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Assessment of the Dairy Potential of Zebu in a Herd from Sancti Spíritus Province, Cuba

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ABSTRACT

Background: The growing need to produce food under the current conditions of Cuban livestock farming requires cattle that express adaptability and efficient production in tropical environments. **Aims**. To characterize milk yield of the White Zebu (Cb), Bermejo Zebu (Cbe) and Sardo Negro (SN) breeds at the Agro Production Cooperative (CPA) Juan González, Cabaiguán, Sancti Spíritus province. **Methods:** A database of 1,032 monthly milk-production records (PDC) from 108 Zebu cows, daughters of 36 sires, was used to characterize milk yield and lactation length (DLAC), to estimate repeatability (Γ) and heritability (h^2) of the traits, and to compute the genetic value (GV) of each cow and her parents. Random-regression models were applied to analyze milk production. **Results:** Accumulated production: 791 kg (Cb), 621 kg (Cbe), and 711 kg (SN). Lactation length (DLAC): ranged from 127 to 283 days. Heritability (h^2) across lactation: from 0.15\pm 0.01 to 0.26\pm 0.02. Genetic correlations between PDC measurements in adjacent time intervals were very close to unity, but later became negative at the ends and beginnings of lactation. Genetic value (VG) per PDC ranged from +2.6 kg to −1.4 kg. Cumulative production up to 250 days of lactation varied between −140 kg and +190 kg. **Conclusions:** This is the first study in Cuba assessing the dairy potential of Zebu cattle in a CPA in Sancti Spíritus. Broader participation by regional breeders is needed to increase the effectiveness and scope of selection programs.

Keywords: Zebu; milk production; repeatability; heritability; genetic value. (*Source*: *MeSH*)

INTRODUCTION

Cuban livestock farming has faced multiple challenges. What had been a predominantly Zebu population—reported by Funes Monzote (2023) to account for about 90% of the national herd in the mid-20th century—was transformed into a dairy population that, by 1990, included roughly

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60% Holstein crossbreeding as part of a national development program in state enterprises (Perez, 1999). More recently, major structural changes in animal ownership have taken place, with over 84% of animals now held by individual producers (Vázquez Hernández and Martínez Rivero, 2025); management and feeding practices have changed dramatically, making it evident that animals adapted to climate change are required (Torres Triana, 2025).

In this context, Zebu and Creole cattle have historically demonstrated adaptation to the Cuban environment and continue to exhibit adequate productive performance. However, there is no evidence in Cuba regarding the dairy potential of Zebu cattle. Consequently, in 2022, the first individual performance-recording program for milk production and calf weaning weight in Zebu animals was implemented under the management conditions at CPA Juan González.

After one year of data collection, a database was compiled and used to estimate the dairy potential of these animals and the extent of existing genetic variation. The aim was to present the first parameter estimates in Cuba for this breed maintained under relatively non-specialized management conditions; the results are reported in this study.

MATERIALS AND METHODS

CPA Juan González is located in the municipality of Cabaiguán at 22.07623° N (22° 4′ 34″ N) and 79.56853° W (79° 34′ 7″ W), at 154 m above sea level. The farm covers 1,582.07 ha, of which 986 ha are dedicated to Zebu cattle; animals have year-round access to drinking water from the Santa Lucía River, small reservoirs, and wind-driven wells. Predominant natural grasses include Mexican grass (*Paspalum notatum*), faragua (*Hyparrhenia rufa*), and camagüeyana (*Bothriochloa pertusa*); forages comprise sugarcane (*Saccharum officinarum*), forage cassava (*Manihot esculenta*) and King Grass (*Pennisetum purpureum* × *P. typhoides*). All paddocks provide natural shade from guasimal (*Guazuma ulmifolia*) and carob (*Ceratonia siliqua*), and include silvopastoral areas planted with eucalyptus (*Eucalyptus*) and mango (*Mangifera indica*). Milking is manual, performed once daily with calf assistance; weaning is based on the dam’s body condition and typically occurs at seven months of age. Breeding is by natural mating using sires registered in the National Register of Pure Breeds.

The database comprised 1,032 monthly milk-production records (PDC) collected from January 2023 to September 2024 for 108 Zebu cows, daughters of 36 sires. Records corresponded to three groups: White Zebu (Cb; 635 PDC from 62 cows), Bermejo Zebu (Cbe; 282 PDC from 34 cows), and Sardo Negro Zebu (SN; 115 PDC from 12 cows). The PDC underwent a thorough editing process to validate primary production data and each animal’s pedigree, which was cross-checked with official information from the Genetics and Livestock Control Department of the provincial delegation of the Ministry of Agriculture.

Mixed linear random-regression models (RR) were used to estimate genetic parameters and the genetic value (VG_k) of each cow and their parents for weekly milk yield and cumulative production at different stages of lactation; the statistical model was as follows:

$$\boldsymbol{Y_{ijklm} = FPDC_i + f(dim_w{:}\, r)_j + r(a; dim_w{:}\, q)_k + perm_l + e_{ijklm}}$$

where:

Y_{ijklm} denotes the i^{th} observation of the dependent variable (PDC) along the lactation trajectory, expressed in weeks (dim_w).

$FPDC_i$ is a fixed effect for the herd–year–month of recording (test month); the model also includes the animal's breed and parity (number of calvings).

$f(dim_w{:}\ r)_j$ denotes the j^{th} fixed covariate of the population-level lactation trajectory expressed in weeks (dim_w), modeled using a Legendre (Φ_r) polynomial of order r=3.

$r(a;\ dim_w{:}\ q)_k$ are the k-th random-effect vectors representing the animal's additive genetic function across the covariates dim_w: q, modeled by a Φ_r of order r=1, 2. This term represents the random deviation of each animal from the previously specified population-level curves, originating from additive genetic effects.

$perm_l$ represents the random effect accounting for repeated monthly milk-production records (PDC) within the same i^{th} animal with available data.

e_{ijklm} is the random residual error common to all i^{th} observations.

The model of order r=2 provided the best fit to the data according to the information criteria LogL, AIC and BIC, as indicated by the Echidna software (Gilmour, 2021). Convergence was reached in nine iterations, and the solution supplied the elements necessary to estimate the genetic parameters and the genetic value (GV) of all animals with records and their ancestors without information. The results from this model yielded a matrix of random-regression coefficients (Kg) which, when multiplied by the relationship matrix (A), produce the (co)variance components, according to V(a)= Kg; $\otimes$ A for additive genetic variances; the permanent-environment variance is $V(p)=I\sigma^2_p$ and the residual error is V(e)= residual.

With these elements, an additional procedure is required to estimate the basic parameters throughout lactation, expressed as weekly milk production dim_w (days in milk):

$\boldsymbol{\sigma^2_{a_i} = \Phi_i K_g \Phi_i'}$For the genetic variances of each genotype across the lactation trajectory dim_w

$\boldsymbol{\sigma_{a_{ij}} = \Phi_i K_g \Phi_j'}$For the genetic (co)variances between each week in milk (dim_w)

From these indicators and using classical formulas, heritability (h^2) and genetic correlations (r_g) were estimated for each PDC along the trajectory of the i^{th} dim_w in the polynomial coefficients, taking into account the corresponding permanent-environment and residual variances.

$$\mathbf{h^2_i} = \frac{\boldsymbol{\Phi_i K_p \Phi_i'}}{\boldsymbol{\Phi_i K_g \Phi_i' + \sigma^2_{p_i} + \sigma^2_{e_i}}} \text{ y } \mathbf{r_{g_{ij}}} = \frac{\boldsymbol{\Phi_i K_g \Phi_j'}}{\sqrt{\boldsymbol{\Phi_i K_g \Phi_i' * \Phi_j K_g \Phi_j'}}}$$

Using the solution of this model, the genetic function f_{a_i}= [a_o a_s a_q] was estimated for each animal, in which a_o a_s a_q represent the elements of a quadratic equation; these can be combined with the individual elements of Φ_i to estimate GVa_i for cumulative milk production at different points of lactation.

$$\mathbf{GVa_i = 7 * \sum_{PDC=1}^{n} \Phi_i f_{a_i}}$$

This GVa_i was estimated for cumulative milk at 50, 100, 150, 200, and 250 days of lactation.

RESULTS AND DISCUSSION

All effects of breed, herd–year–month of calving, parity, and the random cow effect were highly significant ($p < 0.001$). The lactation curve showed stability during the first 90 days; cumulative production over the entire lactation reached 791 kg, 621 kg, and 711 kg for Cb, Cbe, and SN, respectively. Although calf birth weight (34.1 kg) and weaning weight (171.8 kg) were not the focus of the study, they were used to estimate calf milk intake, which was 5.2 kg of milk per kg of live weight, allowing a generalization that the expected milk yield potential of this sample was 1,400 kg, with a range from 830 kg to 2,420 kg. These results are comparable to those reported by Rota (2023) for herds in Camagüey province, where 305-day milk yields were 1,533 kg, 1,329 kg, and 1,490 kg for the Mambí, Siboney, and Holstein breeds, respectively. They also fall within reported ranges for the Sardo Negro in Mexico (1,300 kg in 240 days of lactation; Domínguez-Viveros *et al.*, 2023) and 2,125 kg in Holstein × Gyr crossbred females (Torres *et al.*, 2022).

The random-regression results showed that the model of order r=2 provided the best fit to the data according to the information criteria LogL, AIC, and BIC (Gilmour, 2021). The estimates of h^2, repeatability (Γ), and genetic correlations r_g along lactation are presented in Figure 1.

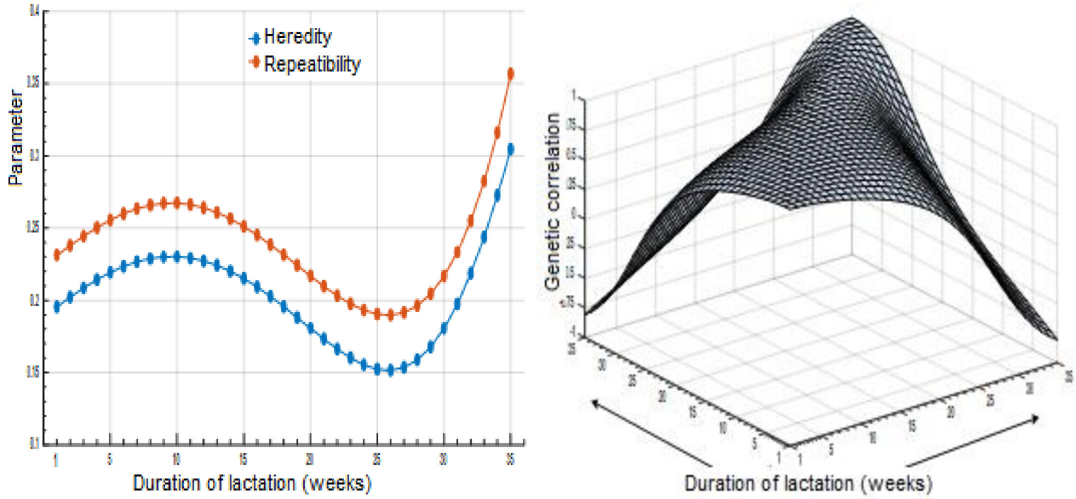

Figure 1. Evolution of heritability and repeatability (left) and genetic correlations (right) of weekly milk production in Zebu cows under the cooperative's conditions.

The estimates of h^2 ranged from $0.15_{\pm 0.01}$ to $0.23_{\pm 0.03}$, showing a decreasing trend during the first 25 weeks; Γ followed the same pattern. The h^2 value was similar to that reported by Hernández and León (2020) for Siboney cattle from three farms in western Cuba ($0.16_{\pm 0.01}$) and to the values reported by Pereira *et al*. (2021) for Gyr cattle in Brazil (0.15 to 0.21). The r_g between PDC measurements in adjacent or nearby time periods are very close to unity (vertical position on the right side of Figure 1); however, they fall to significantly negative levels between the end and the beginning of lactation. These results were similar to those found by Pereira *et al*. (2021) in Gyr cattle in Brazil.

This type of response can have several implications:

- It indicates genetic variation in the kind of lactation and, consequently, in its persistence, measured as the relationship between production levels at different stages of lactation; both types of behavior are highly useful in breeding programs (Mrode and Pocrnic, 2023).
- It can change the ranking (order of merit) of sires at different stages of lactation (Menéndez Buxadera *et al*., 2022).

In this study, phenotypic expressions of PDC were used over 35 weeks, which generated a large number of genetic parameters and GV_{ai} for all animals and a genetic-correlation matrix of 595 elements. Under these circumstances, the use of a principal component analysis (PCA) is recommended; its main advantage is to estimate a set of linear combinations that retain most of the variance of the original data (Hair *et al*., 2009). In this case, PCA was applied to the r_g matrix shown on the right side of Figure 1.

The results of this procedure indicated that only two eigenvectors (VP_K) captured the entirety of the genetic variance of the 35 original estimates of GV_{ai} (Figure 2).

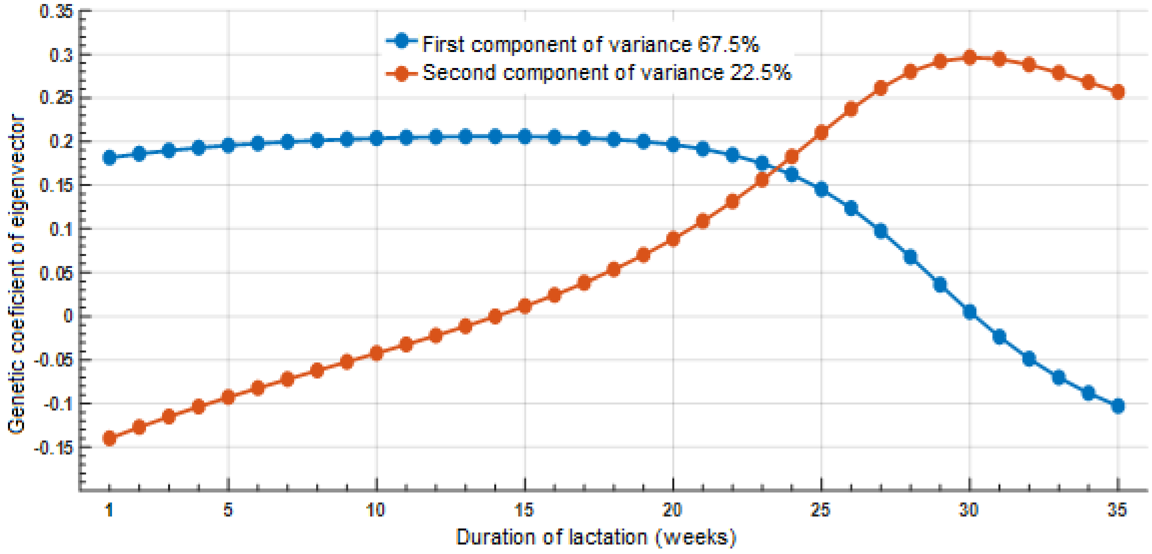

Figure 2. Results of the two principal components of the genetic-correlation matrix for weekly milk production in Zebu cows.

The first principal component explains 68% of the genetic variance, which remains practically unchanged between weeks 1 and 25, while the second shows an opposite pattern with greater importance at the end of lactation.

Another feature of PCA is that the coefficients of the VP_K are uncorrelated, so they can be summed and used as weighting factors, and an index (I_{PDC_k}) can be constructed. In this way, with only two values all the original genetic variances of the genetic merit of each PDC in this example are captured. This I_{PDCk} was estimated as follows:

$$\mathbf{I_{PDC_k} = \sum_{PDC=1}^{35} EV_{ij} GV_{ik}}$$

Where the e_{vij} and GV_{ik} correspond to the eigenvectors and the genetic values of the dataset expressed in standardized form. Note that I_{PDC_k} incorporate the 35 original values and the interpretation can be simpler. According to the recommendations of Mrode and Pocrnic (2023), selection based on this I_{PDC_k} can increase milk production throughout lactation. The sample studied showed substantial genetic variability in GVai and in I_{PDC_k} (Figure 3).

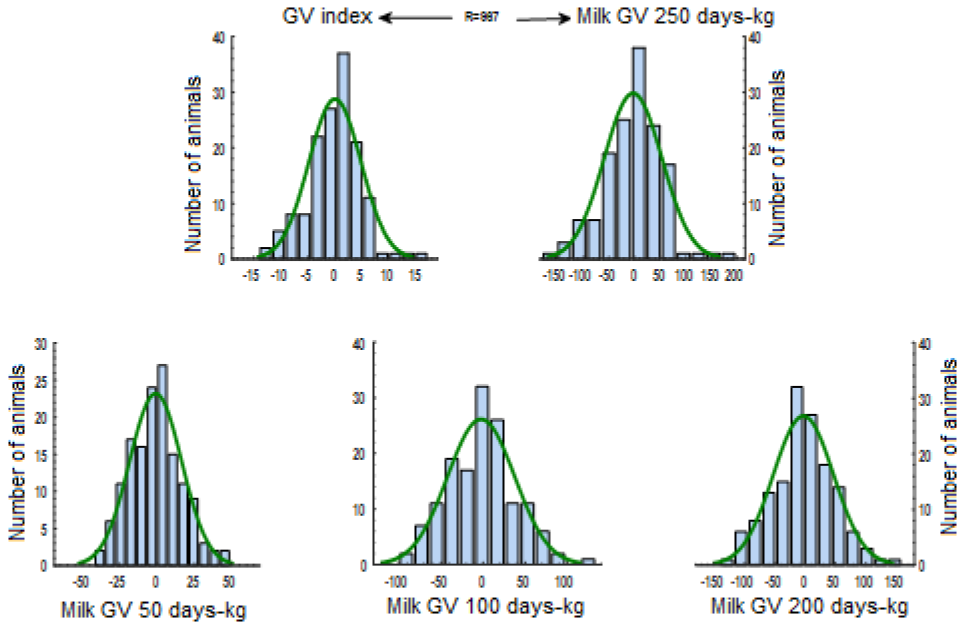

Figure 3. Variability in genetic values across different lactation stages and in the index

The differences between the best and worst animals for accumulated milk at each stage, particularly at 250 days of lactation, ranged from +190 kg to −149 kg, which is practically half of the previously reported mean productions. Even though these were reduced to only five indicators, a question may arise about which ones should be used to take positive or negative selection action.

The results of the I_{PDCK} show a distribution very similar to the previous ones and a correlation of 0.983, so the top animals by the index are also the top animals for total production; therefore, the breeder can rely on the latter result. Finally, by applying the procedures described in Materials and Methods it is possible to produce a better representation of the full range of results to assist the breeder in their work; to this end, Figure 4 was prepared showing the response curves of the GV_{ai} for the three best and three worst animals across the entire lactation.

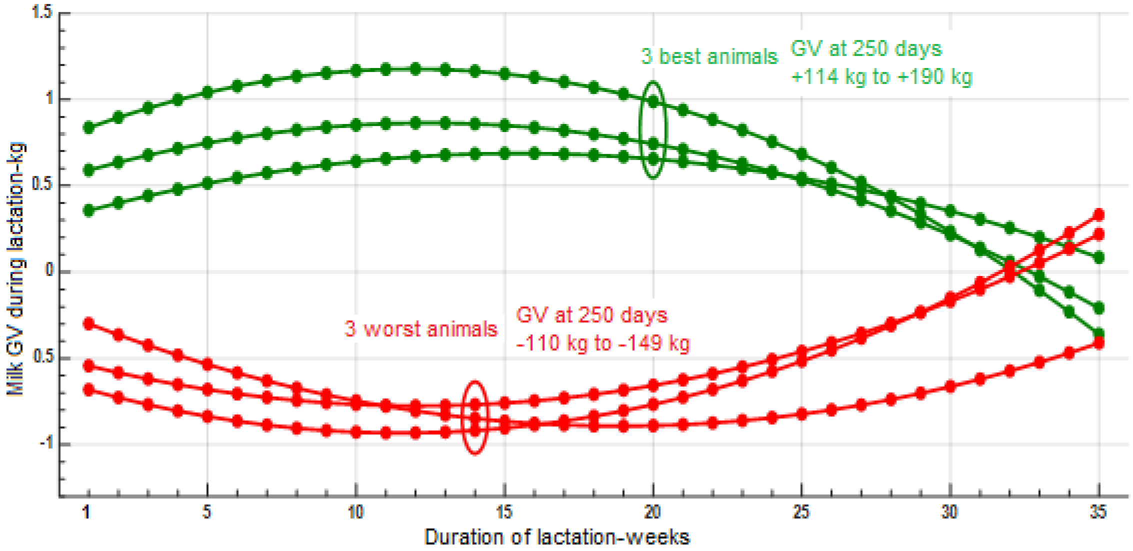

Figure 4. Evolution of the genetic value of six extreme animals throughout lactation

Representation of what breeders observe daily at milking: the differences between cows and how persistence in PDC levels is highlighted during the first 25 to 30 weeks of lactation.

CONCLUSIONS

This work constitutes the first evidence of the genetic potential for milk production of a Zebu herd in a CPA in the province of Sancti Spíritus. However, the participation of more breeders from the region is needed to increase the scope of the selection work. Given the country's difficult overall situation, it is also recommended to include individual breeders under strict, verifiable controls to expand the use of the Zebu breed nationwide; this would help ensure more productive animals which are better adapted to the new conditions of Cuban livestock farming.

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AUTHOR CONTRIBUTION STATEMENT

Research conception and design: AMB, RB, JCV, AMV, LPO; data analysis and interpretation: AMB, RB, JCV, AMV, LPO; writing of the manuscript: AMB, RB, JCV, AMV, LPO.

CONFLICT OF INTEREST STATEMENT

The authors state there are no conflicts of interest whatsoever.