GENETIC CORRELATIONS OF DAYS OPEN WITH MILK YIELD AND METABOLIC WEIGHT IN HOLSTEIN AND BROWN SWISS COWS

Correlaciones genéticas de días abiertos con producción de leche y peso metabólico en vacas Holstein y Pardo Suizo

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ABSTRACT

The aim of the present study was to estimate (co)variance components and genetic correlations of days open with milk yield per lactation, lactation length and metabolic weight in Holstein and Brown Swiss cows under subtropical conditions of Mexico. Cows were kept in an intensive rotational grazing system in which the principal feed was Star grass (*Cynodon plectostachyus*). Cows were milked twice daily, by machine. Analyses of data were made applying a series of bivariate animal models in the MTDFREML program. Models for days open, milk yield per lactation and metabolic weight included breed of cow, calving year, calving season and lactation number as fixed environmental effects, and animal direct genetic, cow's permanent environmental, and residual as random effects. For lactation length the model included the same fixed and random effects, except cow's permanent environmental effect. The estimates of genetic correlations of days open with milk yield per lactation and metabolic weight were moderate and positive (0.45 and 0.33, respectively), suggesting that genes that control milk yield per lactation and metabolic weight also control days open. Estimates of phenotypic and permanent environmental correlations were smaller than estimates of genetic correlations. Results of the present study evidence that poor genetic potential for reproductive performance is associated with high genetic potential for milk production and metabolic weight.

Key words: Genetic correlations, days open, milk yield, cattle, subtropics, metabolic weight.

RESUMEN

El objetivo del presente estudio fue estimar componentes de covarianza y correlaciones genéticas entre días abiertos y producción de leche por lactancia, duración de la lactancia y peso metabólico en vacas Holstein y Pardo Suizo en condiciones subtropicales de México. Las vacas se mantuvieron en un sistema de pastoreo rotacional intensivo, en el cual el alimento principal fue zacate Estrella de África (*Cynodon plectostachyus*). Las vacas fueron ordeñadas dos veces al día con ordeñadora mecánica. Los análisis de los datos se realizaron aplicando una serie de modelos animal bivariados en el programa MTDFREML. Los modelos para días abiertos, producción de leche por lactancia y peso metabólico incluyeron raza de la vaca, año de parto, época de parto y número de lactancia como efectos ambientales fijos, y los efectos aleatorios genético directo, ambiental permanente de la vaca y residual. Para duración de la lactancia el modelo incluyó los mismos efectos fijos y aleatorios, excepto el efecto del ambiente permanente de la vaca. Los estimadores de las correlaciones genéticas de días abiertos con producción de leche por lactancia y peso metabólico fueron moderados y positivos (0,45 y 0,33, respectivamente) sugiriendo que los genes que controlan la producción de leche por lactancia y peso metabólico también controlan días abiertos. Los estimadores de las correlaciones fenotípicas y ambientales permanentes fueron menores que los estimadores de las correlaciones genéticas. Los resultados del presente estudio demuestran que un bajo potencial genético para comportamiento reproductivo está asociado a alto potencial genético para producción de leche y peso metabólico.

Palabras clave: Correlaciones genéticas, días abiertos, producción de leche, bovinos, subtrópico, peso metabólico.

INTRODUCTION

Cow's fertility is one of the most important factors that affect herd efficiency and genetic gain under most production systems, including those for beef and dairy. Abroad studies related to genetic evaluation of dairy cows (*Bos taurus*) have reported antagonistic correlations between fertility and milk production (MP) traits, meaning that selection for high MP leads to decline in fertility. Such studies include those by Nebel and McGilliard [19], Marti and Funk [16], Kadarmideen *et al*. [13], Kadarmideen and Wegmann [14], and Zink *et al*. [30], among others. In Mexico, Cienfuegos-Rivas *et al*. [6], using data from Holstein cows found similar results, reporting that the genetic correlation for first-lactation milk and calving interval (CI) was unfavorable. In contrast, in a more recent study carried out with Mexican Holstein cows under cold weather conditions, Montaldo *et al*. [17] found that mature equivalent MP and CI were not correlated genetically. This result means that single trait selection for higher MP will leave CI unaltered. No information, however, is available in Mexico on (co)variance components and genetic correlations between fertility and MP traits of dairy cows under tropical or subtropical conditions. In the future, a genetic selection index based on reproductive parameters and MP could be used to improve both traits, if a genetic correlation exists between them. Estimation of genetic correlations between fertility and MP traits is a requirement for the creation of such a selection index. The aim of the present study was to estimate (co)variance components and genetic correlations of days open with MP per lactation, lactation length and metabolic weight in Holstein and Brown Swiss cows under subtropical conditions of Mexico. Because of the similarity between days open and CI where a strong genetic correlation was estimated in a previous study [24], the genetic correlation between CI and MP was not estimated.

MATERIALS AND METHODS

Location and climate

The present study was carried out at Las Margaritas research station of the National Institute for Forestry, Agriculture and Livestock Research (INIFAP). The experimental site is located in the Municipality of Hueytamalco, State of Puebla, Mexico, at 450 m above sea level [8]. The climate is classified as subtropical humid [8]. Average annual temperature is 20.8°C, the minimum temperature is 15.3°C in winter, and the maximum temperature is 24.2°C in summer [8]. Also, the region is characterized by abundant rainfall from July to October and a low temperature period with drizzle from November to the end of February. From March to June, high temperatures combined with low humidity and solar radiation generates stressful conditions [8].

Population of study

Productive records of 304 Holstein Friesian and Brown Swiss cows were used in the present investigation. The cows were daughters of 128 sires and 203 dams. The 203 dams were mated to the 128 sires through artificial insemination (mainly) and natural service. The 304 cows evaluated were born from 1986 to 2005, and calved from 1989 to 2009. Females of both breeds were managed together in the same way.

Breeding management

Heifers were first bred when they reached about 350 kg. Heat detection was performed one hour (h) in the morning (from 06:00 to 07:00) and one h in the afternoon (from 17:00 to 18:00), with the help of a chin-ball bull. Breeding of cows was in the following manner: those coming on oestrus in the morning were served in the afternoon, and those coming on oestrus in the afternoon were served the following day in the morning, approximately 12 h after visual observation of oestrus. Cows were confirmed pregnant by rectal palpation after 45 days (d) of last service.

Feeding management

Cows were kept in an intensive rotational grazing system in which the principal feed was Star grass (*Cynodon plectostachyus*). Grazing and non-grazing periods for each pasture (1-2 hectares each) lasted 2-3 and 35-40 d, respectively, depending on the season of the year (climate conditions). Stocking handled on average 2.5 animal units per hectare per year throughout the study. During the cold season (November to February), each cow received 20-30 kg of fresh, chopped Japanese cane (*Saccharum sinense*) per d. Also, each lactating cow received 3.5 kg of a commercial supplement (16% crude protein and 70% total digestible nutrients) per milking (twice a d), while non-lactating cows received 2 kg of the same supplement per d.

Milking management

Calves were taken away from their dams three d after calving. Cows were managed according to the following groups: 1) lactating cows from calving to the fifth month of lactation, 2) lactating cows from the sixth month of lactation to drying-off, and 3) dry-off cows. Milking of cows initiated four d after calving. Cows were milked twice daily by machine, between 05:00 and 07:00 h and between 15:00 and 17:00 h. Measurement of the individual cow's MP was carried out automatically during each milking with Waikato type proportional flow meters. Total MP per d was calculated adding the MP of the first milking to the MP of the second milking. Lactating cows were dried off when they were seven month pregnant or when their milk yield was less than 2 kg per d.

Cow measurements

Variables measured on each cow were: 1) milk yield per lactation, defined as the total kilograms of milk per cow per lactation; 2) lactation length, defined as the number of d from

calving to drying off; 3) d open, defined as the days gone by from calving to conception; and 4) cow's metabolic weight, defined as calving weight of the cow to the 0.75 power [15].

Data editing

All milk yield records were included irrespective of length, but records affected by illness or death were excluded. Ngere *et al*. [20] demonstrated that the customary procedure of deleting short lactations when evaluating native breeds in India led to serious biases, which could affect conclusions drawn about breed or herd. TABLE I shows descriptive statistics for each trait. Days open, MP per lactation, lactation length and cow's metabolic weight varied from 23 to 250 d, 1113 to 8533 kg, 186 to 780 d, and 62.1 to 135.8 units, respectively. The number of records, cows, sires, dams, and animals in the pedigree are presented in TABLE II.

TABLE I
DESCRIPTIVE STATISTICS FOR FERTILITY, MILK YIELD AND WEIGHT TRAITS[a]

	Trait[a]			
	DO	MY	MW	LL
Mean	105.3	3612.0	105.2	323.4
Minimum value	23.0	1113.0	62.1	186.0
Maximum value	250.0	8533.0	135.8	780.0
Standard deviation	54.7	1019.2	9.6	81.7
Coefficient of variation, %	52.0	28.2	9.2	25.3

[a]DO= Days open; MY= Lactation milk yield; MW= cow's metabolic weight; LL= Lactation length.

TABLE II
DATA STRUCTURE FOR BIVARIATE ANALYSES OF FERTILITY, MILK YIELD AND WEIGHT TRAITS[a]

	DO-MY	DO-MW	DO-LL
Number of records for each trait	956	942	956
Number of cows	304	299	304
Number of sires	128	122	128
Number of dams	203	195	203
Pedigree size	525	510	525

[a]DO= Days open; MY= Lactation milk yield; MW= cow's metabolic weight; LL= Lactation length.

Models for bivariate analyses

(Co)variance components and genetic and phenotypic correlations were obtained from bivariate analyses. Estimates of variance components from single-trait analyses were used as priors to carry out two-trait analyses. Linear mixed models for days open, lactation MP and cow's metabolic weight were similar and included the same four fixed environmental effects: breed of cow, calving year, calving season and lactation number. The breed effect consisted of two classes, Holstein and Brown Swiss. Calving year comprised 21 classes, from

1989 to 2009, while calving season consisted of three, cold (from November to February), dry (from March to June), and rainy (from July to October). Lactation number was classified as 1, 2, 3, and ≥ 4. Random effects in the linear model were: animal direct genetic, uncorrelated permanent environmental effects to allow for repeated records of the cow, and residual. The animal model for lactation length included animal direct genetic and residual as random effects, and breed of cow, calving year, calving season and lactation number as fixed environmental effects.

In matrix algebra, the animal model assumed for days open, lactation MP and cow's metabolic weight was: $y = X\beta + Za + Wc + e$, while the animal model assumed for lactation length was: $y = X\beta + Za + e$. The bivariate animal model for days open and lactation MP, for example, was:

$$\begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} X_1 & 0 \\ 0 & X_2 \end{bmatrix} \bullet \begin{bmatrix} \beta_1 \\ \beta_2 \end{bmatrix} + \begin{bmatrix} Z_1 & 0 \\ 0 & Z_2 \end{bmatrix} \bullet \begin{bmatrix} a_1 \\ a_2 \end{bmatrix} + \begin{bmatrix} W_1 & 0 \\ 0 & W_2 \end{bmatrix} \bullet \begin{bmatrix} c_1 \\ c_2 \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \end{bmatrix},$$

where y_1 and y_2 are vectors of single trait phenotypic observations, β_1 and β_2 are vectors of fixed effects (breed of cow, calving year, calving season, and lactation number), a_1 and a_2 are unknown vectors of random direct additive genetic effects, c_1 and c_2 are unknown vectors of random cow's permanent environmental effects, e_1 and e_2 are unknown vectors of random temporary environmental effects; X_1 and X_2 are known incidence matrices relating fixed effects in β_1 and β_2, respectively; Z_1 and Z_2 are known incidence matrices relating additive genetic effects in a_1 and a_2, respectively; and W_1 and W_2 are known incidence matrix relating permanent environmental effects of the cow in c_1 and c_2, respectively.

For random effects, the following (co)variance structure was assumed:

$$Var \begin{bmatrix} a_1 \\ a_2 \end{bmatrix} = G = G_0 \otimes A,$$

$$Var \begin{bmatrix} c_1 \\ c_2 \end{bmatrix} = P = P_0 \otimes I,$$

$$Var \begin{bmatrix} e_1 \\ e_2 \end{bmatrix} = R = R_0 \otimes I,$$

$$G_0 = \begin{bmatrix} \sigma_{a1}^2 & \sigma_{a1,a2} \\ \sigma_{a1,a2} & \sigma_{a2}^2 \end{bmatrix},$$

$$P_0 = \begin{bmatrix} \sigma_{c1}^2 & \sigma_{c1,c2} \\ \sigma_{c1,c2} & \sigma_{c2}^2 \end{bmatrix},$$

$$R_0 = \begin{bmatrix} \sigma_{e1}^2 & \sigma_{e1,e2} \\ \sigma_{e1,e2} & \sigma_{e2}^2 \end{bmatrix},$$

where A is the matrix of Wright's additive numerator relationships among all animals in the pedigree; σ_{a1}^2 is the additive genetic variance for direct effects for days open; $\sigma_{a1,a2}$ is the additive genetic covariance between direct effects for d open and direct effects for lactation MP; σ_{a2}^2 is the additive genetic variance for direct effects for lactation MP; I is an identity matrix of appropriate order; σ_{c1}^2 is the variance due to permanent

environmental effects of the cow for days open; $\sigma_{c1,c2}$ is the co-variance between permanent environmental effects of the cow for days open and permanent environmental effects of the cow for lactation milk yield; σ_{c2}^2 is the variance due to permanent environmental effects of the cow for lactation MP; σ_{e1}^2 is the re-sidual error variance for days open; $\sigma_{e1,e2}$ is the covariance be-tween residual effects for d open and residual effects for lacta-tion MP; and σ_{e2}^2 is the residual error variance for lactation MP.

Genetic and phenotypic parameters were estimated by Restricted Maximum Likelihood with a derivative-free algorithm [9, 26] with the MTDFREML set of programs [4]. The conver-gence criterion for maximization of the likelihood function was set at 10^{-8}. After first convergence, several restarts were per-formed to ensure a global rather than a local maximum had been reached. In each new analysis, resulting estimates of the parameters from the previous analysis were used as new pri-ors. Solutions of random effects were obtained from the last it-eration cycle where a global maximum was reached.

RESULTS AND DISCUSSION

Estimates of genetic, permanent environmental, residual and phenotypic covariances between days open and lactation MP, lactation length and cow's metabolic weight are shown in TABLE III. TABLE IV presents estimates of genetic, permanent environmental, residual and phenotypic correlations between days open and lactation MP, lactation length and cow's meta-bolic weight.

The estimate of the genetic correlation for days open and lactation MP was moderate and positive (0.45), suggesting that genes that control lactation MP also control days open. This phenomenon is known as pleiotropic gene effects. Therefore, it

is expected that selection for high MP would lead to decline in fertility (increased days open). However, Veerkamp *et al*. [28] proposed that linkage of genes may be another phenomenon involved in the determination of the genetic correlation between MP and fertility, even though pleiotropy is thought to be more important than gene linkage. The estimate of the genetic corre-lation between days open and lactation MP obtained in the present study is similar to corresponding estimates reported by Hansen *et al*. [11], who reported estimates of 0.42, 0.44 and 0.47 for first-, second- and third-parity yield of American Hol-stein cows. Similarly, from more recent studies, VanRaden *et al*. [27] and Zink *et al*. [30] also obtained moderate and positive (unfavorable) estimates of genetic correlations for days open and lactation MP (0.38 and 0.39, respectively). Present genetic correlation estimate between days open and lactation MP, however, is greater than those found by Campos *et al*. [5], Grosshans *et al*. [10], Hermas *et al*. [12], Kadarmideen *et al*. [13], and Raheja *et al*. [23], whose estimates were: 0.27, 0.25, 0.19, 0.27, and 0.05, respectively. Abdallah and McDaniel [1], Berger *et al*. [3], Dematawewa and Berger [7], Seykora and McDaniel [25], and Veerkamp *et al*. [29] reported estimates of genetic correlations for days open with lactation MP of 0.60, 0.62, 0.63, 0.54 and 0.61, which are greater than the current corresponding estimate. The difference among present esti-mate of genetic correlation and corresponding estimates re-ported in the literature may be due, among other factors, to dif-ferences in the statistical model applied, since most cited stud-ies did not include the permanent environmental effect of the cow in the analytical model to account for repeated records of cows (repeatability animal model). Another reason for the dif-ference between current and literature estimates could be that the present study was carried out with experimental data, in-stead of field data.

The estimated genetic correlation between days open and lactation length was also positive (0.87), but much stronger than the estimates of the genetic correlations of days open with lactation MP and cow's metabolic weight, indicating that cows with longer lactations take more time to get preg-nant after calving. Days open and cow's metabolic weight were moderately and positively correlated genetically (0.33). This result suggests that enhancement of cow's weight through selection is expected to decrease reproductive effi-ciency. Pryce *et al*. [22] argued that cows with high genetic potential for MP are likely to undergo marked body tissue mo-bilization, with increasing risk of impairment of reproductive

TABLE III
ESTIMATES OF GENETIC (C_g), PERMANENT ENVIRONMENTAL (C_c), RESIDUAL (C_e) AND PHENOTYPIC COVARIANCES (C_p) FOR DAYS OPEN WITH LACTATION MILK YIELD, LACTATION LENGTH AND COW'S METABOLIC WEIGHT

Trait	C_g	C_c	C_e	C_p
Lactation milk yield	173.3	134.3	1470.2	1777.7
Lactation length	251.2	-	1787.9	2039.1
Cow's metabolic weight	13.4	6.3	-26.5	-6.8

TABLE IV
ESTIMATES OF GENETIC (r_g), PERMANENT ENVIRONMENTAL (r_c), RESIDUAL (r_e) AND PHENOTYPIC CORRELATIONS (r_p) FOR DAYS OPEN WITH LACTATION MILK YIELD, LACTATION LENGTH AND COW'S METABOLIC WEIGHT

Trait	r_g	r_c	r_e	r_p
Lactation milk yield	0.45 ± 0.94	0.22 ± 0.47	0.38 ± 0.05	0.35
Lactation length	0.87 ± 0.80	-	0.48 ± 0.06	0.48
Cow's metabolic weight	0.33 ± 0.60	0.11 ± 0.37	-0.10 ± 0.04	-0.02

performance. Present estimate of the genetic correlation for days open and cow's metabolic weight is in accordance with the unfavorable estimate of the genetic correlation between services per conception and cow's body weight (0.37) reported by Badinga *et al*. [2], for lactating Holstein and Jersey cows under subtropical conditions of Florida (USA). In contrast, Núñez *et al*. [21] found that calving weight was moderately and negatively correlated genetically with CI (-0.51) and d to first service (-0.34), suggesting that selection for greater weight of cow would result in more fertile cows. On the other hand, Moore *et al*. [18] obtained near-zero estimates of the genetic correlation between days open and cow weight, which suggests lack of pleiotropic gene effects among weight and fertility of the cow.

Estimated permanent environmental, residual and phenotypic correlations between days open and lactation MP, lactation length and cow's metabolic weight had a similar direction of relationship, however, they were much smaller in magnitude than estimated genetic correlations. This result is in agreement with those reported by Hansen *et al*. [11], Kadarmideen *et al*. [13], VanRaden *et al*. [27], and Veerkamp *et al*. [29] who reported that estimates of genetic correlations were greater than estimates of phenotypic correlations for days open and lactation milk yield.

CONCLUSIONS

Estimates of genetic correlations of days open with MP per lactation and cow's metabolic weight reported in the present research are within the range of corresponding estimates reported in the literature for dairy cows under cold weather environments. Within the investigated population, the genetic correlation estimate between days open and MP per lactation was moderately antagonistic, revealing that single-trait selection for high MP would result in lower genetic merit for cow fertility. Similarly, selection for high MP would be expected to result in correlated changes in cow's metabolic weight. Therefore, days open or an equivalent fertility trait should be integrated into future selection programs for our experimental herd.

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