

## ASSOCIATION BETWEEN REPRODUCTIVE TRAITS AND MILK YIELD, IN CROSSBRED HEIFERS

## ASOCIACIÓN ENTRE CARACTERÍSTICAS REPRODUCTIVAS Y PRODUCCIÓN DE LECHE, EN NOVILLAS MESTIZAS

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### Abstract

This research was carried out in heifers from a crisscrossing program between the red Holstein and Brahman breeds, in Venezuela. (Co)variance components were estimated and the relationship between milk yield (P305), age (AGE1) and fertility at first service (FERT1) in virgin heifers was investigated. The analysis methodology was restricted maximum likelihood (REML), under a multivariate animal model. The mixed model included: the random effect of the animal; and the fixed effects of racial group, year-seasons of the event occurrence; for P305, the duration of lactation was also included as a covariate in quadratic form. Heritabilities were:  $0.498 \pm 0.022$ ;  $0.436 \pm 0.020$  and  $0.024 \pm 0.008$ , for P305, AGE1 and FERT1 respectively. Genetic correlations between: P305-AGE1; P305-FERT1 and AGE1-FERT1, were:  $-0.281 \pm 0.040$ ;  $0.238 \pm 0.117$  and  $-0.076 \pm 0.123$ , these results suggest a favorable genetic association between P305-AGE1, as well as, between P305-FERT1. Weighted regression analysis of the averages breeding values on years, showed an improvement in P305 of 10.85 kg/year and a reduction of  $-0.1150$  month/year in AGE1 representing 0.60 and 0.41% of the population means for those traits ( $p < 0.01$ ); the annual genetic change for FERT1 was not significant ( $p > 0.05$ ). The phenotypic changes in P305 and AGE1 were not significant ( $p > 0.05$ ). It is concluded that there is no genetic antagonism between P305 and FERT1 and that it is possible to reduce AGE1 for decreasing the costs for generating replacement heifers, improving the rate of genetic change in P305.

*Keywords:* Milk yield, fertility, age first service, crossbred cattle.

### Resumen

Esta investigación se realizó con novillas de un programa de cruzamiento entre las razas Holstein y Brahman roja, en Venezuela. Se estimaron los componentes de (co)varianza y se investigó la relación entre producción de leche (P305), edad (AGE1) y fertilidad al primer servicio (FERT1) en novillas vírgenes. La metodología de análisis fue bajo máxima verosimilitud restringida (REML), bajo un modelo animal multivariado. El modelo lineal incluía: el efecto aleatorio del animal; y los efectos fijos de grupo racial, años-temporadas de ocurrencia del evento; para P305, la duración de la lactancia también se incluyó como covariable en forma cuadrática. Las heredabilidades fueron:  $0.498 \pm 0.022$ ;  $0.436 \pm 0.020$  y  $0.024 \pm 0.008$ , para P305, AGE1 y FERT1 respectivamente. Las correlaciones genéticas entre: P305-AGE1; P305-FERT1 y AGE1-FERT1, fueron:  $-0.281 \pm 0.040$ ;  $0.238 \pm 0.117$  y  $-0.076 \pm 0.123$ , estos resultados sugieren una asociación genética favorable entre P305-AGE1, así como entre P305-FERT1. El análisis de regresión ponderada de los valores genéticos promedios en años, mostró una mejora en P305 de 10.85 kg/año y una reducción de  $-0.1150$  mes/año en AGE1 lo cual representa 0.60 y 0.41% de las medias poblacionales para esos rasgos ( $p < 0.05$ ), el cambio genético anual para FERT1 no fue significativo ( $p > 0.05$ ). Los cambios fenotípicos en P305 y AGE1 no fueron significativos ( $p > 0.01$ ). Se concluye que no existe antagonismo genético entre P305 y FERT1 y que es posible reducir AGE1 para disminuir los costos de generación de vaquillas, mejorando la tasa de cambio genético en P305.

*Palabras clave:* Producción de leche, fertilidad, edad primer servicio, ganado mestizo.

## INTRODUCTION

Reproduction is a complex multifactorial process, with high phenotypic variance, very little genetic variation, hence is very sensitive to environmental effects. The parturition of the cow triggers lactation, which is the fundamental source of income in dairy farms, therefore, breeder's objective must be focused on having efficient reproduction in the herd, this includes an early pregnancy with the least number of services. The cost of raising replacement heifers in farms are between 15 to 20% of the total costs in dairy farms (Fodor *et al.*, 2020). In an experiment with dairy tropical creole heifers managing the feeding system has proved to improve age and weight at puberty and at the same time follicular dynamics (Severino *et al.*, 2017). An age at first service of 17.7 months with a range between 14.5 and 23.8 months was reported for heifers (Muller *et al.*, 2017). In Israel it has been suggested that the optimal age at first calving in Holstein is between 22 and 24 months (Weller *et al.*, 2022a).

Heritability for milk yield at 305 days of lactation have been reported in the range of 0.15 to 0.50 in different populations of dairy cattle (Shalaby, 2005; Montaldo *et al.*, 2010; Ayalew *et al.*, 2017; Weller *et al.*, 2022b). For reproductive traits, on the contrary, the additive variance is very low: a heritability of 0.012 has been reported for the 56-day non-return rate (Sun *et al.*, 2009); for age at first service, values close to 0.06 have been published (Ayalew *et al.*, 2017; Weller *et al.*, 2022b), although a value of 0.128 was previously published (Abe *et al.*, 2009). Heritability for first service fertility for this crossbred cattle and age group was estimated to be 0.03 by using a Gaussian model and 0.07 with a threshold model (Román *et al.*, 2010). Despite having low heritability, reproductive and health traits are being incorporated into selection programs in some countries, it is interesting to see the evolution of selection indices in dairy cattle in Israel from 1985 to the present (Weller *et al.*, 2022a; 2022b).

In dual purpose cattle, evidence of deterioration reproductive behavior was found when classifying the cows, according to the level of milk yield and recording first service fertility, a significant reduction was observed, with the increase of production level (Soto & Perea, 2014). Previously, studying a cause-effect relationship between production level and fertility, evaluating the effects of milk yield at 120 days in milk, on the number of services per conception, it was found that more services were required in Holstein, Jersey and Guernsey cows per each 100 kg of extra milk (Olds *et al.*, 1979).

Negative estimates of the genetic correlation between age at first artificial insemination and milk yield, and therefore favorable, were reported previously (Abe *et al.*, 2009; Weller *et al.*, 2022b). However, some studies suggest a

genetic antagonism between milk yield and reproductive performance (Shalaby, 2005; Windig *et al.*, 2006; Getahun and Beneberu, 2023). Reports of the genetic correlations between age at first service and age at first calving are high and positive (Abe *et al.*, 2009; Brzáková *et al.*, 2019; Weller *et al.*, 2022b; Getahun and Beneberu, 2023).

At the experimental level, working with the Jersey breed a genetic change of 39.90 Kg/year was reported by Román *et al.* (1999), representing 1.48% of the population average, which is very close to the maximum possible for this trait as it was suggested previously (Rendel and Robertson, 1950). Despite the change achieved on milk yield, correlated favorable changes, for age at first heat and duration of the period from parturition to first service were observed, only the change in the number of services per conception showed a positive slope, but very close to zero (Román *et al.*, 1999).

The foregoing has motivated this research with the aims of estimating the genetic, environmental and phenotypic correlations between: milk production at 305 days; age and fertility at first service, as well as, the changes with time, in virgin heifers from a crisscrossing program in a tropical environment.

## MATERIAL AND METHODS

This research was carried out using the databases of the "Mompox" farm which belongs to the Santa Ana farming, during the period 1989-2016. The records are kept electronically with the GanSoft© Software. The production unit is located in a sub-humid zone in the Lake Maracaibo basin, at 14 m.a.s.l, at 9° 30' 3" north latitude and 72° 20' 39" west longitude, further details may be found on previous work (Soto and Perea, 2014).

The animals belong to a population generated by a crisscrossing program between the Holstein and the red Brahman breeds mainly, as a strategy to combine the production levels of *Bos taurus*, with the adaptation ability of *Bos indicus* to hard weather conditions, hence, in this work, the records from the two resulting subpopulations at the time of the stabilization of the crossbreeding program were used.

For this research, only records belonging to first calving animals were used, corresponding to the variables: Milk yield at 305 days (P305), which was estimated by monthly supervision, but truncated to a maximum duration of 305 days; Age at first service (AGE1) by artificial insemination (AI), which was estimated as the difference between the date of the first recorded service and the date of birth expressed in months; finally, the fertility at first service (FERT1) was evaluated as a binomial variable coded as 0, for empty and 1 for pregnant, these last two variables were taken when the heifers were virgin. In

addition, lactation length (LL) and age at parturition (AGE1P) were reordered.

The model included the fixed effects of: predominant breed group in the animals with two levels, 2/3 Holstein 1/3 Brahman and 2/3 Brahman 1/3 Holstein; The months of the year were grouped into four seasons, based on the rainfall records of the farm, namely: season 1, months of December and January; season 2, months of February March; season 3, months of April, May and June; season 4, months of July, August, September and October. Contemporary groups were structured concatenating years and seasons, groups with less than four observations in each contemporary group were excluded.

The multivariate model can be written as:

$$y = X\beta + Zu + e$$

If we partition the data vector as  $y' = [y'_1 \ y'_2 \ y'_3]$ ; and conveniently the incidence matrices of the fixed effects as:  $X' = [X'_1 \ X'_2 \ X'_3]$ ; and the random effects matrix as:  $Z' = [Z'_1 \ Z'_2 \ Z'_3]$ , and if 1, 2 and 3, represent the variables: P305; AGE1 and FERT1, the statistical model can be expressed as the following linear combination (Searle, 1971; Mrode 2005):

$$\begin{bmatrix} y_1 \\ y_2 \\ y_3 \end{bmatrix} = \begin{bmatrix} X_1 & 0 & 0 \\ 0 & X_2 & 0 \\ 0 & 0 & X_3 \end{bmatrix} \begin{bmatrix} \beta_1 \\ \beta_2 \\ \beta_3 \end{bmatrix} + \begin{bmatrix} Z_1 & 0 & 0 \\ 0 & Z_2 & 0 \\ 0 & 0 & Z_3 \end{bmatrix} \begin{bmatrix} a_1 \\ a_2 \\ a_3 \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \\ e_3 \end{bmatrix}$$

The sub-matrices for the allocation of the fixed effects for P305 had the effect of racial group with two levels as above, the effect of year-calving season with 93 levels, and the LL as a quadratic covariate; the sub-matrices for the allocation of the fixed effects for AGE1 and FERT1, in addition to racial group, included 111 and 105 levels of year-seasons of the event occurrence, respectively.

For the estimation of the (co)variance components, the Wombat software was used (Meyer, 2022), selecting in the estimation strategy the option -pxai, a hybrid algorithm consisting of a few initial expectation-maximization iterations followed by iterations with the REML average information algorithm. First, univariate analyzes were performed, estimating the additive variance of each trait from  $\hat{\sigma}_A^2 = h^2 \hat{\sigma}_p^2$ , where  $\hat{\sigma}_p^2$  is the phenotypic variance of the random variable, estimated from the data of table 1 for each trait; the environmental component was estimated by difference. Subsequently, the univariate estimators were used as initial values and the genetic covariance components were estimated by using the equation:  $\sigma_{A,y} \sigma_{Ax} r_{a(x,y)} = \sigma_{A(x,y)}$ . analogously, the initial values for the environmental covariance components were estimated. The convergence criterion established a priori was  $1 \times 10^{-6}$ .

For the description of the dispersion of the random effects of the model, it was considered that  $G_0$  is the additive genetic variance covariance matrix among the three traits submitted to the multivariate analysis, and likewise,  $R_0$  is the variance covariance matrix for the residuals;  $A$  is the matrix of the additive genetic relationships between the animals,  $I$  is an identity matrix and  $\otimes$  represents the Kronecker product, the variances of the random effects are defined by the expression:

$$Var \begin{bmatrix} u_i \\ e_i \end{bmatrix} = \begin{bmatrix} G_0 \otimes A & 0 \\ 0 & R_0 \otimes I \end{bmatrix}$$

The required data files were built with the Statistical Analysis System (SAS, 2016), including one with the information of the three traits for the multivariate analysis.

## RESULTS AND DISCUSSION

The Pedigree file contained the identification of 17,544 animals with their ancestors, of the total number of animals 2024 belonged to the base population. There were 680 descendants of related animals, with an average inbreeding coefficient of 0.2976%, the average inbreeding among inbred animals was 7.68%.

Table 1 shows the averages and standard deviations for: P305, FERT1 and AGE1, used as dependent variables in these analyses, in addition, LL and AGE1P are included.

The P305 of these animals is below the previously published value of 3504.02 for Holstein cattle in Ethiopia (Ayalew *et al.*, 2017) and very inferior to publications for the same breed in Israel, Egypt and Japan (Shalaby, 2005; Abe *et al.*, 2009; Weller *et al.*, 2022a) and in the Mexican republic with an average of 11499 kg milk equivalent adult (Montaldo *et al.*, 2010). In tropical conditions it is difficult to reach these figures because the diet is mainly based on forage, with supplementation only at the milking time according to the level of production.

The age at which these heifers begin their reproductive life is considerably high, which is affecting the costs of raising replacements, compromising genetic progress and contributing to shortening the length of the lifespan of the animals. The AGE1 average is much higher than those published for Holsteins (Muller *et al.*, 2017; Brzaková *et al.*, 2019; Weller *et al.*, 2022a; Abe *et al.*, 2009); This variable responds satisfactorily to feeding programs as has been published in creole dairy cattle in Mexico (Severino *et al.*, 2917). Despite the delay in reaching the weight required to be included in the reproductive program, the FERT1 in these heifers of 62% is higher than that published in Israel for Holsteins and slightly lower than the 69% reported for Holstein heifers in Japan (Abe *et al.*, 2009).

The dairy aptitude of this crossbreed cattle is reflected in LL with an average of  $295.09 \pm 23.54$  days, which indicates that the dairy temperament of the *Bos taurus* breed has been inherited in this population, despite the introduction of Brahman genes, which is a breed that tends to have shorter lactations.

**Table 1.** Means  $\pm$  standard deviations for productive and reproductive traits of heifers from a crisscrossing program between the Holstein and Red Brahman breeds

Traits	Statistics		
	N	Mean	S.D
P305	10599	1798.65	534.90
AGE1	14300	27.14	3.67
FERT1	15427	0.62	0.49
LL	10599	295.09	23.54
AGE1P	10599	37.30	4.44

### Heritability estimates

The additive and environmental genetic (co)variance components are shown together with their standard errors, for each trait on tables 2 and 3. The corresponding proportions and their standard errors are in tables 4 and 5. In the case of P305, the ratio of the additive variance to the total was 50%. Our estimator is identical to the reported for Holstein heifers in Israel (Weller *et al.*, 2022b), higher than the reported for the same type of animals in Egypt, Mexico and Ethiopia (Shalaby, 2005; Montaldo *et al.*, 2010; Ayalew *et al.*, 2017).

**Table 2.** Estimates of the additive (co)variance components  $\pm$  standard errors, for a population resulting from a crisscrossing program between the Holstein and Red Brahman breeds

Component	Genetic	
	Estimates	S.E
$\hat{\sigma}_{A(P305)}^2$	81614.9000	4716.6900
$\hat{\rho}_{A(P305,AGE1)}$	-168.8640	24.8790
$\hat{\rho}_{A(P305,FERT1)}$	5.0695	2.4707
$\hat{\sigma}_{A(AGE1)}^2$	4.4157	0.2485
$\hat{\rho}_{A(AGE1,FERT1)}$	0.0119	0.0191
$\hat{\sigma}_{A(FERT1)}^2$	0.0056	0.0018

$\hat{\sigma}_{A(i)}^2$  = additive genetic variance for the *i*<sup>th</sup> trait,  $\hat{\rho}_{A(i,j)}$  = additive genetic covariance between the *i*<sup>th</sup> and *j*<sup>th</sup> traits.

**Table 3.** Estimates of the environmental (co)variance components  $\pm$  standard errors for a population resulting from a crisscrossing program between the Holstein and Red Brahman breeds

Component	Environmental	
	Estimates	S.E
$\hat{\sigma}_{E(P305)}^2$	82332.4000	3006.5200
$\hat{\rho}_{E(P305,AGE1)}$	-3.3747	16.8075
$\hat{\rho}_{E(P305,FERT1)}$	-7.0711	2.2601
$\hat{\sigma}_{E(AGE1)}^2$	5.7043	0.1640
$\hat{\rho}_{E(AGE1,FERT1)}$	0.0618	0.0164
$\hat{\sigma}_{E(FERT1)}^2$	0.2222	0.0029

$\hat{\sigma}_{E(i)}^2$  = environmental variance for the *i*<sup>th</sup> trait,  $\hat{\rho}_{E(i,j)}$  = environmental covariance between the *i*<sup>th</sup> and *j*<sup>th</sup> traits.

**Table 4.** Estimates of the heritabilities and genetic correlations  $\pm$  standard errors, for a population resulting from a crisscrossing program between the Holstein and Red Brahman breeds

Estimates	Genetic	
	Proportion	S.E
$\hat{h}_{(P305)}^2$	0.498	0.022
$\hat{r}_{A(P305,AGE1)}$	-0.281	0.040
$\hat{r}_{A(P305,FERT1)}$	0.238	0.117
$\hat{h}_{(AGE1)}^2$	0.436	0.020
$\hat{r}_{A(AGE1,FERT1)}$	-0.076	0.123
$\hat{h}_{(FERT1)}^2$	0.024	0.008

$\hat{h}_{(i)}^2$  = heritability for the *i*<sup>th</sup> trait,  $\hat{\rho}_{A(i,j)}$  = additive genetic covariance between the *i*<sup>th</sup> and *j*<sup>th</sup> traits.

**Table 5.** Estimates of the proportion of the environmental (co)variance components  $\pm$  standard errors and environmental correlation for a population resulting from a crisscrossing program between the Holstein and Red Brahman breeds

Estimates	Environmental	
	Proportion	S.E
$\hat{e}_{(P305)}^2$	0.502	0.022
$\hat{r}_{e(P305,AGE1)}$	-0.005	0.025
$\hat{r}_{e(P305,FERT1)}$	-0.052	0.017
$\hat{e}_{(AGE1)}^2$	0.564	0.020
$\hat{r}_{e(AGE1,FERT1)}$	0.055	0.015
$\hat{e}_{(FERT1)}^2$	0.976	0.008

$\hat{e}_{(i)}^2$  = proportion of the environmental variance from the phenotypic variance for the *i*<sup>th</sup> trait,  $\hat{r}_{e(i,j)}$  = environmental correlation between the *i*<sup>th</sup> and *j*<sup>th</sup> traits.

In the particular case of this population, having a high genetic variability was to be expected, if we consider that these animals came from crossing individuals of very extreme genotypes: firstly, the best red Holstein bulls available on the market of semen, with positive and high values in their expected progeny difference for milk yield; secondly, bulls of the Brahman breed, paying attention mainly to have high weaning weights, which are raised in the Brahman breeding center of the “Mompox” farm.

The phenotypic values, in their simplest form, are due to the action of the genotype and the environment (Falconer and MacKay, 2001), we must say that the management and feeding conditions, as well as, medical-veterinary assistance and control of production records in this herd, is well above average for the herds in this sub-tropical zone; observation which is made, because it could be thought that, since we are dealing within a region in a tropical weather usually with poor management practices, the tendency would be for the heritabilities to be low.

These results are encouraging and hence: livestock associations, development corporations and entities that promote livestock development in the country, should see this population as the strategy to follow in national programs, to consolidate the livestock that sustains more than 75% of the national supply of milk and around 45% of that corresponding to meat. From here the initiatives for the formation of local tropical dairy breeds could come



out; an issue that has not been achieved because simple decisions have not been taken yet, such as reducing the number of breeds to the minimum required.

For AGE1 the heritability estimator indicates that 44% of the variability in this trait has an additive genetic component and therefore a substantial amount of response is to be expected if this trait is included in a selection index to obtain replacements for the farm. Our estimator is much higher than those previously reported (BrzÁková *et al.*, 2019; Weller *et al.*, 2022b). This must be looked at carefully, if the aim is to improve the productivity of this livestock, since heifers are beginning their reproductive life, when they should already be lactating. This is compromising: productivity of the farm, duration of the productive life of cows and genetic progress. This trait is a developmental characteristic and is simply a function of growth rate, combined with the onset of puberty, an event that must have occurred well in advance. It can be inferred that with rational feeding plans AGE1 can be reduced and weight increased at puberty (Severino *et al.*, 2017). We could expect that if we manage to make heifer's grow, as close as, possible to the "optimum", they will have an efficiently developed hypothalamus-pituitary-gonad-uterus axis so that the feedback mechanisms that determine cyclicity and pregnancy occur.

The heritability for FERT1 was 0.024; ratifying the almost null genetic variability in this trait; only slightly lower than the previously reported estimated for this population (Román *et al.*, 2010), however, in this case, the estimate is more precise due to the increased number of observations. Previously comparing linear and threshold models a very low heritability for fertility was found, observing slightly higher estimates with the latter model; however, the correlations between the predictions by both methodologies were greater than 0.99 (Weller & Ron, 1982).

There are sufficient reasons to suppose that the additive variance for reproductive traits to be low, since these characters have been subject to natural selection for hundreds of years, because they are determinants in the survival of the species, and as a result, any gene that affect the proportional contribution of offspring of a particular genotype to the next generation is dropped from the population (Falconer & MacKay, 2001). It is striking that in some countries reproductive and other health characteristics have been added into the selection plans; knowing that the magnitude of the response to selection must be negligible given the high homozygosity. In the case of tropical herds, like this one, the crisscrossing program has as objectives: to give stability to the production system generating within it the replacement females; to maintain maximum expression of heterosis and to combine the desirable characteristics of two populations. Genetic improvement must be supported both in the crossing program and in the selection plans. Over

the years, efforts have been made in both directions in this population.

The fact that some animals stand out from their contemporaries, achieving acceptable levels of production in P305, and that they also get pregnant at the right time, with fewer services, makes us suppose that they have a genetic system in harmony with the environment in which that unfold; therefore, they should be left for replacement. This justifies the inclusion of reproductive and health characters as have done in Israel (Weller *et al.*, 2022b). Another way of interpreting this is the search for an indirect response to selection for "adaptation" to the environment and its inclusion in the improvement plans would be justified; Otherwise, it would be worthless to include them, even in an index, because it compromises the annual progress in the traits of interest (Rendel & Robertson, 1950), mainly affecting the selection differential for the economic traits.

### Genetic, environmental and phenotypic correlations

The genetic correlation between P305 and AGE1 was - 0.28, rather low but favorable and much higher than that found for Holstein cattle in Israel and Japan respectively (Abe *et al.*, 2009; Weller *et al.*, 2022b). It has been reported that younger heifers at the time of pregnancy had a higher probability of calving, produced more milk, and less likely to be culled from the herd (Fodor *et al.*, 2010). On the other hand, a moderate antagonism of 0.29 has been reported in crossbred cattle in Ethiopia (Getahun & Beneberu, 2023) and a very extreme one for Holstein cattle in Egypt of 0.93 (Shalaby, 2005).

The genetic correlation between P305 and FERT1 was 0.24 with a high standard error. A negative estimate of 0.34 was found for Holstein heifers in Israel (Weller *et al.*, 2022b); a positive but small value was found for heifers of the same breed in Japan (Abe *et al.*, 2009). For practical purposes our positive estimate is also favorable, since it suggests an increase in fertility at first service with the increase in milk yield.

In a review on the causes of poor fertility in high producing dairy cows, authors make a clear distinction between virgin heifers with a high non-return rate compared to adult cows, and they also point out the importance of non-genetic factors as responsible for the possible antagonism between reproduction and milk production, exposed by some authors (Walsh *et al.*, 2011). On the other hand, it has been pointed out that many of the studies in this field are observational and consequently there is the possibility of entanglement from the statistical point of view among the multiple factors affecting the complex reproductive process and lactation (Bello *et al.*, 2012). The genetic correlation between AGE1 and FERT1 was -0.08 and due to the magnitude of the standard error, it is essentially zero, therefore, it indicates that there are

very few genes that act on both physiological processes at the same time.

The environmental correlations were close to zero in agreement with previous work (Abe et al., 2009; Weller et al., 2022b). The phenotypic correlations were very low, the highest being -0,13 between P305 and AGE1, the others were almost zero.

AGE1 is strongly correlated with AGE1P phenotypically and genetically, the latter being close to 0.99 (Abe et al., 2009; Brzáková, et al., 2019; Weller et al., 2022b; Getahun and Beneberu, 2023). This implies that they are the same trait genetically. That was the reason for incorporating AGE1 in the multivariate analysis instead of AGE1P, if we intend to reduce the costs of generating replacements on the farm and to shorten the interval between generations in order to accelerate annual genetic progress. With these data, in a bivariate analysis including AGE1 and AGE1P, the phenotypic correlation was  $0.876 \pm 0.002$  and the genetic one  $0.991 \pm 0.003$ , confirming the above rationale, furthermore, AGE1 is less subject to bias (Weller et al., 2022b).

### Genetic and phenotypic changes

Table 6 shows the estimates of the weighted regression coefficients of the average genetic values for each trait on years, along with their standard errors. The weighting factor was the reciprocal of the standard errors of each year. With all the selective effort put into milk yield, the regression slope for P305 may represent the direct genetic response for P305, with a significant increase of 10.85 kg/year ( $p < 0.01$ ), which represents 0.60% of the population average, being therefore much lower than that achieved in Jersey (Román et al., 1999) or the maximum possible previously reported (Rendel and Robertson, 1950). This implies that the selection program in this population must be reviewed, especially at the level of females and in Brahman bulls, seeking in this case to identify within this breed the best genotypes with dairy aptitude, since at the Holstein breed level they are using the best bulls available. In table 7 are the phenotypic changes for milk P305 was only 5.89 kg/year, but not significantly different from zero ( $p > 0.05$ ). This implies, the possibility of improving management and feeding conditions with the purpose that animals adequately express their genotypic value and hence minimizing erroneously selecting the wrong females.

**Table 6.** Annual genetic change for P305 and correlated response for AGE1 and FERT1, in a population resulting from a crisscrossing program between the Holstein and Red Brahman breeds

Trait	Genetic trends			
	$\Delta_{A/year}$	S.E	"t"	
P305	10.8475	1.4189	7.41	**
AGE1	-0.1150	0.0097	-11.84	**
FERT1	0.0008	0.0004	2.02	NS

$\Delta_{A/year}$ = Annual genetic change, S.E= standard error, t=computed value for "t"

**Table 7.** Annual phenotypic changes P305, AGE1 and FERT1, in a population resulting from a crisscrossing program between the Holstein and Red Brahman breeds

Trait	Phenotypic trends			
	$\Delta_{p/year}$	SE	"t"	
P305	5.8882	6.3657	0.88	NS
EDAD1	0.0014	0.0016	0.83	NS
FERT1	-0.0104	0.0022	-4.71	**

$\Delta_{A/year}$ = Annual phenotypic change, S.E= standard error, t=computed value for "t"

The regression slopes for AGE1 and FERT1 in table 6 would represent correlated genetic changes; In the first case, the regression coefficient is negative, therefore favorable, suggesting a downward trend in the age at which heifers reach puberty and are ready to enter to the reproductive program, the percentage magnitude of the change is, however, very low, representing only 0.41% of the population average ( $p < 0.001$ ). The regression coefficient for the genetic change in FERT1 was not significant; this seems to be associated with the low additive variability estimated in this population for this trait ( $p > 0.05$ ), however, the sign of the regression coefficient is favorable.

The phenotypic changes for P305 and AGE1 in table 7 were not significant ( $p > 0.05$ ), the change for FERT1 represents 1.69% of the population mean ( $p < 0.01$ ), this change is unfavorable, however, since it contributes to the reduction of the probability of pregnancy of the heifers, this implies reviewing the management factors, since favorable changes can be canceled by changes in management.

From the review by (Walsh et al., 2011), we conclude that in countries like the USA and the Netherlands, the genetic improvement of dairy cattle has been very accelerated; consequently, it is relatively easy to obtain replacement heifers of high or similar genotypic value and therefore it is justified to include in the selection programs health and reproductive traits. Furthermore, according to these authors, the trend should be that by the year 2050 it will be possible to maintain the same supply in milk production, reducing the number of cows. It is to be expected, therefore, an increase in the metabolic expenditure of these animals, which must be compensated through management and at the same time improve reproductive programs in order to avoid reproductive failures.

In the Venezuelan case, in recent years, a series of events have discouraged the dual-purpose cattle production sector, with a notable reduction in the operations of the dairy industry, this is reflected by the drop in the supply of fluid or powdered milk on the shelves in the market. Many dual-purpose livestock producers have dedicated their activity to cheese production, some of them have shifted their activities to buffalo farming.

## CONCLUSIONS

Milk yield in this population has a high heritability, with possibilities of improvement through the selection procedures in males and females.

The heritability for age at first service suggests enough variability to reduce the average age at first breeding through a selection process. This should improve the development of females in the growth phase prior to weaning and around puberty, in order to reduce the age for starting reproduction.

The age at first service could be considered in the elaboration of selection indices for the incorporation of replacement heifers in this population, due to a possible favorable correlated response due to adaptation to the tropical environment.

The heritability for fertility at first service is very close to zero and consequently little genetic change is to be expected if this trait is included in selection plans.

There is no evidence of genetic antagonism between milk yield and reproductive behavior measured by the association of this variable with age and fertility at first service.

The crisscrossing program, like the one developed in this population should be taken as a model for the consolidation of dual-purpose livestock, a fundamental axis for supplying the national demand and the country's milk and meat.

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## CONFLICTS OF INTEREST

None of the authors of this paper had a personal or financial interest with organizations that could inappropriately influence or bias the results of this research.

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