Original

Multi-Trait Selection in Cuban Dairy Cattle

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ABSTRACT

Aim. Perform a multi-trait selection of dairy production, reproduction, and longevity traits by creating selection indexes (SI) through principal component analysis. **Materials and methods:** Phenotypic and genealogical data from female Mambí de Cuba cattle (3/4 Holstein 1/4 Zebu), Siboney de Cuba cattle (5/8 Holstein 3/8 Zebu), and Holstein cattle were used for multi-trait selection of dairy production, reproduction, and longevity traits, by creating selection indices (SI) through principal component analysis (PCA). A multi-trait animal model was used to estimate the parameters and genetic values (GV) of 5 445 Mambí de Cuba cows, 6,425 Siboney de Cuba cows, and 1 571 Holstein cows, for accumulated milk production up to 305 days (GV_{L305}), lactation duration (GV_{DL}), age at first calving (GV_{AFC}), calving interval (GV_{CGI}), lifetime accumulated milk (GV_{LM}), and productive life (GV_{PL}). **Results:** The linear correlations between the GVs in Mambí cows with each principal component showed that GV_{L305}, GV_{LM}, and GV_{DL} are highly related to PC_1, while GV_{CI} was more associated with PC_2. "GV_{PL} and GV_{AFC} were related to PC_3. In Siboney de Cuba, GV_{L305} and GV_{DL} were highly related to PC_1, while GV_{CGI}, GV_{LM}, and GV_{AFC} were more associated with PC_2. GV_{PL} and GV_{AFC} were related to PC_3. In Holstein, GV_{L305}, GV_{DL}, and GV_{LM} were related to PC_1, while GV_{CGI} and GV_{PL} were related to PC_2. **Conclusion:** In dairy cattle, it is possible to construct selection indices based on PC_{1-3}. These showed genetic variation, so they could be used in a multi-trait selection program.

Keywords: principal components, selection indexes, genetic improvement (**Source**: *AGROVOC)*

INTRODUCTION

The two basic tools available to the geneticist and the rancher to help increase the productivity of their herd in an animal genetic improvement program are the combination of mating systems and selection (Ossa, 1998).

Traditional selection indexes (Hazel, 1943) are used to select animals based on linear combinations of genetic values with economic weights. Although this methodology has been used by various authors (Betancur-Zambrano *et al.*, 2012; Peripolli *et al*., 2016), it is sometimes difficult to obtain economic weights. Therefore, the use of principal component analysis (PCA) has recently been incorporated into the construction of selection indexes in dairy cattle (Bignardi *et al*., 2012; Khan *et al*., 2013). PCA analysis is thought to allow for the reduction of the dimensionality of variables, facilitates the interpretation of data into a few principal components, and identifies the type of relationship between the original variables.

Selection indexes are widely used, with each country placing different emphasis on each of the included traits; generally, they combine traits of production, reproduction, conformation, type, health, longevity, and fertility (Betancur-Zambrano *et al*., 2012).

Although several studies have demonstrated that selection solely for milk production has negative effects on udder health (Heringstad *et al*., 2003) and reproductive performance (Haile-Mariam *et al.*, 2003; Kadarmideen *et al.*, 2003), in Cuban dairy cattle, the selection criterion used is solely milk production. "Therefore, this study aimed to perform a multi-trait selection of dairy production, reproduction, and longevity traits by creating selection indexes (SI) through principal component analysis.

MATERIALS AND METHODS

Information on milk production and reproduction, recorded in the Livestock Control System (SISCOP), was used for Mambí de Cuba cows (¾ Holstein ¼ Zebu) that calved between 1986 and 2016, Siboney de Cuba cows (5/8 Holstein 3/8 Zebu) that calved between 1984 and 2016, and Holstein cows that calved between 1984 and 2016. These cows were located in three farms (The Matanzas Genetic Project, in Matanzas Province, Los Naranjos in Mayabeque, and Camilo Cienfuegos in Pinar del Río) in the western region of the Republic of Cuba.

Records of the living animals as well as those that had been culled were used. From the milk production data file (living + culled), the following traits were obtained: accumulated milk production up to 305 days (L305), lactation duration (DL), and age at first calving (AFC1). Meanwhile, from the reproduction data file (living + culled), the calving interval (CGI) was calculated. From the culling data file for milk production, lifetime accumulated milk (LM) was calculated; as well as the longevity trait known as productive life (PL), determined as the months from the first to the last calving.

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Data Editing and Contemporary Groups

To ensure greater accuracy in the estimation of genetic parameters, data with low frequencies were removed, such as lactations with less than 30 days, ages at first calving under 24 months, milk productions under 100 kg, CSI and CGI under 24 days, and ICC under 300 days. Lactations beyond the tenth were grouped into this last category. The pedigree file consisted of a total of 153 963 individuals.

The least squares method was used in a general linear model (GLM) through the statistical package SAS (2010) version 9.3 (SAS Institute, Cary, NC, USA) to define the significant fixed effects (P<0.01) to be included in the contemporary group (CG). The combination of herd-year-season of calving was considered as CG, and groups with fewer than 3 animals were removed. Two calving seasons were determined: the rainy season (from May to October) and the dry season (from November to April).

Table 1 shows the number of observations used in each data file, the number of animals, the number of contemporary groups (CG), the calving years (CY), and the means and standard deviations for each trait.

Table 1 Number of observations (N), calving years (CY), mean and standard deviation (SD) in milk production, reproduction, and longevity traits of Mambí de Cuba, Siboney de Cuba, and Holstein cows.

Traits	N	Cows	Bulls	CG	CY	Mean	SD
Mambí de Cuba							
L305 (kg)	46 260	13 945	249	4 410	1987-2016	1861.19	857.06
DL (days)	46 260	13 945	249	4 410	1987-2016	280.83	93.20
LM (kg)	10 549	10 549	242	2 951	1984-2015	5591.95	4904.87
AFC (months)	10 542	10 542	226	2 509	1987-2015	51.48	19.75
CGI (days)	54 113	15 339	271	6 104	1985-2016	201.80	150.12
PL (months)	8 072	8 072	235	2 474	1984-2014	49.84	29.19
Siboney de Cuba							
L305 (kg)	47 567	17 235	348	3 292	1987-2016	1545.55	805.62
DL (days)	47 567	17 235	348	3 292	1987-2016	271.89	83.07
LM (kg)	13 171	13 171	339	2 553	1984-2015	3894.70	3741.95
AFC (months)	14 383	14 383	332	1 899	1987-2016	45.10	15.07
CGI (days)	47 032	14 118	313	3 915	1986-2016	232.51	170.70
PL (months)	8 437	8 437	228	1 586	1984-2014	47.46	26.77
Holstein							
L305 (kg)	29 480	25 959	672	4 110	1987-2015	2415.99	1160.94
DL (days)	29 480	25 959	672	4 110	1987-2015	290.99	78.74
LM (kg)	31 386	31 386	718	5 235	1984-2015	2833.75	1566.29
AFC (months)	21 695	21 695	585	3 025	1987-2015	34.81	12.00
CGI (days)	12 060	3 721	353	2 786	1986-2015	262.25	187.79
PL (months)	1 920	1 920	284	897	1984-2013	46.83	28.70

L305: Accumulated milk production up to 305 days; LD: Duration of lactation; LM: Leche acumulada por vida; AFC: Age at first calving; CGI: Calving gestation interval; PL: Productive life

The ASREML program (Gilmour *et al*., 2003) was used to estimate genetic values. The following multi-trait animal model was used:

$$
\begin{bmatrix} y_1 \\ y_2 \\ y_3 \\ y_4 \\ y_5 \\ y_6 \end{bmatrix} = \begin{bmatrix} x_1 & 0 & 0 & 0 & 0 & 0 \\ 0 & x_2 & 0 & 0 & 0 & 0 \\ 0 & 0 & x_3 & 0 & 0 & 0 \\ 0 & 0 & 0 & x_4 & 0 & 0 \\ 0 & 0 & 0 & 0 & x_5 & 0 \\ 0 & 0 & 0 & 0 & 0 & x_6 \end{bmatrix} \begin{bmatrix} b_1 \\ b_2 \\ b_3 \\ b_4 \\ b_5 \\ b_6 \end{bmatrix} + \begin{bmatrix} z_1 & 0 & 0 & 0 & 0 & 0 \\ 0 & z_2 & 0 & 0 & 0 & 0 \\ 0 & 0 & z_3 & 0 & 0 & 0 \\ 0 & 0 & 0 & z_4 & 0 & 0 \\ 0 & 0 & 0 & 0 & z_5 & 0 \\ 0 & 0 & 0 & 0 & 0 & z_6 \end{bmatrix} \begin{bmatrix} a_1 \\ a_2 \\ a_3 \\ a_4 \\ a_5 \\ a_6 \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \\ e_3 \\ e_4 \\ e_5 \\ e_6 \end{bmatrix}
$$

Where:

y_i = vector of observations for the *i-th* trait, b_i = vector of fixed effects (herd-year-season of calving and age at calving as a linear and quadratic covariate) for the *i-th* trait, a_i = vector of random animal effects for the *i-th* trait.

e_i = vector of random residual effects for the *i-th* trait, x_i and Z_i = design matrices that relate the data to the fixed and random effects, respectively

The estimated GV were imported into the SAS statistical package (2010) version 9.3 (SAS Institute, Cary, NC, USA) and subsequently all files were merged, leaving only those cows that had information on the GV for all traits studied. The final file included a total of 5 445 Mambí de Cuba cows, 6 425 Siboney de Cuba cows, and 1 571 Holstein cows.

The principal component analysis was performed using the SPSS statistical package (2002) version 11.5. It was conducted as a way to condense or summarize the information contained in several original variables (in this case the GV) into a smaller set of new composite dimensions or variants called principal components, with minimal loss of information, and to explore the relationships between the obtained GV (GV_{L305}, GV_{DL}, GV_{LM}, GV_{AFC}, GV_{CGI}, GV_{PL}) to explain the data structure (Hair *et al*., 2009).

Due to differences in measurement units, the GVs for all traits were standardized using the standard normal distribution ('z'). The Kaiser criterion (1960) was used to select the principal component that explains the greatest genetic variation in the data. This criterion considers only those principal components with self-values greater than one. The value of a principal component is associated with the variance of all the traits included in the principal component. Each eigenvalue is associated with a unit vector called an eigenvector. Eigenvectors represent the strength and direction of the variance of each trait with the principal component. In this study, a variable correlation matrix was used to obtain the eigenvalues.

By using the standardized GVs in this analysis, each principal component can generate a new value called the principal component score, which is the sum of the standardized GV of each trait's weight by its respective standardized scoring coefficient (SSC). That way, the principal

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component can be used as an index to evaluate animals for multiple traits. The standardized scoring coefficients of each GV in each principal component were obtained using the following formula:

$$SSC_{ij}= \frac{eigenvector_{ij}}{\sqrt{eigenvalue_{j}}}$$

Where:

SSC_{ij} = Standardized scoring coefficients of the GV for each trait in the *j-th* principal component

The principal component score (index) was calculated as: $PC_{jl}=\sum SSC_{ij} VG_{il}$

Where:

CP_{jl} = Principal component score (index score) for the *l-th* animal in the *j-th* principal component, SSC_{ij} = Standardized scoring coefficients of the GV for the *i-th* trait in the *j-th* principal component,

VG_{il} = Standardized estimated genetic value of the *i-th* trait in the *l-th* animal

RESULTS AND DISCUSSION

The construction of traditional selection indexes is sometimes difficult due to the lack of economic weights, and these are also subject to constant market variations. An alternative was to incorporate principal component analysis in the construction of selection indices. Buzanskas *et al*. (2013) stated that the use of principal components (PC) is a methodology to construct linear combinations among the genetic values of traits available in a database, taking into consideration the eigenvalues of the principal component and the eigenvectors of the traits in each principal component, which are measures of variability. One of the advantages of its use is that traits with low heritability estimates, which are rarely considered in a direct selection process, can be included in the principal component.

In the Mambí de Cuba, principal components 1 and 2 (PC_1, PC_2) met the Kaiser criterion (Table 2), and component 3 (PC_3) presented a value close to 1, so it was also selected. Of the 6 original dimensions (e.g., VG_{L305}, VG_{DL}, VG_{LM}, VG_{AFC}, VG_{CGI}, VG_{PL}), 69.6% of the total variance of the GV was explained by PC_1 to PC_3. PC_1 made the greatest contribution, with 33.5% of the total variance. In the Mambí de Cuba, principal components 1 and 2 (PC_1, PC_2) met the Kaiser criterion (Table 2), and component 3 (PC_3) presented a value close to 1, so it was also selected. In the Siboney de Cuba, the first three principal components (PC_1, PC_2, PC_3) met the Kaiser criterion. Meanwhile, in the Holstein, the first two principal components (PC_1, PC_2) met the Kaiser criterion. They accounted for 53.7% of the total variance of the GV.

Table 2. Eigenvalues for each principal component, total and cumulative proportion of additive genetic variance, from the first to the sixth principal component (PC$_{1-6}$), in Mambí de Cuba, Siboney de Cuba, and Holstein cows

Components	Eigenvalues		
	Total	Additive genetic variance %	Cumulative %
Mambí de Cuba			
PC$_1$	2.015	33.5	33.5
PC$_2$	1.173	19.5	53.1
PC$_3$	0.988	16.4	69.6
PC$_4$	0.869	14.4	84.0
PC$_5$	0.589	9.82	93.9
PC$_6$	0.366	6.09	100
Siboney de Cuba			
PC$_1$	1.945	32.414	32.414
PC$_2$	1.252	20.862	53.276
PC$_3$	1.055	17.585	70.861
PC$_4$	0.765	12.743	83.604
PC$_5$	0.662	11.038	94.642
PC$_6$	0.321	5.358	100.000
Holstein			
PC$_1$	2.098	34.972	34.972
PC$_2$	1.127	18.781	53.753
PC$_3$	0.974	16.232	69.985
PC$_4$	0.938	15.632	85.617
PC$_5$	0.509	8.479	94.096
PC$_6$	0.354	5.904	100.000

Khan *et al*. (2013) in Vrindavani cattle (50 to 75% Holstein-Friesian, Brown Swiss, Jersey - 25 to 50% Hariana cattle) in India, noted that the first 3 principal components accounted for 93.08% of the total variance. In the Nelore breed, the first three principal components covered 100% of the additive genetic variance of nine traits related to meat production (Boligon *et al*., 2013). These results are probably due to the fact that, in the first case, only traits related to milk production were used (partial milk yields at 100, 170, and 240 days in the first lactation, in the second lactation, and their respective total yields), and in the second case, only traits related to meat production were used.

The results of the present study are consistent with others that have also demonstrated that with the use of principal component analysis (PCA), the dimensionality of traits can be reduced. Bignardi *et al*. (2012) in Holstein cows, found that only two principal components (PC) were required to summarize the genetic variation of the bulls across the 10 evaluated traits (10 monthly milk yields). In Canchim cows, Buzanskas *et al*. (2013) reported that 73.37% of the total variance of the GV for three reproductive traits and one growth trait was covered by two principal components (PC). Moreover, Agudelo-Gómez *et al*. (2015) observed that the first three principal components (PC) accounted for 65.78% of the original variance of the genetic values for 270-day

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milk production, age at first calving, weaning weight, and weight at different ages (12, 18, and 24 months).

The linear correlations between the GV of the studied traits with each principal component (Table 3) showed that in the Mambí de Cuba, the traits related to milk production and lactation duration were highly related to PC_1, while the reproductive trait was more associated with PC_2. The PL and AFC were related to PC_3. Thus, PC_1 could be interpreted as a genetic index related to milk production traits and lactation duration, while PC_3 could be a genetic index related to longevity and age at first calving. In this sense, it might be better to select the animals for CGI, considering only their GV instead of using the PC_2 index.

Table 3. Linear correlations of the standardized GV with principal components 1 to 3 (PC_{1-3}) in Mambí de Cuba, Siboney de Cuba, and Holstein cows

GV	PC_1	PC_2	PC_3
Mambí de Cuba components			
GV_{L305}	0.843	0.067	0.030
GV_{DL}	0.842	0.189	-0.034
VG_{LM}	0.641	-0.457	0.027
GV_{CGI}	0.368	0.633	0.066
VG_{PL}	0.141	-0.572	0.635
GV_{AFC}	-0.169	0.444	0.760
GV	**Mambí de Cuba components**		
	PC_1	PC_2	PC_3
GV_{L305}	0.867	-0.100	0.004
GV_{DL}	0.881	-0.005	-0.043
VG_{LM}	0.405	0.586	-0.320
GV_{CGI}	0.448	-0.654	0.039
VG_{PL}	0.083	-0.015	0.917
GV_{AFC}	0.214	0.686	0.331
GV	**Mambí de Cuba components**		
	PC_1	PC_2	
GV_{L305}	0.842	-0.159	
GV_{DL}	0.717	0.337	
GV_{LM}	0.728	-0.478	
GV_{CGI}	0.284	0.564	
GV_{PL}	0.255	0.639	
GV_{AFC}	-0.446	0.184	

The linear correlations between the GV of the studied traits in Siboney de Cuba cows with each principal component showed that traits related to milk production and lactation duration were highly related to PC_1, while CGI, LM, and AFC were more associated with PC_2. The PL was related to PC_3. Thus, PC_1 could be interpreted as a genetic index related to milk production traits and lactation duration, while PC_2 could be a genetic index related to reproduction and lifetime milk production. In PC_3, it would be better to select the animals considering only their GV for PL, instead of using an index, given that the correlations of the GV of the other traits with this component were low.

The linear correlations between the GV of the studied traits in Holstein cows with each principal component showed that traits related to milk production and lactation duration were highly related to PC_1, while CGI and PL were more associated with PC_2.

The weights of these indices are standardized scoring coefficients (SSC) for each standardized GV of the cows of the three studied breeds (Table 4). The highest absolute value of the SSC is of the greatest relative importance of the standardized GV in the principal component. This relevance is explained by the higher linear correlation between the traits and the principal component (Table 3).

The principal component score (index value) for every Mambí de Cuba animal, in each principal component, was calculated as:

$PC_1 = 0.418 \ (GV_{L305}) + 0.418 \ (GV_{DL}) + 0.318 \ (GV_{LM})$

$PC_3 = 0.643 \ (GV_{PL}) + 0.770 \ (GV_{AFC})$

The principal component score (index value) for every Siboney de Cuba animal, in each principal component, was calculated as:

$PC_1 = 0.446 \ (GV_{L305}) + 0.453 \ (GV_{DL}) + 0.318 \ (GV_{LM})$

$PC_2 = 0.469 \ (GV_{LM}) - 0.522 \ (VG_{CGI}) + 0.548 \ (VG_{AFC})$

The principal component score (index value) for each Holstein animal, in each principal component, was calculated as:

$PC_1 = 0.401 \ (GV_{L305}) + 0.342 \ (GV_{DL}) + 0.347 \ (GV_{LM})$

$PC_2 = 0.500 \ (GV_{CGI}) + 0.567 \ (VG_{PL})$

Table 4. Standardized scoring coefficients (SSC) of every estimated standardized GV for all traits in each principal component (PC_{1-3}), in Mambí de Cuba, Siboney de Cuba, and Holstein cows

GV	SSC (PC_1)	SSC (PC_2)	SSC (PC_3)
	Mambí de Cuba		
GV_{L305}	0.418	0.057	0.030
GV_{DL}	0.418	0.161	-0.034
GV_{LM}	0.318	-0.389	0.028
GV_{CGI}	0.183	0.539	0.067
GV_{PL}	0.070	-0.487	0.643
GV_{AFC}	-0.084	0.379	0.770
	Siboney de Cuba		
GV_{L305}	0.446	-0.080	0.004
GV_{DL}	0.453	-0.004	-0.041
GV_{LM}	0.208	0.469	-0.303
GV_{CGI}	0.230	-0.522	0.037

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GV$_{PL}$	0.043	-0.012	0.869
GV$_{AFC}$	0.110	0.548	0.313
	Holstein		
GV$_{L305}$	0.401	-0.141	
GV$_{DL}$	0.342	0.299	
GV$_{LM}$	0.347	-0.424	
GV$_{CGI}$	0.135	0.500	
GV$_{PL}$	0.122	0.567	
GV$_{AFC}$	-0.213	0.164	

The selection of Mambí de Cuba cows for GV$_{L305}$, GV$_{LM}$, and GV$_{DL}$ through PC$_1$ could be carried out separately from the selection for GV$_{AFC}$ and GV$_{PL}$ through PC$_3$, considering the linear correlation between the GVs and each principal component (Table 3). Selection for CGI can be done directly by its genetic value. These results also correspond with the genetic correlations between the studied traits (Hernández *et al*., 2011), which revealed a medium genetic correlation between L305, LM, and DL (0.33 to 0.46) and between AFC and PL (-0.56); while the genetic correlations between these five traits and CGI were low (between 0.12 and 0.26), so they will change almost independently.

While the selection of Siboney de Cuba cows for GV$_{L305}$ and GV$_{DL}$ through PC$_1$ could be performed separately from the selection for GV$_{CGI}$, GV$_{AFC}$, and GV$_{LM}$ through PC$_2$, considering the linear correlation between the GVs and each principal component (Table 3). Selection for PL can be done directly by its genetic value.

In Holstein cows, the selection for GV$_{L305}$, GV$_{LM}$, and GV$_{DL}$ through PC$_1$ could be carried out separately from the selection for VG$_{CGI}$ and GV$_{PL}$ through PC$_2$, considering the linear correlation between the GVs and each principal component (Table 3).

Using principal component analysis, animals can be selected based on only two generated scores (in Mambí de Cuba by PC$_1$ and PC$_3$; and in Siboney de Cuba and Holstein by PC$_1$ and PC$_2$) instead of the six genetic values. According to Buzanskas *et al*. (2013), when this approach is used, animals can be selected in a balanced manner since the scores of each principal component are linear combinations of all the genetic values of the evaluated traits, and not empirical weights typically used in improvement programs.

In Mambí de Cuba cows, PC$_1$ can be considered a genetic index for milk production because it favors genetically superior animals for GV$_{L305}$, GV$_{LM}$, and GV$_{DL}$; while PC$_3$ can be a genetic index related to longevity and age at first calving. The greater variability for GV$_{L305}$, GV$_{LM}$, and GV$_{DL}$ can be explained by the fact that currently, emphasis is only placed on selection for GV$_{L305}$ and a high selection intensity is not applied. Significantly, negative GV$_{AFCs}$ in PC$_1$ are interesting because the objective is to reduce the age of first calving, as this trait has a medium genetic

correlation with lifetime milk production (-0.37) and longevity (-0.56). So, they will change together in some way, but in opposite directions.

In Siboney de Cuba cows, PC_1 can be considered a genetic index for milk production because it favors genetically superior animals for VGL305 and GV_{DL}; while PC_2 can be a genetic index related to reproduction and lifetime milk production. In Holstein cows, PC_1 can be considered a genetic index for milk production because it favors genetically superior animals for GV_{L305}, GV_{LM}, and GV_{DL}; while PC_2 can be a genetic index related to reproduction and longevity.

CONCLUSION

In dairy cattle (Mambí de Cuba, Siboney de Cuba, and Holstein), the construction of selection indices based on PC_{1-3} is possible. They underwent genetic variation, so they could be used in a multi-trait selection program.

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AUTHOR CONTRIBUTION STATEMENT

Research conception and design: AHR, RPLS, data analysis and interpretation: AHR, RPLS, redaction of the manuscript: AHR, RPLS.

CONFLICT OF INTEREST STATEMENT

The authors state there are no conflicts of interest whatsoever.