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Bias and future trends of pig carcass classification methods

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Abstract

Bias of the present formula approved for Spain using the Fat-O-Meater (FOM) grading probe applied to extremely wide sub-populations of pure lines and crosses. A new equation was calculated adding to FOM backfat and loin depth the percentage lean of the ham (LH), as a new predictor. Biases were calculated when applying both equations to the different sub-populations studied. In general, when comparing the differences between estimated and actual lean percentages, the very lean breeds and crosses are underestimated and the very fat ones are overestimated. These differences were lower when the FOM + LH equation was used. The reduction of biases by linear corrections of both equations was analysed. The mean square error (MSE) was decomposed into error in central tendency, error due to regression, and error due to disturbances. For the FOM equation, it was not possible to reduce MSE by means of linear corrections. However, a reduction of 16.5% of MSE was obtained by linear correction with FOM + LH equation. In practice, LH cannot be included in a grading scheme because it was obtained by dissection. However, these results indicate that new predictors including measurements of wider anatomical regions should be included in new technological developments. Furthermore, the meat industry is interested in predicting the lean percentage of the main joints in order to optimise their commercial cutting. © 2000 Elsevier Science Ltd. All rights reserved.

Keywords: Pig; Carcass; Classification; Bias

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1. Introduction

During the last two decades automatic grading probes have been the most widely technological devices used in national classification schemes for pig carcass grading. In the EU member states carcass lean percentage is the base line for pig carcass classification and it should be predicted by objective carcass measurements. The automatic probes in general satisfy the main statistical criterion for accuracy (RMSE $<2.5\%$ lean) as far as EC regulations are concerned (Commission of the European Communities [EC], 1984, 1985). The Commission of the European Communities (1985) proposed to measure and dissect a representative sample of the national or regional pig population of at least 120 carcasses in order to estimate the coefficients (intercept and slopes) through multiple linear regression analysis.

When using regressions, the coefficients and the errors should be unbiased, though there are no restrictions about the bias of the equations in the EC regulations. In multiple linear regressions the y_i residuals or differences ($\hat{e}_i$) of estimated lean ($\hat{y}_i$) minus actual (y_i) values ($\hat{e} = \hat{y}_i - y_i$) should not be correlated with estimated values ($\hat{y}_i$). However, there are several causes, which provoke some correlations of the estimated carcass lean with the errors indicating the existence of biases. There are two main sources of biases, a group originating from the operation (i.e. slaughter conditions, instruments, operators) and another group in which reference biases are included (i.e. sub-population, dissection, sampling, and statistical approaches). In this paper, we will study biases coming from the pig sub-populations assigning in their genetic background.

The aim of this paper is to study the bias of the present formula approved for Spain using the Fat-O-Meater (FOM) grading probe applied to extremely wide sub-populations of pure lines and crosses. Also, the reduction of biases by linear corrections of the prediction equation was analysed. A new predictor was added representing a wider anatomical region in order to advance future technological developments.

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2. Materials and methods

2.1. Animals

2.1.1. National representative sample

This sample was used to build a new equation (predictors taken at 60 mm from the mid line between the 3rd and 4th last rib level) for estimating the percentage of carcass lean with the Fat-O-Meater (FOM, SFK Technology, Denmark) according to the EC regulations. A total of 120 carcasses were selected in 4 abattoirs in order to represent all major crossbreed types, sexes and carcass weights. The carcasses were selected over the criteria of fat depths (FD) measured at the last rib level at 60 mm of the mid-line, so that approximately 40% (FD >20 mm) represented the fattest, 40% the leanest (FD <13 mm) and 20% the average fatness of the national population (Gispert & Diestre, 1994).

2.1.2. Sub-populations

Commercial crosses: this sub-sample was obtained from 133 carcasses (63 gilts and 70 castrated) from five different crosses including Duroc (DU), Landrace (LR), Large White (LW), and Belgium Landrace (BL). The crosses were DU (LW × LR), LW (DU × LW), LW (LR × LW), BL (DU × LW) and BL (LR × LW) (Blasco et al., 1994).

Commercial crosses: a total of 93 carcasses of barrows were slaughtered at 90 and 120 kg l.w. from three crosses provided by a breeding company. Cross A were products from a conformated synthetic sire and LW × LR sows. Cross B were products of a less conformated sire including DU with the same source of sows. Cross C were from the same genetic source as the sows used to produce A and B products (Garcia-Macias et al., 1996).

Pure lines: these 169 carcasses were from entire male pigs from pure lines provided by several nucleus herds of national breeders. They were slaughtered at 90 and 110 kg l.w. The following breeds were included: LR, LW, DU and Pietrain (Pi) (Tibau et al., 1997).

Pure lines: these 130 carcasses were from gilts provided by a breeding company representing pure lines from their genetic nucleus.

2.2. Carcass cutting and dissection

All the left half carcasses were divided into 12 joints after removing the flare fat, kidneys and diaphragm. The main joints (leg, loin, shoulder and belly) were dissected into subcutaneous fat with skin, intermuscular fat, lean and bone and weighed separately. The tenderloin was removed from the carcasses and added to the lean weight of the dissected joints. Carcass lean percentage was calculated according to the new EU reference dissection method (Walstra & Merkus, 1995). Some adjustments have been applied in order to achieve the scale of lean percentage because some changes in the dissection method have been carried out during recent years. In those carcasses which were dissected before the new method was establish the weight of the connective tissue removed from the muscles was added to the lean weight of the dissected joints.

2.3. Statistics

The Spanish official equation to predict carcass lean percentage using FOM is the following:

$$\hat{y} = 61.56 - 0.878 \times \mathrm{G34} + 0.157 \times \mathrm{M34} \quad \mathrm{RMSE} = 1.56$$

where G34 is the backfat thickness and M34 is loin depth, both measured at the level of 3/4 last rib 60 mm from the mid-line (Gispert & Diestre, 1994).

From the same representative sample a new equation was calculated including additionally the percentage of lean in the ham obtained by dissection (LH):

$$\hat{y}_{\mathrm{i}} = 27.2 - 0.49 \times \mathrm{G34} + 0.085 \times \mathrm{M34} + 0.46 \times \mathrm{LH}$$
$$\mathrm{RMSE} = 1.14$$

For both equations the mean values of the residuals (estimated lean–actual lean) for each genotype within the sub-populations studied were calculated.

The mean square error (MSE) was decomposed into error in central tendency (ECT), error due to regression (ER), and error due to disturbances (ED). These three fractions were calculated as follow:

$$\mathrm{ECT} = (\bar{P} - \bar{A})^2$$
$$\mathrm{ER} = (S_{\mathrm{p}} - r \times S_{\mathrm{A}})^2$$
$$\mathrm{ED} = (1 - r^2) \times S_{\mathrm{A}}^2$$

where P and A are the averaged predicted and observed values, respectively; S_{p} and S_{A} are the standard deviations of the predicted and observed values respectively; and r is the coefficient of correlation between predicted and observed values. Error in central tendency indicates how the average of predicted values deviates from the average of observed values. Error due to the regression measures the deviation of the least squares regression coefficient ($r \times S_{\mathrm{A}}/S_{\mathrm{p}}$) from one, the value it would have been if the predictions were completely accurate. Error due to disturbances is the variation in observed values that are not accounted for by a least squares regression of observed on predicted values. In fact, this error is the "unexplained variance" and represents the portion of MSE that cannot be eliminated by linear corrections of the predictions (Theil, 1966). Generally, the tendency and regression errors are due to the fact that the reference sample, used to obtain the prediction equation, is not representative of the studied population.

All calculations were performed using the appropriate statistical procedures of SAS (1990)

3. Results and discussion

In Table 1 the main carcass characteristics are presented for each of the genotypes included in the sub-populations analysed. There is an extreme variation in all the variables studied. Carcass of Pi and f pure lines had very high lean percentage (> 60%) and on the other hand, carcasses from crosses B and C had very low lean percentage (< 50%). In general, when comparing the differences between estimated and actual carcass lean percentage, the very lean carcasses are underestimated and the very fat ones are overestimated. However, these differences were lower when the FOM + LH equation was used to estimate carcass lean percentage.

In Table 2 the decomposition of the mean square error (MSE) is shown. When using the official FOM equation the error in central tendency (ECT) and the error due to regression (ER) are not very important with respect to the total error (MSE). They account for only 1.9% of MSE. This indicates that it is not possible to significantly reduce the MSE using only linear corrections of the prediction equation. This indicates that the national reference sample which was selected using backfat depths is representative of the population studied when the reference equation is used. Including a new predictor such as LH, the RMSE was reduced from 3.068 to 2.205. Furthermore, as shown in Table 1, lower biases were found for the different genotypes studied.

Table 2
Decomposed mean square error (MSE) of both equations

	FOM	FOM + LH
ECT[a]	0.090	0.360
ER[b]	0.092	0.442
ED[c]	9.233	4.062
MSE	9.415	4.864
RMSE[c]	3.068	2.205

[a] ECT: error in central tendency.

[b] ER: error due to regression.

[c] ED: error due to disturbances; RMSE: root mean square error.

Table 1
Means and standard deviation (S.D.) of the main carcass characteristics and bias in different sub-populations

		Carcass weight		FOM (mm)				Actual lean (%)				Bias[a]	
	N	C. weight (kg)		G34 backfat (mm)		M34 loin (mm)		Carcass		Ham		FOM	FOM + LH
		Mean	S.D.	Mean	S.D.	Mean	S.D.	Mean	S.D.	Mean	S.D.		
National sample	120	78.1	11.05	17.8	5.21	51.2	6.11	54.7	4.80	69.0	5.05		
Crosses													
Du (LW × LR)	30	76.7	3.89	16.7	3.46	50.6	5.72	56.4	2.67	70.7	2.52	−1.57	−0.57
LW (Du × LW)	28	76.1	1.85	19.9	5.09	47.8	4.93	52.4	4.54	65.5	4.53	−0.84	−0.33
LW (LR × LW)	25	75.4	2.56	17.2	3.73	48.0	4.38	56.2	3.67	69.4	4.45	−2.20	−1.41
LB (Du × LW)	28	77.4	3.18	15.8	2.91	52.4	5.09	58.7	3.56	72.6	3.77	−2.71	−1.34
LB (LR × LW)	22	77.4	3.20	14.6	3.61	54.3	5.09	59.8	4.60	73.2	4.05	−2.57	−1.50
Crosses													
A	50	85.3	13.09	17.4	3.74	47.1	6.26	51.5	3.35	67.1	3.66	2.25	2.13
B	48	84.8	13.66	19.4	3.92	46.9	7.40	49.6	2.60	65.0	2.81	2.27	1.97
C	55	84.0	13.69	17.8	3.84	42.3	5.51	48.0	2.73	63.4	3.30	4.58	3.25
Pure lines													
LR	52	78.3	9.36	19.3	4.28	50.6	5.23	52.6	3.45	67.5	3.43	−0.05	0.48
LW	48	77.9	9.37	17.1	4.63	50.1	7.36	54.7	4.45	69.8	4.27	−0.27	0.53
Du	38	78.5	8.84	18.8	3.37	47.8	5.95	51.9	2.92	67.4	2.62	0.65	1.15
Pi	31	81.2	8.07	10.8	2.05	65.9	5.17	66.1	2.62	79.0	2.40	−3.70	−2.25
Pure lines													
a	15	71.4	8.63	13.8	2.76	47.6	6.54	55.0	2.86	69.9	2.09	1.89	1.63
b	24	71.2	7.00	11.8	2.43	52.5	11.07	58.3	3.71	72.5	3.39	1.17	0.96
c	24	73.2	7.55	12.8	2.57	47.8	6.29	57.8	3.18	72.2	2.76	−0.02	0.38
d	16	74.1	5.27	14.7	2.41	50.2	6.23	55.7	2.95	70.6	2.38	0.83	1.06
e	18	76.3	4.80	16.8	3.41	50.8	4.74	54.6	3.71	69.7	3.36	0.21	0.78
f	33	77.3	6.62	12.4	1.87	59.0	5.39	60.8	2.50	73.7	2.54	−0.84	−0.72

[a] Estimated–actual carcass lean percentage.

Moreover, the decomposition of the MSE for this new equation shows that applying linear corrections could reduce it even more, because the tendency and regression errors accounted for 16.5 of MSE. This means that if LH is included in the equation it may be considered in the selection criteria of the reference sample

Brondum, Egebo, Agerskov and Busk (1998) indicate that the Autofom ultrasound system, which can measure automatically 3200 positions to a depth of approximately 12 cm and 0.19 mm of resolution depth, provides predictions of carcass meat percentage of 1.58–1.95%. Furthermore, good estimations of the fat thickness and primal meat cuts have been also achieved.

4. Conclusion

The use of the present FOM equation in extreme subpopulations does not fulfil the accuracy required by the regulations (RMSE <2.5) and very important biases are observed. Furthermore, it is not possible to improve this equation significantly by only applying linear corrections.

The addition of a new variable, in this case the lean percentage of the ham, significantly reduces the RMSE and the biases observed. These results indicate that new technological developments should be focused on searching for predictors that can measure wider anatomical regions to estimate the total carcass lean percentage. It is very important that these new variables should be taken into consideration when selecting a representative sample. Furthermore, the abattoirs in the near future will need to predict lean yields of the main cuts to optimise their commercial cutting so the new developments of classification devices should offer this alternative.

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