Estimation of heritabilities and genetic correlations between weights and carcass traits in beef cattle in Uruguay.

A. Dartayete[1], I., Aguilar[2] & D. Gimeno[3].
[1] *Private consultant.*
[2] *Instituto Nacional de Investigación Agropecuaria, 90200 Canelones, Uruguay*
[3] *Secretariado Uruguayo de la Lana, Montevideo, Uruguay , dgimeno@sul.org.uy (Corresponding Author).*

Summary

A total of 1058 animals from 23 different breed combinations (86% steers, 14% heifers) were slaughtered with an average age of 2½ years between 1996 and 2001. Heritabilities and genetic correlations were estimated for the following traits: weight at 12, 15 and 18 months of age, slaughter and carcass weights (hot carcass weight, pistola weight, valuable cuts weight), ribeye area, subcutaneous fat thickness and subcutaneous fat thickness at P8.

The posterior mean of the heritability for live weights increases with age, from 0.33 at 12mo to 0.58 at the slaughter weight. The hot carcass weight had the highest posterior mean of 0.64 followed by the pistola weight (0.57) and valuable cuts weight (0.34).

The lowest estimates of heritability were for the fat traits; 0.22 for subcutaneous fat thickness and 0.18 for fat thickness at P8.

Hot carcass weight presented high genetic correlations (> 0.7) with the live weight traits, while the pistola weight and the valuable cuts weight had practically equivalent correlation estimates with the live weight traits (> 0.65). This is supported by the genetic correlations obtained between the hot carcass weight, the pistola cut weight and the valuable cuts weight, which were 0.94 to 0.96.

These results determine the possibility of using live weight measurements as selection criteria to improve the hot carcass weight, so that the pistola cut weight and the valuable cuts will be improved. Likewise, the ribeye area would also be improved, while the subcutaneous fat thickness would not be substantially modified. This would not be an inconvenience at present, considering the data provided by the industry regarding adequate fat levels according to their demand, as well as the current conditions of production in the primary sector.

Keywords : beef cattle, weights , carcass, fat, heritability, genetic correlation.

Introduction

Genetic improvement programs for beef cattle in Uruguay currently have EPDs for live animal weight and ultrasound measurements of ribeye area and fat thickness.

Slaughter price of animals are based on hot carcass weight, age (dentition), conformation (visual scale with 5 levels) and degree of fat (visual scale with 6 levels).

These subjective scales show little variation at national level with 89.3% and 81.25% of the animals in a single level and 96.8% and 95.4% when grouping two levels of conformation and degree of fat, respectively (INIA, 2017). The price is thus determined mainly by the hot carcass weight. Presently, the ribeye area and fat thickness do not affect the formation of the price paid by the animals slaughtered; however EPDs for these traits are generated.

The main objective of this work was to estimate genetic heritabilities and correlations between live animal weights and quality carcass traits.

Material and Methods

The data used in the present study was obtained from the Crossbreeding Beef Cattle Project developed between the Social Security Notarial Fund and the Faculty of Agronomy of the University of the Republic, with the support of the National Institute of Agricultural Research (INIA). Data came from two experiments involving 23 breed combinations of Hereford (HH), Angus (AA), Red Poll (RR), Salers (SS), Limousin (LL), Charolais (CC) and Nellore (NN) born between 1993 and 1999.

The information of 1058 animals (handled jointly from birth within each experiment and sex) involves performance records of 909 steers and 149 heifers as live and slaughtered animals. Slaughter was carried out at an approximate age of 2 and a half years.

The first experiment involved 758 steers of 17 breed combinations, HH and AA purebreds, three crosses between AA, HH and NN sires with HH dams, 6 first backcrosses between AH, SH and NH, three F2 groups with AH, SH and NH. and three groups crosses (NH)H, (SH)H and (AH)A product of the use of sires crosses NH, SH and AH on pure females HH and AA. While the other experiment, involved 151 steers and 149 heifers, of seven breed combinations progeny of LL, SS and CC sires with Hereford cows and LL, SS sires with RH and SH heifers.

The steers and heifers were progeny of 101 sires, six pure-breed and three F1 cross-breed sires (22 HH, 21 AA, 17 NN, 18 SS, 7 LL, 3 CC, 4 AH, 5 NH and 4 SH). At least one sire of each breed or cross was repeated per year, and also to generate half-sib across different breed combination, e.g same AA sire used to generate AH and A(AH) progeny. The two experiments were connected by eight Salers sires.

The traits analyzed in the live animals were the weights (kg) that are usually included in the genetic evaluations in Uruguay adjusted at 12 (12W), 15 (15W) and 18 (18W) months of age. In addition the slaughter weight (SW) was used.

Traits collected in the slaughter house were the following:

Hot carcass weight (HW, kg): measurement of the weight of the animal on the 2nd scale, after removal of the leather, head, extremities and viscera. The left and right stockings were measured.

Pistola weight (PW, kg): The weight of the hindquarter without the rib. It is prepared from a hindquarter by the removal of the thin flank, lateral portion ribs and a portion of the navel end brisket. A cut is made commencing at the superficial inguinal lymph node separating the M. *rectus abdominus* and following the contour of the hip, running parallel to the bodies of the vertebrae and the M. *longissimus dorsi* (eye muscle) to the specified ribs (INAC,2012).

Ribeye area (REA, cm ^{2}): is the measure of the total area of the loin or ribeye (*longissimus dorsi*) between the 10th and 11 ribs. The area was drawn on a transparent sheet of acetate, then scanned and measured with a specific program.

Fat thickness (FT, cm): measured at the tenth rib with a millimeter ruler, two measurements were taken, at ¼ and ¾ of the largest length of the REA, considering for this study the average value of the two measurements.

P8 : Measurement of fat thickness (cm) at the level of the rump, using a specific graduated ruler to take this measurement.

Valuable cut weights (VCW, kg): the sum of the individual weight measurements of the tenderloin, striploin and top sirloin (D-rump) and striploin (INAC, 2012).

Criteria for slaughtering was based on weight and fat cover, by visual assessment, which is the criteria used when marketing cattle for slaughter in Uruguay.

A multiple trait model including 12W, 15W,18W, SW, HCW, PW,VCW, P8, FT and REA was used to estimate parameters. All traits include effect of contemporary group defined by slaughter year, experiment, breed group and sex as "fixed". For carcass traits, days to the slaughter was included as a "fixed" covariate.

Breeding values were predicted for 2524 animals in the pedigree file of which 1058 had their own records and the rest are ancestors of these.

The additive genetic and residual covariances were estimated by Gibbs sampling using the MTGSAM program (Van Tassel & Van Vleck, 1995).

Prior distributions of genetic and residual variance components were assumed to be inverted Wishart with 12 degrees of belief. A priori knowledge of covariances was assumed to be zero given the variability of estimates of correlations found in the literature. A priori additive genetic variances used were 482, 836,1531, 538, 14.8, 3.6, 15.6, 7.5, 0.7, 0.9 for 12W, 15W, 18W, SW, HCW, REA, FT, PW, P8, VCW, respectively. The residual prior variances used were 536, 931, 1704, 597, 33.0, 5.4, 25.4, 9.5, 4.4, 1.3 for 12W, 15W, 18W, SW, HCW, REA, FT, PW, P8 and VCW, respectively.

For the "fixed" effects the program used assumed prior "flat" distributions (Van Tassel and Van Vleck, 1995).

Tests were performed to determine the length of the chain. A high dependence was observed between samplings of the different traits, resulting in slow convergence. In the end, 2,500,000 iterations were carried out with a burn in of 558,000 samples, the chain was sampled every 5 iterations, resulting in 388,400 samples. The convergence analysis was performed graphically for each heritability and genetic correlation. By means of descriptive statistics and distribution charts, the posterior distributions of each heritability and genetic correlation were characterized.

Results and Discussion

Table 1 shows estimates of heritabilities and additive genetic correlations. 12W, 15W, REA and VCW had mean posterior heritability between 0.33 and 0.34. Higher values were obtained for 18W (0.41), SW (0.58) and PW (0.57) and the highest mean posterior estimate was HCW with 0.64 (Table 1). An increase in heritability in weight is observed as the animal increases in age with HCW being the largest, similar trend to that observed in the review by Koots et al. (1994).

Table 1Mean and standard deviations of the posterior distribution of heritability and additive genetic correlations of live weight, carcass weights, fat thickness in the carcass and rib eye area of steak.

Trait.[1]	12W	15W	18W	SW	HCW	REA	FT	PW	P8	VCW.
12W	**0.33 ±0.10**									
15W	0.75 ±0.09	**0.33 ±0.09**								
18W	0.72 ±0.09	0.78 ±0.07	**0.41 ±0.09**							
SW	0.65 ±0.13	0.66 ±0.11	0.76 ±0.08	**0.58 ±0.11**						
HCW	0.69 ±0.12	0.72 ±0.10	0.80 ±0.06	0.94 ±0.03	**0.64 ±0.10**					
REA	0.39 ±0.19	0.36 ±0.19	0.46 ±0.16	0.51 ±0.16	0.52 ±0.14	**0.34 ±0.10**				
FT	0.26 ±0.21	0.29 ±0.20	0.28 ±0.19	0.32 ±0.19	0.30 ±0.19	-0.08 ±0.21	**0.22 ±0.06**			
PW	0.67 ±0.12	0.68 ±0.10	0.77 ±0.07	0.92 ±0.03	0.96 ±0.01	0.59 ±0.13	0.22 ±0.19	**0.57 ±0.08**		
P8	0.10 ±0.24	0.17 ±0.24	0.10 ±0.23	0.07 ±0.23	0.13 ±0.23	-0.59 ±0.19	0.32 ±0.20	0.02 ±0.23	**0.16 ±0.06**	
VCW.	0.67 ±0.12	0.69 ±0.10	0.78 ±0.07	0.90 ±0.04	0.95 ±0.01	0.60 ±0.13	0.22 ±0.19	0.94 ±0.16	0.02 ±0.23	**0.34 ±0.07**

[1] 12W, 15W, 18W: weights at 12,15,18 months of age, respectively; SW: slaughter weight; HCW: hot carcass weight; REA ribeye area; FT: fat thikness; PW: pistola weight; VCW: valuable cut weight

Fat measurements were those with the lowest mean averages, with FT with an average of 0.22 and the lowest, P8 with an average of 0.18. Genetic correlations of SW with live animal weights (12W, 15W and 18W) ranged from 0.65 to 0.76, with values increasing with age of weight (Table 1). Regarding the carcass traits, it is important to highlight the high estimates (above 0.9) obtained between the carcass weight measurements (HCW, PW and VCW). These traits had also high but smaller genetic correlation estimates (between 0.5 and 0.6) with REA which in turn presented negative genetic correlations with the two measures of fat thickness considered, -0.08 for FT and -0.59 for P8. Posterior distributions of genetic correlations of fat thickness (FT, P8) with the other traits were those with the highest posterior standard deviation. The FT trait showed low genetic correlations with the other traits, being the highest with P8 (0.32). On the other hand, P8 presented low estimates of 0.02 to 0.07 with measures of weight HCC, PW and VCW.

From the results obtained (Table 1), it should be noted that the highest genetic correlations were obtained between the live weight traits (12W, 15W, 18W and SW) and carcass weights (HCC, PW and VCW) increasing in the three carcass traits mentioned above from the first measurement of live weight considered towards the slaughter weight; the lowest estimate for this group was between HCC and 12W (0.67), while the highest was that of HCC and SW (0.94).

Conclusions

These results confirm the possibility of using live weight measurements as selection criteria to improve hot carcass weight, pistola cut weight and valuable cuts weight. Likewise, ribeye area would also be improved, while subcutaneous fat thickness would not be substantially modified. This should not be an inconvenience at present, considering information provided by industry regarding adequate fat levels, as well as the current conditions of production in the primary sector.

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