



Selection index for meat and milk traits of buffaloes in Colombia



Divier A. Agudelo-Gómez^a, Jorge H. Agudelo-Trujillo^b, Mario F. Cerón-Muñoz^{c,*}

^a Corporación Universitaria Lasallista, College of Administrative Sciences and Agriculture, Research Group on Production, Development, and Agricultural Transformation, 055440 Caldas, Colombia

^b Universidad de Antioquia, School of Agricultural Sciences, Medellín, Colombia

^c Universidad de Antioquia, School of Agricultural Sciences, Research Group on Genetics, Breeding and Animal Modeling (GaMMA), Medellín, Colombia

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ABSTRACT

Genetic parameters and breeding values from univariate, multivariate, and reduced principal component models for weaning weight, yearling weight, weight at 18 months, weight at two years, age at first calving, milk yield, and maternal genetic effects for weaning weight and yearling weight were estimated for dual purpose buffaloes in Colombia. With those values we constructed selection indices (SI) and estimated genetic progress obtained through mating-modeling under various selection criteria and weighted values for each trait. Comparison of SI was performed using duality diagrams in principal components of breeding values obtained by pseudo-simulation of mating with animals selected with the constructed SIs. The index constructed with the first principal component of the reduced range model led to improved meat, milk yield, and age at first calving.

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1. Introduction

Genetic evaluations in buffalo herds in Colombia can be enumerated as follows: two evaluations have been conducted for milk yield since 2006 (Cerón-Muñoz et al., 2006; Hurtado-Lugo et al., 2006), one has been conducted for meat production since 2008 (Agudelo-Gómez et al., 2009), and one more has been conducted to evaluate reproductive traits since 2010 (Bolívar-Vergara et al., 2010). It is noteworthy that none of those evaluations have not included weaning weight (WW), yearling weight (W12), weight at 18 months (W18), weight at two years (W24), age at first calving (AFC), and milk yield to 270 days (MY).

Despite of the existence of national genetic evaluations, Colombian farmers have traditionally conducted phenotypic selection based only on milk yield because this trait is most directly related with income. They do not perform selection based on body weight gain, although most males in the country are destined for meat production. Since weaned males are commonly used for meat, it is important to consider growth-associated traits; thus, selection would allow a parallel improvement of milk yield and meat traits without neglecting reproductive traits (Bolívar-Vergara et al., 2010; Cerón-Muñoz et al., 2006; Agudelo-Gómez et al., 2009).

Selection indices (SI) integrate all available information (genetic, phenotypic, and economic data) into a single value, so the lack of merit for a particular objective can be balanced by its preeminence in others, allowing to obtain a single value known as aggregate genotype (Falconer and Mackay, 1996; Cerón-Muñoz and Vergara, 2012).

Indices used in breeding programs focused on selection consist of a linear combination of phenotypic values for the traits of interest, and were originally developed for multi-character selection in plants (Smith, 1936). SI measure the net merit of improving selection units in a particular species. In short, SI measure the economic gain resulting from the use of breeding animals (Hazel, 1943).

The index, which is based on principal component (PC) analysis (Buzanskas et al., 2013), is a multivariate technique for evaluating relationships between quantitative traits. It reduces the number of variables to analyze by grouping them into a new set named principal components (Kaiser, 1960). This way it improves precision and reduces the computational burden inherent to the analysis of large and complex datasets (Kirkpatrick and Meyer, 2004). The PC approach has also been proposed as a possible solution to the variance component estimation for genetic evaluation of dairy bulls, which is of special interest because it allows for a dimension reduction (Tyrisvä et al., 2011). A reduction of the multi-dimensional distribution of breeding values provides information to understand genetic associations between traits (Savegnago

* Corresponding author.

E-mail address: mario.ceron@udea.edu.co (M.F. Cerón-Muñoz).

et al., 2011). Genetic gain could be maximized by keeping all boars intact and selecting animals based on an estimated breeding value calculated from SI (Newcom et al., 2005). The objective of this study was to construct SI based on genetic evaluations using univariate, multivariate, and reduced range models, and to estimate genetic progress for each trait to define which methodology generates the greatest genetic progress for several traits in a population of buffaloes destined for beef and milk production.

2. Materials and methods

Genealogy databases and breeding values (BV) of males and females estimated by univariate (Agudelo-Gómez et al., 2015a) and multivariate reduced range models (Agudelo-Gómez et al., 2015b) were used. The traits taken into account for the construction of the indices were weaning weight (WW), yearling weight (W12), weight at 18 months (W18), weight at two years (W24), age at first calving (AFC), milk yield to 270 days (MY), maternal genetic effects for weaning weight (MGWW), and maternal genetic effect for yearling weight (MGW12). Females (70%) and males (5%) were chosen from the genealogy base, considering the following criteria:

No selection (S_0): females and males were chosen with Bernoulli simulations.

Selection by milk yield breeding value (IMY): individuals with superior genetic merit for milk yield were chosen.

Selection indexes (SI) were constructed as proposed by Hazel (1943), as follows:

$$SI = h_{WW}Y_{WW} + h_{W12}Y_{W12} + h_{W18}Y_{W18} + h_{W24}Y_{W24} + h_{AFC}Y_{AFC} + h_{MY}Y_{MY} + h_{MGWW}Y_{MGWW} + h_{MGW12}Y_{MGW12}$$

where Y are animal breeding values and h are regression coefficients, given by:

$$h_i = P^{-1}Gv$$

where:

h_i = regression coefficient for the i th trait, used to construct the index.

P and G are the matrices of phenotypic and genetic (co) variances, respectively, obtained from the multivariate model, as described by Agudelo-Gómez et al. (2015b), with the following structure:

$$P = \begin{bmatrix} 1107.5 & 891.3 & 960.0 & 582.0 & -679.4 & 479.0 & 0.0 & 0.0 \\ 891.3 & 1277.7 & 1124.2 & 762.0 & -830.7 & 382.2 & 0.0 & 0.0 \\ 960.0 & 1124.2 & 1605.2 & 1158.4 & -1410.4 & 922.9 & 0.0 & 0.0 \\ 582.0 & 762.0 & 1158.4 & 1930.0 & -1529.5 & 1491.9 & 0.0 & 0.0 \\ -679.4 & -830.7 & -1410.4 & -1529.5 & 11174.0 & 2475.9 & 0.0 & 0.0 \\ 479.0 & 382.2 & 922.9 & 1491.9 & 2475.9 & 36831.0 & 0.0 & 0.0 \\ 0.0 & 0.0 & 0.0 & 0.0 & 0.0 & 0.0 & 1107.5 & 0.0 \\ 0.0 & 0.0 & 0.0 & 0.0 & 0.0 & 0.0 & 0.0 & 1277.7 \end{bmatrix}$$

$$G = \begin{bmatrix} 270.0 & 282.2 & 418.8 & 310.3 & -389.1 & 699.0 & 0.0 & 0.0 \\ 282.1 & 349.3 & 432.1 & 340.7 & -340.1 & 1091.1 & 0.0 & 0.0 \\ 418.8 & 432.1 & 717.4 & 554.2 & -591.5 & 1372.2 & 0.0 & 0.0 \\ 310.3 & 340.7 & 554.2 & 588.7 & -753.4 & 1218.2 & 0.0 & 0.0 \\ -389.1 & -340.1 & -519.5 & -763.4 & 1699.9 & -571.3 & 0.0 & 0.0 \\ 699.0 & 1091.1 & 1372.2 & 1218.2 & -571.3 & 9482.0 & 0.0 & 0.0 \\ 0.0 & 0.0 & 0.0 & 0.0 & 0.0 & 0.0 & 2700.0 & 0.0 \\ 0.0 & 0.0 & 0.0 & 0.0 & 0.0 & 0.0 & 0.0 & 349.3 \end{bmatrix}$$

v is a relationships vector with weights of each trait in the fourteen proposed SI. The first seven SI (SI1 to SI7) were constructed using the first seven weighted values from Table 1 and the respective regressors from Table 2, and BV were obtained from univariate analyses with MTDFREML software (Boldman et al., 1995). The random effects for WW and W12 were: direct additive genetic, maternal additive genetic, maternal permanent environmental, and residual effect. The fixed effects were: sex (male or female), number of calving (1 to 14), and contemporary group (farm, year, and calving season: January to April, May to August, or September to December). Age at weighing was used as a covariate (linear effect). Random effects for W18 and W24 were the additive genetic random and the residual effect. The fixed effects were sex, number of calving, and contemporary group. Age at weighing was used as a covariate. Random effects for AFC were the same as for W18 and W24, and the fixed effect of contemporary group was included (farm, year, and season of first birth).

Random effects for MY270 were the additive genetic, permanent environmental, and residual effect. The fixed effects were parity (1 to 14) and contemporary group (farm, year, and season of birth). These models were described by Agudelo-Gómez et al. (2015a).

Additionally, the other seven SI (SI8 to SI14) were constructed with the last seven weighting values described in Table 1 and the respective regressors from Table 2 and the BV obtained by the multivariate model with Wombat software (Meyer, 2007a) described by Agudelo-Gómez et al. (2015b), whose fixed and random effects for each trait were the same as indicated above for the univariate analysis.

Selection indexes by principal components:

Three selection indices (PCI_1 , PCI_2 and PCI_3) were constructed using the first three components described by Agudelo-Gómez

Table 1
Weighted values of the traits evaluated in Colombian buffaloes, used for constructing the selection indexes (SI) proposed by Hazel (1943).

Trait	SI ₁	SI ₂	SI ₃	SI ₄	SI ₅	SI ₆	SI ₇	SI ₈	SI ₉	SI ₁₀	SI ₁₁	SI ₁₂	SI ₁₃	SI ₁₄
WW, kg	1.0	1.0	1.0	1.0	1.0	1.0	2.0	1.0	1.0	1.0	1.0	1.0	1.0	2.0
W12, kg	1.0	1.0	1.0	0.0	1.0	1.0	0.0	1.0	1.0	1.0	0.0	1.0	1.0	0.0
W18, kg	1.0	1.0	1.0	1.0	1.0	1.0	0.0	1.0	1.0	1.0	1.0	1.0	1.0	0.0
W24, kg	1.0	1.0	1.5	1.0	1.0	1.0	2.0	1.0	1.0	1.5	1.0	1.0	1.0	2.0
AFC, days	1.0	-2.0	-1.5	-2.0	0.0	0.0	0.0	1.0	-2.0	-1.5	-2.0	0.0	0.0	0.0
MY, kg	1.0	5.0	2.0	3.0	3.0	0.0	0.0	1.0	5.0	2.0	3.0	3.0	0.0	0.0
MGWW, kg	1.0	1.0	0.0	1.0	1.0	0.0	0.0	1.0	1.0	0.0	1.0	1.0	0.0	0.0
MGW12, kg	1.0	1.0	0.0	0.0	1.0	0.0	0.0	1.0	1.0	0.0	0.0	1.0	0.0	0.0

WW: weaning weight, W12: yearling weight, W18: weight at 18 months, W24: weight at 2 years, MY: milk yield to 270 days, AFC: age at first calving, MGWW: maternal genetic effect for weaning weight, MGW12: maternal genetic effect for yearling weight.

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