DEXA) is an alternative technique that has been used successfully to predict the chemical composition of pig carcasses as well as the composition of freshly dissected tissues. DEXA is usually applied in human medical field for measuring bone mineral density and human body composition. It is the attenuation of the two X-ray energy through the tissue (bone, muscle and fat) that permits determination of the proportion of each tissue type. The aim of the present study was therefore to evaluate the effect of genetic line on the quality of regression models using DEXA variables for predicting carcass and primal cut composition.

Material and Methods

Ninety-six gilts from three genetic lines, namely 32 Large White (LW), 32 Synthetic Genex 3000 (SG) and 32 Meishan-derived dam line (M), were provided by Hypor Inc. (Regina, SK) and raised and slaughtered (109.6 ± 3.78 kg liveweight) at the Agriculture and Agri-Food Canada (AAFC) Research Centre in Lennoxville (QC). The carcasses were fabricated into 4 primal cuts (shoulder, ham, loin and belly) following conventional breaking lines. The four primal cuts were scanned laterally using a Lunar DPX-L osteodensitometer (Lunar Corp. Madison, WI) in "adult slow" mode. For each primal cut and the entire carcass, the analyses provided the estimated total weight, lean weight, fat and bone mineral content (BMC), as well as the ratio between the attenuation coefficients of the two X-ray energy levels (R-value).
Following DEXA scanning of the carcass, primals were dissected to determine the weight of the lean, fat and bone. Backfat thickness was measured with a ruler (1) on the ham along a straight line corresponding to the leg axis, (2) on the dorsal midline at the point where the shoulder is separated from the loin and (3) on the chop cut between the 3rd and 4th last ribs 7 cm away from the dorsal midline and perpendicular to the skin (Canadian grading site). The depth of the *Longissimus thoracis* muscle was measured on the same chop and at the same site as fat thickness. Loin eye area (cm^2), including the aponeurosis, was obtained by computer image analysis on the scanned surface of a loin chop removed from the same location.

Results and Discussion

Carcass conformation and primal cut composition (fat, lean and bone) of the three genetic lines differed considerably, although the live weight of the animals during fasting prior to slaughter did not differ much, with a mean difference of 3.09 kg between the heaviest LW line and the lightest SG line. The M line differed the most from the other two lines (LW and SG), the fat thickness at different carcass sites and the quantities of fat dissected from all the primal cuts being higher ($P < 0.005$) (data not shown). LW and SG lines, instead, showed to have a deeper and larger ($P < 0.005$) longissimus muscle and a higher amount of lean dissected from the four primal cuts ($P < 0.005$) (data not shown).

To account for the wide variability in conformation and tissue composition among the different genetic lines, it was important to determine

whether the genetic line had an effect on the quality of the prediction models. This involved determining whether it is justifiable to adjust the prediction equations for genetic line or whether a common equation covering all the genetic lines is appropriate for these variables. We therefore conducted slope and intercept heterogeneity tests of the three regression lines obtained for the genetic lines (LW, SG and M) in order to construct a relationship between the predicted variables and the observed variables. In all the slope heterogeneity tests, i.e. for the prediction of total weight, lean, fat and bones, none of the results indicated significant slope differences ($P > 0.1172$) between the genetic lines. In terms of evaluating intercept heterogeneity, the statistical tests enabled us to determine that, for some variables, at least one intercept differed significantly for the LW, SG or M regression lines (Table 1). Notwithstanding that the intercept revealed a significant heterogeneity for several variables, the improvement in prediction accuracy was nonetheless limited taking into account the decrease in error (RSD) and the increase in the coefficients of determination (R^2) between a corrected prediction model (equation adjusted for genetic line) and an uncorrected model (same equation for the three genetic lines) (Table 1). The improvement in prediction quality as quantified by the decrease in the error relative to the cut weight or tissue weight to be predicted is higher for the loin in all cases. Furthermore, only when predicting the bone-in loin needs a corrected predictive regression model (Table 1) to be used. For this case, the RSD decreased from 0.118 kg to 0.085 kg and the coefficient of determination increased from 0.37 to 0.68.

Since we found that correcting the prediction equations for genetic line to the prediction models was not justified except in the case of the loin bone prediction, the regression model without correction shows that the weight of the half-carcass and each primal cut (shoulder, belly, loin and ham) are accurately predicted by the corresponding variable measured by DEXA, the coefficients of determination are high ($R^2 > 0.95$), and the residuals expressed as a percentage of the weight of the dependent variable to be predicted (CV%) are low. The lean, fat and bone weight follow in terms of prediction accuracy. DEXA-determined lean weight accurately predicts the weight of dissected tissues ($R^2 > 0.74$). Table 1 also shows the high quality of the predictions of fat weight for the half-carcass and primal cuts. The *R*-value, derived from the DEXA results, was not selected at any time as the primary explanatory variable in the regression models predicting the weight of a cut or tissues.

Conclusion

This technology can be used to estimate the lean and fat content of carcasses and primal cuts irrespective of variability in the conformation and tissue composition of the cuts. This indicates that correcting the prediction equations for the different weights based on genetic line is not justified. Because of its speed, reliability and ease of use, DEXA holds promise as an indirect technology that could replace carcass dissection.

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Table 1
Intercept heterogeneity test for the genetic line effect and comparison of model prediction quality with and without equation correction for the genetic lines (LW, M,SG)

Dependent variable dissection (kg)	Independent variable DEXA (kg)	Significance[a]	Without correction RSD	Without correction R^{2b}	With correction RSD	With correction R^{2b}	Decrease RSD (kg)	Decrease Predicted Error[d] (%)	Increase R^{2b}(%)
Weight	**Weight**								
Half carcass		***	0.355	0.96	0.309	0.97	0.046	0.11	1.04
Shoulder	Shoulder	***	0.117	0.97	0.098	0.98	0.019	0.16	0.88
Loin	Loin	***	0.132	0.98	0.098	0.98	0.035	0.30	0.30
Ham	Ham	NS	0.058	0.996	0.058	0.996	-0.001	-0.01	0.00
Belly	Belly	***	0.116	0.95	0.102	0.96	0.014	0.20	1.26
Muscle	**Muscle**								
Half carcass		***	**0.689**	**0.93**	**0.642**	**0.94**	**0.046**	**0.11**	**1.18**
Shoulder	Shoulder	*	0.195	0.91	0.187	0.92	0.008	0.15	1.08
Loin	Loin	***	0.310	0.85	0.260	0.90	0.050	0.87	5.38
Ham	Ham	*	0.243	0.93	0.233	0.94	0.010	0.16	0.68
Belly	Belly	***	0.203	0.74	0.185	0.80	0.018	0.86	6.94
Fat	**Fat**								
Half carcass		***	0.823	0.87	0.715	0.90	0.108	0.27	3.97
Shoulder	Shoulder	NS	0.230	0.83	0.219	0.85	0.011	0.34	2.28
Loin	Loin	***	0.409	0.83	0.345	0.88	0.064	1.43	6.19
Ham	Ham	NS	0.168	0.70	0.170	0.71	-0.002	-0.07	0.38
Belly	Belly	***	0.216	0.90	0.200	0.91	0.017	0.48	1.95
Bone	**Bone**								
Half carcass		***	0.205	0.66	0.191	0.71	0.014	0.03	8.03
Shoulder	Shoulder	NS	0.122	0.48	0.123	0.48	-0.002	-0.14	1.07
Loin	Loin	***	0.118	0.37	0.085	0.68	0.034	2.98	84.86
Ham	Ham	***	0.054	0.66	0.050	0.71	0.004	0.59	8.76

[a] Most significant intercept heterogeneity between LW, SG and M. NS; P>0.05;* P<0.05;** P<0.01;*** P<0.001
[b] Non ajusted
[c] calculated on RSD difference only
[d] calculated on RSD difference based on predicted pound of tissue