Volume 58, January-December 2024, ISSN: 2079-3480

ANIMAL SCIENCE

CUBAN JOURNAL OF AGRICULTURAL SCIENCE

Journal site: https://cjascience.com Cu-ID: https://cu-id.com/1996/v58e02

SELECTION INDEX BY FINAL AND WEANING WEIGHT IN BUFFALO PERFORMANCE TESTS IN CUBA

ÍNDICE DE SELECCIÓN POR PESO AL DESTETE Y FINAL EN PRUEBAS DE COMPORTAMIENTO DE BÚFALOS EN CUBA

L.M. FRAGA[1]*, O. LÓPEZ[2], YENNY GARCÍA[1]

[1]*Instituto de Ciencia Animal, C. Central km 47 ½, San José de las Lajas, Mayabeque, Cuba*
[2]*Empresa Genética Los Naranjos, Carretera Caimito-Vereda, km 4 ½, Artemisa, Cuba*

**E-mail:* luismfb48@gmail.com

Performance tests were carried out on 241 male buffaloes from the Empresa Pecuaria Genética Los Naranjos, in Cuba, during the years 2011/2012 and 2017. The evaluated indicators were weight at weaning at eight months, final weight at 20 months of age, weight gain from eight to 20 months, weight per age at 20 months and milk production of their mothers at 244 days, as well as the percentage values, calculated from their respective annual means. A mixed model was used (Proc Glimmix of SAS 2013), which considered the year of entry into testing as a fixed effect, and the individual nested in the year of entry as random effect. The genetic values (GV) with their precision were estimated using a two-character model, compiled in IML (Interactive Matrix Language) of SAS. This considered genealogy (250 males and females), which, together with the 241 observations of tested animals, formed a kinship matrix of 491 individuals. Weaning (136.43 and 151.92 kg) and final (285.39 and 333.35 kg) weights were low, while the production of their mothers was acceptable (944.04 and 1,135.42 kg). It is concluded that the selection index, constructed from the variances and covariances of phenotypic and genetic values, economically weighted as a regression of the observed deviations from their means of weaning and final weight, is a reliable method for the selection of buffaloes in performance tests.

Keywords: *buffaloes, indexes, live weights, performance tests*

Se realizaron pruebas de comportamiento a 241 búfalos machos de la Empresa Pecuaria Genética Los Naranjos, en Cuba, que comprendieron los años 2011/2012 y 2017. Se evaluaron los indicadores peso al destete a los ocho meses, final a los 20 meses de edad, ganancia en peso de ocho a 20 meses, peso por edad a los 20 meses y producción de leche de sus madres a los 244 días, así como los valores porcentuales, calculados a partir de sus medias anuales respectivas. Se utilizó un modelo mixto (ProcGlimmix del SAS 2013), que consideró como efecto fijo el año de entrada en prueba, y como aleatorio el individuo anidado en el año de entrada. Se estimaron los valores genéticos (VG) con su precisión mediante un modelo bicarácter, compilado en IML (Interactive Matrix Language) del SAS. Este consideró la genealogía (250 animales machos y hembras), que unida a las 241 observaciones de animales probados, conformó una matriz de parentesco de 491 individuos. Los pesos al destete (136.43 y 151.92 kg) y final (285.39 y 333.35 kg) estuvieron bajos, mientras que la producción de sus madres fue aceptable (944.04 y 1135.42 kg). Se concluye que el índice de selección, construido a partir de las varianzas y covarianzas de los valores genéticos y fenotípicos ponderados económicamente como regresión de las desviaciones observadas de sus medias del peso al destete y final, es un método confiable para la selección de los búfalos en las pruebas de comportamiento.

Palabras clave: *búfalos, índices, pesos vivos, pruebas comportamiento*

Introduction

Selection indexes have been shown to constitute a highly precise way of conducting animal selection, considering several traits. In this way, the relationship among all characters is considered, which includes their genetic values and economic weights, to simultaneously improve a group of characters in different species. The main objective of selection is to improve the total economic value or aggregate genotype (H) of the population, which is defined for each animal as the sum of each of the genotypes for the selected characters, weighting each one by its relative economic value

Received: August 25, 2023
Accepted: December 29, 2023
Conflict of interests: The authors declare that there is no conflict of interests.
CRediT authorship contribution statement: L. M. Fraga: **Conceptualization, Data curation, Investigation, Formal analysis, Writing - original draft.** O. López: **Data curation, Investigation, Formal analysis.** Yenny García: **Data curation, Investigation, Formal analysis.**

(Hazel and Lush 1942 and Hazel 1943). Currently, to form the indexes, the principal components procedure is used with the genetic values, as applied by Bignardi *et al.* (2012) and Khan *et al.* (2013). In Cuba, Hernández and Ponce de León (2018, 2020) have also used it.

Currently, the buffalo genetic improvement program in Cuba is based on genetic evaluations of mothers for milk production and the results of performance tests of grazing males. The males that enter performance tests come from the best mothers for milk production. Performance tests are evaluations of male (calves) growth from different herds, from the same company, from weaning to eight months, and extend over a year under grazing conditions. At the end of the test, the best animals for future sires are determined, considering their growth and milk production of their mothers during lactation in percentage terms, both respectively weighted (60:30) according to Mitat *et al.* (2010).

Selection methods that consider bovine milk production have evolved in the last 100 years (Weigel *et al.* 2017), although less so in buffalo species, in which meat production is beginning to be of particular interest, in addition to milk, due to its productivity and profitability, which has been pointed out by Ranjhan (2004) when referring to global commercial production, and more recently by García *et al.* (2017) as far as Cuba is concerned. According to Mrode and Thompson (2005) and Miglior *et al.* (2017), most of the selection indexes in the world focus on increasing the production of milk and its constituents, having a lower focus on meat production. According to the cited authors, this reality applies to most countries, except for Scandinavia, which selection indexes also include conformation. The ANASB (2020a) catalog is a sample of the method used in Italy for buffalo production in the country, specifically aimed at legs, mammary system, milk, fat, protein and yield.

Improvements have been found in all traits when the indices are used, but in growth traits they have been less used, and much less in buffaloes, despite the fact that some pre-weaning and post-weaning growth traits have shown the possibility of genetic improvement. The selection and use of indexes have been recommended in the bubaline species (Ramos and Fraga 2008). Specifically, in Colombia, Agudelo *et al.* (2016) have advocated it, as well as Taheri and De Seno (2016) in Iran. Endris (2020) have applied it in Ethiopia, and the ANASB (2020b) catalog in Italy is evidence of its use. However, this methodology is rarely used, because a large part of the buffalo population is in the hands of small producers with low resources and little or no application of management and genetic selection technologies (Reggeti 2004). This important method depends on the definition of the selection objectives, as well as the feasibility of measuring the selection criteria to be used and the economic control by producers.

The objective of this study was to describe the evolution of the indicators that have occurred in the buffalo species during a period of six years in a enterprise in Cuba, and from this information to build an index for buffalo selection in performance tests.

Materials and methods

The information was taken from the Empresa Pecuaria Genética Los Naranjos, in Cuba, from performance tests carried out on buffaloes grazing *Cynodon nlemfuensis*, at a rate of 0.6 to 1.0 animals/ha, for an average of 12.72 months. The animals subjected to this test were those that, during the birth campaign, on three occasions, had good weights at weaning and came from mothers that phenotypically had higher milk productions during the birth years (between 2011 and 2017), for a total of 241 individuals. This database records the indicators weight at weaning at eight months (WW), final weight (FW) at 20 months, daily weight gain (DWG) 8-20 months, weight per age (WPA) and total milk production of their mothers (MPM) at 244 d of lactation, as well as their percentage values in relation to the mean for each year.

SAS (2013) mixed model was used with Proc GLIMMIX (Wolfinger and O'Connell 1993 and Schabenberger 2006) to process the measures of WW, FW, DWG, WPA and MPM after identifying with Proc SEVERITY the most adjusted distribution to the data, which resulted in gamma, and use of the log link. The Proc IML of SAS (2013) was used with a program developed from the procedure indicated by Duangjinda (2007) and Elzo and Vergara (2007) to obtain the genetic values or predicted transmittingability (GV/PTA) of a two-character model (weaning weight and final live weight) with its precision, with a kinship matrix composed by the genealogy (35 fathers and 215 mothers) and the 241 observations of tested animals, which formed a kinship matrix of 491 individuals, obtained with the application of SAS INBRED Proc (2013). The year of entry to the performance test was taken as fixed effect in both procedures (Glimmix and two-character), which had six levels corresponding to the years 2011 and 2012 until 2017 (united due to insufficient information from the first year).

Differences among means of year fixed effects were estimated by Kramer (1956). With these objectives, the following mixed model was used in Glimmix:

$$Y_{ijkl} = \mu + a_i + a_j \quad (a_i) + e_{ijk}$$

where:

μ = Constant or general mean, common to all observations

α_i = Fixed effect of the i-th year of start of the test (i=2011/2012…, 2017)

$a_j(\alpha_i)$ = Random effect of the j-th animal (j=1.2…, 241) nested on the i-th starting year (in the case of the two-character to obtain the GVs, no nesting was performed).

e_{ijkl} = Random error associated with observations normally distributed with mean 0 and variance $\delta^2{}_e$.

$$I = b'\left[\begin{bmatrix} Pd \\ Pf \end{bmatrix} - \begin{bmatrix} \mu Pd \\ \mu Pf \end{bmatrix}\right]$$

y

$$b = \begin{pmatrix} VPd & CovPdPf \\ CovPdPf & VPf \end{pmatrix}^{-1} * \begin{vmatrix} VGPd^2 & CovVGPdVGPf \\ CovVGPdVGPfVGPf^2 & \end{vmatrix} * \begin{bmatrix} 1.00 \\ 8.37 \end{bmatrix}$$

Pd and Pf represent the weight at weaning and at the end of the test, their means (μPd and μPf), their phenotypic variances (VPd, VPf) and covariances (CovPdPf), variances (VGPd2 and VGPf2) and covariances (CovVGPdVGPf) of their genetic values, as well as the respective relative economic values. All represented in a matrix form.

Results and discussion

The relative results of the performance of the variables processed by year of entry into testing are shown in table 1. Although these values are acceptable, they are still below the objectives of the genetic improvement plan for buffaloes in Cuba (Mitat *et al.* 2010). A variable performance was recorded for all the evaluated indicators, which decreased in recent years, partly due to the low selection index applied (Mitat 2022) and for unspecified reasons. For these reasons, it is considered that measures should be adopted to achieve higher weights. In particular, with regard to genetics, a more precise selection than the one currently carried out should be proposed, regardless of whether work is done on other possible non-genetic improvement paths.

The phenotypic and genetic correlations of the index of milk production of mothers (%) were low for all the evaluated indicators (table 2), so it was considered that their inclusion in a selection index was not advisable. It was determined to give it more importance through other selection methods in the program, and to consider the weight at weaning and final weight at 20 months. These had a genetic correlation that, although it reached a medium and significant value, showed a certain independence among their own genes, which proved to be completely independent of the milk production of their respective mothers.

In Brazil, Falleiro *et al.* (2013) with Mediterranean buffaloes obtained a higher, equally significant, genetic correlation of 0.75 between weaning weight at 205 d and

Table 1. Performance test results, recorded in a genetic company in Cuba

Years of beginning of the performance test	Weight at weaning, eight months		Final weight, 20 months		Gain 8-20 months		Weight per age, 20 months		Milk production of mothers in eight months	
	Mean, kg	SE ±	Mean, kg	SE ±	Mean, g/day	SE ±	Mean, g/day	SE ±	Mean, kg	SE ±
2011-2012	136.43[a]	1.65	285.39[a]	5.28	317.05[a]	10.53	413.34[a]	7.49	1068.43[ab]	30.01
2013	148.80[b]	1.52	306.48[b]	4.86	390.89[b]	9.70	454.60[b]	6.89	1135.42[a]	27.64
2014	140.17[a]	1.26	326.56[c]	4.03	440.43[c]	8.04	475.52[b]	5.72	1072.55[ab]	22.91
2015	141.07[ac]	1.33	333.35[c]	4.26	496.10[d]	8.50	501.92[c]	6.04	1032.28[abc]	24.21
2016	151.92[b]	1.20	320.62[c]	3.84	320.26[a]	7.65	453.57[b]	5.44	944.04[c]	21.81
2017	145.69[c]	1.48	310.20[d]	4.72	309.84[a]	9.42	459.74[b]	6.70	1013.17[bc]	26.84
Pvalue	<.0001		<.0001		<.0001		<.0001		<.0001	

[a,b,c,d] Values with different letters per column differ at $P<0.05$ (Kramer 1956)

Table 2. Phenotypic (top diagonal) and genetic (bottom diagonal) correlations and their significance among indicators measured in the buffalo performance test.

	Weight at weaning	Weight at 20 months	DWG, %	WPA, %	MPM, %
Weight at weaning	1.00	0.36008 <.0001	0.12397 0.0546	0.17912 0.0053	-0.05434 0.4010
Weight at 20 months	0.31575 <.0001	1.00	0.35679 <.0001	0.41925 <.0001	-0.01493 0.8176
DWG, %	0.11784 0.0684	0.82696 <.0001	1.00	0.80894 <.0001	0.06194 0.3383
WPA, %	0.16026 0.0129	0.90789 <.0001	0.80262 <.0001	1.00	0.07263 0.2614
MPM, %	-0.04504 0.4874	0.02631 0.6851	0.01925 0.7666	0.01349 0.8353	1.00

DWG: daily weight gain WPA: weight per age MPM: milk production of mothers weight after 305 d. Meanwhile, the phenotypic was also high and significant, with a value of 0.67. This is explained by the greater proximity among the ages evaluated (205 vs. 305 d) by these authors in relation to the present study (244 vs. 608 d). As this correlation was not high enough to guarantee a high correlated response, by ignoring one of the two and considering what was suggested by Mrode and Thompson (2005) regarding the elimination bias (culling bias), it would be justified to combine both characteristics in an index that weights them in an added value that minimizes said bias. According to the cited authors, this bias is incurred when selecting by final weight without taking into account the weight at weaning, when only the preselected animals are tested.

It is suggested not to consider the inclusion of the percentage index of the milk production of mothers, as it is currently done in the improvement plan in Cuba, and to consider it in the preselection of the animals to be tested, as well as in a procedure of further selection, which finally considers, together with the proposed index, the genetic value of said mothers. This is estimated, on the other hand, from the information in the database of all the enterprise mothers, and not from those whose offspring were subjected to tests, even based on several lactations.

The selection index carried out like this, combines a characteristic (weight at weaning) that has high maternal genetic determination, due to its direct and indirect effects (Telo da Gama *et al.* 2004 and Mrode and Thompson 2005) with the weight at the end of the performance test at 20 months. With respect to the latter, this study presented a certain independence of genetic nature (rg=0.31575), which with its economic weightings would bring it closer to an ideal of desirable characteristics of an aggregate genotype, so it could replace the currently used method. Thus, this subindex would be combined with a comprehensive index that includes the genetic values corresponding to the mothers of the individuals in performance test, obtained by evaluating all mothers for milk production. This aspect deserves further study. In Brazil, Daher (2010) suggests a similar treatment with buffaloes, but in milk production, with the purpose of modifying the lactation curve in a desirable direction.

Table 3 shows the 20 best and worst individuals, according to the evaluated index that represents all the animals in the analyzed period. However, it is possible that the interest lies in the assessment of a specific period, particularly the last year, although when the assessment considers the entire population over several years, greater precision in the evaluation is guaranteed. This procedure is more reliable than with percentage values as practiced until now, although the weighting values may vary according to the interests of the producer.

With the use of the IML, this procedure could be applied for other characteristics of economic interest in bubaline production, so it represents an example here. Both with the IML and with the multicharacter, which would contemplate an aggregate genotype with more than two characters, its application is preferable where there are no large

Table 3. The best and worst individual indexes, standardized by the genetic values of the two-character model, with the weaning and final weights of buffaloes in the performance test (N=241 and rHI=0.9499)

Merit	Identification	Best	Identification	Worst
1	207-16	2.7757	281-10	-1.3130
2	117-10	2.5739	385-10	-1.3937
3	495-13	2.2385	75 15	-1.4098
4	327-13	2.1560	707-12	-1.4394
5	107-14	2.0502	457-10	-1.4762
6	385-14	1.9811	263-10	-1.5219
7	143-13	1.9793	379 15	-1.5228
8	113-13	1.9578	133-10	-1.5506
9	263-14	1.9560	155 15	-1.5578
10	125-14	1.8618	301-12	-1.6331
11	121-14	1.8484	129-16	-1.6547
12	111-12	1.8313	217-10	-1.7192
13	445-10	1.8143	269-10	-1.7390
14	381-14	1.7390	265-10	-1.7793
15	111-13	1.6591	297-12	-1.8681
16	323-13	1.6403	333-12	-2.0152
17	133-14	1.5686	327-10	-2.0681
18	329-13	1.5443	597 15	-2.0771
19	63-14	1.5399	1405-12	-2.2349
20	113-14	1.5381	295-10	-2.5614

populations with extensive genealogical history. There are various ways or methods of carrying out the selection and fulfill the evaluations with specific and complex programs (ASREML by Gilmour *et al*. 2003) or perform a more precise selection with the covariance adjustment of the growth curve from the weighings carried out at other ages during the test or proceed to form the indexes using the procedure of the principal components of the genetic values, as pointed out by Bignardi *et al.* (2012) and Khan *et al.* (2013).

In Cuba, Hernández and Ponce de León (2018, 2020) have studied the genetic objectives defined by the most important principal components that allow several characteristics to be incorporated into the index.

Shook (2006) pointed out the use of subindexes that are subsequently combined into a general index and can be one more alternative to achieve the objective of total economic merit. These aspects are being analyzed with this same information in order to evaluating more precise selection methods.

Nevertheless, the general index methodology indicated in this paper, based on a sub-index for weaning weight and final weight of the test, as well as another sub-index for the milk production of mothers, although it is not addressed in this article, it is carried out in the country with other procedures, and it constitutes an example of what could happen when populations for improvement are not large at country or enterprise level. This procedure could be a guide or example, taking into consideration other characteristics of economic interest. In this way, the bubaline species in Cuba could have a more precise genetic evaluation and make a greater contribution, as Yadav (2004) points out when referring not only to milk production, but also to meat production of high commercial value and nutritional quality.

Conclusions

It is concluded that the selection index constructed from the variances and covariances of the genetic and phenotypic values, economically weighted as a regression of the deviations from their means of weaning and final weight, is a reliable method for the selection of buffaloes in performance tests.

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