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Original

Bivariate analysis for the improvement of genetic evaluations with incomplete records in Charolais cattle

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ABSTRACT

Objective: Estimate (co)variance components and genetic parameters of live weight traits and examine the effect of selection culling when using bivariate analysis in registered Charolais beef cattle. **Materials and methods:** The effect of incomplete data over accuracies was compared, expected progeny differences (EPD) and standard errors of prediction (SEP) were obtained and evaluated by comparing univariate and bivariate models for birth (BW), weaning (WW) and yearling (YW) weights. **Results:** Bivariate models for WW and YW, improved accuracies of EPDs and reduced the SEPs. Joint analysis for BW and WW increased in a 38% the accuracies and reduced SEP estimators for YW ($p<0.001$). Accuracies of EPD for BW obtained from univariate models were improved when BW was included in bivariate models. **Conclusions:** The results support the use of bivariate genetic analysis in limited or incomplete live weight indicators databases that were registered after birth, such as weaning and yearling weight.

Keywords: Incomplete records; live weights; culling selection (*Sources: USDA, Tesauro ICYT de Biología Animal*).

RESUMEN

Objetivo: Estimar los componentes de (co)varianza y parámetros genéticos de indicadores de peso vivo y examinar el efecto de la selección cuando se utiliza análisis bivariado en ganado Charolais de registro. **Materiales y métodos:** Se comparó el cambio en bases de datos incompletas sobre las exactitudes, se obtuvieron diferencias esperadas de la progenie (DEP) y errores estándar de predicción (SEP), evaluados bajo modelos univariados y multivariados para peso al nacimiento (PN), peso al destete (PD) y peso al año (PA). **Resultados:** El modelo bivariado para PD y PA mejoró las exactitudes para las DEP´s y redujo las SEP. Los análisis conjuntos para PN y PD incrementaron en un 38% las exactitudes y se redujeron los estimadores SEP para PA ($p<0.001$). Las exactitudes

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de las DEP para PN obtenidas mediante modelos univariados mejoraron al incluir PN en modelos bivariados. **Conclusiones:** Los resultados apoyan el uso de análisis genéticos bivariados en bases de datos limitadas en información para indicadores registrados posteriores al nacimiento tales como peso vivo al destete y al año.

Palabras clave: Datos incompletos; Pesos vivos; selección de animales (*Fuentes: USDA, Tesauro ICYT de Biología Animal*)

INTRODUCTION

In Mexico, most of the breeding programs for beef cattle are using BLUP (Best Linear Unbiased Prediction) methodology for the genetic evaluations of the animals using a single trait animal model. Expected progeny differences (EPD) for live weight traits are published in sire catalogs and summaries and these resources are mainly used for the selection of sires.

Charolais cattle are one of the most popular and widespread breeds of cattle in the world and in Mexico was one of the first breeds subjected to genetic evaluations for live traits, by the Charolais Herd Book of Mexico (1,2).

One of the most common issues in a local registered beef production system is the selection and trade (or culling) of young animals, hence incomplete records are processed in genetic evaluations, this has been pointed out in previous studies in Brahman, another important beef cattle breed in Latin America (3). Previously it has been suggested this factor as one of the selection forces that influence the data collected from commercial livestock; consequently may change the null expectation of the Mendelian sampling effects which is an underlying assumption for the properties of individual animal models. This selection (culling) bias can be addressed in part, by multivariate genetic models that may account for selection (4,5).

A multiple trait animal evaluation uses the phenotypic and genetic correlations between the traits and the genetic relationship between the animals included in the pedigree file. This methodology improves the accuracy of the genetic evaluation and consequently the selection response (5,6).

This type of analysis also could help with the particular characteristics of Mexican beef cattle systems, since data structure could present a challenge for the analysis and interpretation of results (7).

The objective of the present paper was to estimate (co)variance components and genetic parameters of live weight traits and examine the effect and selection bias when using bivariate analysis in registered Charolais beef cattle.

MATERIALS AND METHODS

Location. This investigation was based on information obtained from three herds of registered Charolais cattle located in the north of Mexico (Nuevo León and Sonora), at 282 to 500 m.a.s.l. and average temperatures between 20 to 30 °C. Animals were maintained under extensive management.

Type of study and sample size. Data corresponded to Charolais cattle born from 1967 to 2016 were analyzed. Live weight traits considered in this study were birth weight (BW, kg), weaning weight adjusted to 205 d (WW, kg), and yearling weight (YW, kg).

Statistical analysis. Three bivariate animal models were fitted using the MTDFREML program (8). The models included the fixed effects of contemporary group (herd-sex-year-season) and linear and quadratic age of dam, and the random effect of animal. Seasons of birth were grouped accordingly with a method that considers classification criteria defining four seasons as arid, semi-arid, sub-humid and humid (9).

In matrix notation the univariate model for BW was represented as:

$$Y=Xb+Za+e$$

With the assumptions,

$$E[y]=Xb, E[a]=0, E[e]=0, y$$

$$Var\begin{bmatrix}\mathbf{a}\\ \mathbf{b}\\ \mathbf{e}\end{bmatrix}=\begin{bmatrix}\mathbf{A}\sigma_a^2 & \mathbf{0} & \mathbf{0}\\ \mathbf{0} & \mathbf{I}_V\sigma_p^2 & \mathbf{0}\\ \mathbf{0} & \mathbf{0} & \mathbf{I}_N\sigma_e^2\end{bmatrix}$$

The univariate model for WW was,

Y = Xb+Za+Wm+ e

With the assumptions,

E[y]=Xb,E[a]=0,E[m]=0,E[e]=0,and

$$Var\begin{bmatrix}\mathbf{a}\\ \mathbf{m}\\ \mathbf{p}\\ \mathbf{e}\end{bmatrix}=\begin{bmatrix}\mathbf{A}\sigma_{\mathbf{a}}^{2} & \mathbf{A}\sigma_{\mathbf{am}} & \mathbf{0} & \mathbf{0}\\ \mathbf{A}\sigma_{\mathbf{am}} & \mathbf{A}\sigma_{\mathbf{m}}^{2} & \mathbf{0} & \mathbf{0}\\ \mathbf{0} & \mathbf{0} & \mathbf{I}_{\mathbf{V}}\sigma_{\mathbf{p}}^{2} & \mathbf{0}\\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{I}_{\mathbf{N}}\sigma_{\mathbf{e}}^{2}\end{bmatrix}$$

Where: A=numerator relationship matrix; N=number of observations; V=number of animals with records, and I = identity matrix of proper order.

The bivariate models for BW-WW; and YW- WW were:

$$\begin{bmatrix}y_1\\ y_3\end{bmatrix}=\begin{bmatrix}X_1 & 0\\ 0 & X_2\end{bmatrix}\begin{bmatrix}b_1\\ b_2\end{bmatrix}+\begin{bmatrix}Z_1 & 0\\ 0 & Z_2\end{bmatrix}\begin{bmatrix}a_1\\ a_2\end{bmatrix}+\begin{bmatrix}0 & 0\\ 0 & W_2\end{bmatrix}\begin{bmatrix}0\\ m_2\end{bmatrix}+\begin{bmatrix}e_1\\ e_2\end{bmatrix}$$

And for BW, YW:

$$\begin{bmatrix}\boldsymbol{y_1}\\ \boldsymbol{y_3}\end{bmatrix}=\begin{bmatrix}\boldsymbol{X_1} & \boldsymbol{0}\\ \boldsymbol{0} & \boldsymbol{X_2}\end{bmatrix}\begin{bmatrix}\boldsymbol{b_1}\\ \boldsymbol{b_2}\end{bmatrix}+\begin{bmatrix}\boldsymbol{Z_1} & \boldsymbol{0}\\ \boldsymbol{0} & \boldsymbol{Z_2}\end{bmatrix}\begin{bmatrix}\boldsymbol{a_1}\\ \boldsymbol{a_2}\end{bmatrix}+\begin{bmatrix}\boldsymbol{e_1}\\ \boldsymbol{e_2}\end{bmatrix}$$

Where y_i = vector of observations for the i_{th} trait (1= BW, 2=WW, 3= YW), b_i = vector of fixed effects for the i_{th} trait, a_i = vector of random animal effects, m_2 = vector of random maternal (indirect) genetic effects, e_i = vector of random residual effects, and X_i, Z_i, and W_i are incidence matrices relating records of the n^{th} trait to fixed, animal and maternal genetic effects, respectively.

It was then assumed that,

$$var\begin{bmatrix}\mathbf{a_1}\\ \mathbf{a_2}\\ \mathbf{m_2}\\ \mathbf{e_1}\\ \mathbf{e_2}\end{bmatrix}=\begin{bmatrix}\mathbf{g_{11}A} & \mathbf{g_{12}A} & \mathbf{g_{13}A} & \mathbf{0} & \mathbf{0}\\ \mathbf{g_{21}A} & \mathbf{g_{22}A} & \mathbf{g_{23}A} & \mathbf{0} & \mathbf{0}\\ \mathbf{g_{31}A} & \mathbf{g_{32}A} & \mathbf{g_{33}A} & \mathbf{0} & \mathbf{0}\\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{r_{11}} & \mathbf{r_{12}}\\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{r_{21}} & \mathbf{r_{22}}\end{bmatrix}$$

The convergence criterion used was e = $1x10^{-14}$, and three restarts for the program were considered until no changes in Log likelihood were observed. Computed (co)variance components were additive genetic variance direct (σ_d^2) for BW (BWd), WW (WWd) and YW (YWd), additive genetic variance maternal (σ_m^2) for WW (WWm), residual environmental variance (σ_e^2), phenotypic variance (σ_p^2), and genetic covariances between all traits. Genetic parameter estimated were direct heritabilities (h_d^2) for BW, WW, and YW, and maternal heritability (h_m^2) for WW.

To estimate the degree of selection bias, accuracies, expected progeny differences (EPD) and standard errors of prediction (SEP) were compared amongst univariate and bivariate models. A 10% of highest ranked animals by YW EPD and accuracies predicted by univariate analysis were considered in this examination. Complementarily, Spearman rank correlation coefficients were estimated with this data subsets. These analyses were performed by TTEST and CORR procedures, using SAS software v.9.0, respectively, (10).

Ethical aspects: This article does not contain any studies with live animals performed by any of the authors and approval from an Animal Ethics Committee was not required.

RESULTS

Descriptive statistics of traits analyzed in this study are presented in Table 1. The total number of animals in the relationship matrix was 5629 The number of records for YW showed a decrease of 48% and 52%, compared with BW and WW, respectively.

Table 1. Descriptive statistics of live weight traits of Charolais cattle.

Trait	N	Mean	SD	Min	Max
Birth weight (kg)	4186	40.54	7.46	20	66
Weaning weight (kg)	3866	228.40	43.92	99	396
Yearling weight (kg)	2016	375.31	72.74	166	681

Table 2 describes the population structure and pedigree information for this study.

Table 2. Population structure of Charolais population used in this study.

Trait	Pedigree	CG	Sires	Dams
Birth weight	5629	224	142	1665
Weaning weight	5629	213	98	1591
Yearling weight	5629	131	98	1580

CG= Contemporary groups

The estimates of heritabilities, phenotypic and genetic correlations are presented in table 3. The Genetic correlation between WW direct and maternal was negative and low.

WW direct and maternal genetic effects showed higher genetic correlations with YW. Similarly, WW showed a high phenotypic correlation with YW (Table 3).

Table 3. Heritabilities, and phenotypic and genetic correlation for bivariate analysis of live weight traits of Charolais cattle.

Trait	BW	WWd	WWm	YW
BW	0.32	0.26	-	0.27
WWd	0.22	0.22	-	0.67
WWm	0.43	-0.27	0.18	-
YW	0.57	0.66	0.71	0.34

BW: birth weight direct. WWd: weaning weight direct. YW: Yearling weight direct. WWm: weaning weight maternal. Above diagonal: Phenotypic correlation. Below diagonal: Genetic correlations.

Table 4, shows the average EPD, SEP and accuracies estimated from the ten percent highest ranked animals by univariate and bivariate genetic models. In general estimates for bivariate models, showed significant differences, compared to those obtained by the bivariate models. Most relevant differences are the lower means for EPD, and slightly higher accuracies for WW and YW.

Complementary correlation analysis is presented in table 5. Spearman rank correlation coefficients, showed substantial changes in ranking for WW and YW traits. YW showed slight influence on predictors; however, WW direct and maternal predictions were highly influenced by bivariate models with low and even negative correlations between univariate and bivariate models. All correlations were highly significant ($p<0.0001$).

Table 4. Expected progeny differences, standard error of prediction and accuracy averages from univariate and bivariate analysis of live weight traits of Charolais cattle.

Trait		Univariate	BW/WW	BW/YW	WW/YW
BW	EPD	-7.439±2.09 ^{a}	-3.650±1.05 ^{b}	-3.644±1.05 ^{b}	__
	SEP	2.79±0.18 ^{a}	2.76±0.17 ^{b}	2.75±0.18 ^{b}	
	AVG	0.62±0.06 ^{a}	0.62±0.06 ^{a}	0.63±0.06 ^{b}	
WWd	EPD	12.709±5.30^{a}	6.896±7.45 ^{c}	__	7.731±8.62 ^{b}
	SEP	22.26±0.71^{a}	14.28±0.83 ^{c}		14.52±0.88 ^{b}
	AVG	0.34±0.07^{c}	0.47±0.07 ^{b}		0.52±0.07 ^{a}
WWm	EPD	13.447±5.52 ^{a}	5.464±6.08 ^{c}	__	12.228±18.04 ^{b}
	SEP	22.23±1.14 ^{b}	12.93±0.97^{c}		24.41±2.64 ^{a}
	AVG	0.34±0.11 ^{c}	0.47±0.11^{b}		0.60±0.11 ^{a}
YW	EPD	24.424±8.98 ^{a}	__	22.92±12.73 ^{b}	8.495±6.03 ^{c}
	SEP	23.99±1.52 ^{a}		22.73±1.31 ^{b}	10.57±0.73 ^{c}
	AVG	0.49±0.10 ^{c}		0.57±0.06 ^{a}	0.52±0.09 ^{b}

BW: birth weight direct. WWd: weaning weight direct. YW: Yearling weight direct. WWm: weaning weight maternal. Values with different superscripts within the same row are significantly different ($p<0.05$).

Table 5. Spearman rank correlation coefficients of expected progeny differences (accuracies) between univariate and bivariate[1] analysis of live weight traits of Charolais cattle.

Univariate	BW_{ww}	BW_{yw}	WW_{BW}	WW_{YW}	YW_{BW}	YW_{ww}
BW	0.98 (0.97)	0.97 (0.99)				
WWd			0.18 (0.60)	0.08 (0.59)		
WWm			0.35 (0.18)	-0.20 (0.56)		
YM					0.65 (0.96)	0.66 (0.72)

BW: birth weight direct. WWd: weaning weight direct. WWd: weaning weight maternal. YW: Yearling weight direct. [1]Subindex indicate secondary trait in bivariate analysis.

DISCUSSION

In general, for the descriptive evaluation, all means for table 1, were similar to those reported previously in Mexico (9,11), but YW was higher than the value reported in another Charolais population (12).

BW direct heritability was slightly higher to the reports from Mexican Charolais cattle (11), but similar to some reports in French Charolais populations (13). In the case of WW direct heritability, these results are similar to estimators reported for registered Charolais cattle from Mexico (11). Conversely in a French Charolais and Austrian population higher estimators were reported (13,14). Heritability for maternal WW was slightly lower than heritability for direct WW. Similar range estimates for maternal heritabilities (0.12 to 0.18) in different Australian, Canadian American and New Zealand Charolais populations had been published (15).

In this study, negative covariance and correlations between direct and maternal genetic effects for WW were observed. Other studies (8,9) have reported a stronger negative correlation (i.e. -0.72) for Charolais registered cattle from Mexico. Consistently, this trend has been observed in different beef cattle populations like Brown Swiss and Cebu cattle (16,17).

This known negative genetic correlation is attributed to different causes, such as genetic antagonism, missed effects in the model of evaluation, sire by year interactions and data structure (18,19). Some implications of this negative genetic correlations had been related to slow genetic progress for WW (20,21). Some authors, recently discussed the estimated negative genetic response in maternal WW in registered Charolais cattle herds in Mexico, indicating that this trend is perhaps, directly related to the current criterion of selection focused exclusively on direct genetic effects during the sire selection process (2).

The estimate of heritability for YW was similar to the value reported using a different genetic model (12). Although this trait is the most important trait used as a selection criterion for young sires in Mexico, few reports of heritability for the trait in Charolais cattle were found in the literature (22).

BW showed moderate to high genetic correlations among different live weight traits evaluated (Table 3). The genetic correlation between this trait and WWd was lower to that reported in a Canchim population (0.42) (24), and higher than reported in a Spanish Charolais cattle (-0.11) (23). For WWm, moderate and genetic correlation showed a positive association with BWd (0.43), opposed to the genetic correlation previously reported of -0.27 (15). The higher genetic correlation with BW was observed with YW (Table 4). Similarly, YW showed the highest genetic correlations with WWd and WWm (0.66 and 0.71, respectively) suggesting a positive and strong relationship among YW and these traits.

The undesirable high BW negatively related to calving ease (24,25) can explain the observed correlation of BW since this trait is undesirable for most Charolais breeders. However, the limited use of genetic strategies on most breeding herds has guided differential responses for this trait (2).

In the other hand, the highest genetic correlations between WW genetic traits and YW could also be a reflection of the higher valued post-weaning weights. A consequence of this practice may be the considerable reduction on information available in the dataset for genetic evaluations. As documented (7), this is a persistent issue of the beef cattle production systems, where, sequential elimination, culling or selling of animals and selectively reports of information for some traits is a frequent practice. As observed here, analyzed dataset experienced a reduction of 52% of data from BW to YW, from selling young sires and heifers perhaps, hence conducting to a very likely culling (selection) bias (26,27). This is a relevant implication in young

sire trade, since weaning to yearling, with the inevitable loose of unregistered data.

With exception to BW, a bivariate model for WW and YW increases estimates of accuracies and reduces the SEP values. Joint analysis of BW and WW increased 38% of the accuracies and reduced SEP estimators ($p<0.001$). Interestingly, YW and WW bivariate analysis led to the significantly improvement of accuracy in all traits, and a substantial reduction of SEP for YW ($p<0.001$). Theoretically this increase in accuracy with multivariate analysis has been explained by the better connections in the data due to residual covariance between traits (6,27). It provides similar results compared with index selection and makes the multivariate approach reliable for the purpose of selection (28,29,30).

A recent study (22), mentioned the importance of multivariate analysis in WW and YW traits in the monitoring of selected animals for the next breeding generation affected by culling bias, as a decrease in the data can affect the rearrangement of top sires (31). The use of multivariate or at least bivariate analysis will produce better genetics predictions using the covariance in the selection of young animals for better growth performance. Additionally, the significant and substantial change in ranking of animals observed in YW and WW through a more complex model, suggest possible important economic implications when EPD and accuracies are used for selection and buying of young sires and heifers. Furthermore, bivariate models might provide better support of data structure and provide better estimators and predictions.

Some implications derived from the present analysis are that all traits showed moderate to high heritability, suggesting a very likely positive and favorable selection response; however, since not BW increasing is projected and higher post-weaning gains are desired, predictions on WW and YW traits are quite necessary. Some evidences showed that opposite selection on positively related traits is possible (2,32,33). A problem derived relies on the fact that WW and YW are the main criterion for selecting young breeding stock, but these traits are subjected to incomplete records during the estimation of genetic predictions. Therefore, the use of bivariate genetic analysis might help overcome possible information loses for those animals whose pedigrees by uncompleted recording could have been compromised and the use of this information could be used for practical decision making.

In conclusion, genetic parameters for live weight traits achieved from univariate and bivariate mixed models were obtained in this study. A considerable amount of information is reduced from BW to YW perhaps by culling or selling young animals, producing a possible culling bias. The bivariate animal models showed to reduce the standard error of prediction and increase the accuracies of EPD for WW and YW. The national genetic evaluations need to consider the implementation of at least bivariate animal models to overcome the selection bias produced for data reduction in YW traits.

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