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Selection index for meat and milk traits of buffaloes in Colombia

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ABSTRACT

Genetic parameters and breeding values from unitrait, multitrait, 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.

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 (Tyrisevä et al., 2011). A reduction of the multi-dimensional distribution of breeding values provides information to understand genetic associations between traits (Savegnago

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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 unitrait, multitrait, 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 unitrait (Agudelo-Gómez et al., 2015a) and multitrait 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:

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

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 multitrait 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 unitrait 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 multitrait 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 unitrait 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.

Table 2
Trait regressors 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	−0.51	−1.60	−0.37	−0.72	−1.17	0.15	2.0	−0.51	−1.60	−0.37	−0.72	−1.17	0.15	2.0
W12, kg	0.83	3.13	1.03	1.55	2.08	0.08	0.0	0.83	3.13	1.03	1.55	2.08	0.08	0.0
W18, kg	1.62	3.59	2.22	2.44	2.60	1.14	0.0	1.62	3.59	2.22	2.44	2.60	1.14	0.0
W24, kg	−0.29	0.56	0.57	0.64	0.02	0.05	2.0	−0.29	0.56	0.57	0.64	0.02	0.05	2.0
AFC, days	0.04	−0.35	−0.26	−0.31	−0.10	−0.05	0.0	0.04	−0.35	−0.26	−0.31	−0.10	−0.05	0.0
MY, kg	0.34	1.39	0.63	0.85	0.86	0.09	0.0	0.34	1.39	0.63	0.85	0.86	0.09	0.0
MGWW, kg	0.03	0.03	0.00	0.00	0.03	0.0	0.0	0.03	0.03	0.00	0.00	0.03	0.0	0.0
MGW12, kg	0.10	0.10	0.00	0.00	0.10	0.0	0.0	0.10	0.10	0.00	0.00	0.10	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.

et al. (2015a), using the following formula:

$$IPC_{jl} = \sum_{i=1}^{l} eig_{ij} * BV_{il}$$

where:

PCI_{jl} is the index corresponding to the *Ith* animal in the *jth* principal component.

eig_{ij} is the eigenvector (linear correlation) of the *ith* trait in the *jth* principal component. BV_{il} is the breeding value of the *ith* trait in the *lth* animal.

BV were estimated using unitrait models (Agudelo-Gómez et al., 2015a) and the coordinates (linear correlation) in Table 3.

Three selection indices were also constructed with the principal components obtained in the reduced range multitrait analysis (ICR_1, ICR_2 and ICR_3), as reported by Agudelo-Gómez et al. (2015b), considering the linear correlations described in Table 4.

The best 70% females and 5% males from each index were mated using pseudo simulation processes with uniform distribution and 200 replicates. Genetic values were generated for each trait of the progeny by averaging the genetic values of their parents. The SI comparison was performed with a duality diagram of the relationship of genetic values for each trait in each SI in the PC analysis using the "ade4" library (Dray and Dufour, 2007) of R project software (R Core Time, 2014).

3. Results

Average breeding values (kg) varied as follows: from −0.05 (RPCI3) to 16.22 (SI13) for WW, from 0.44 (IPCR2) to 10.64 (SI9) for W12, from 1.89 (IPCR2) to 27.04 (SI1) for W18, from −0.09 (S0) to 8.21 (SI14) for W24, from −0.91 (IPC3) to 1.96 (SI6) for MGWW, from −1.9 (IPC3) to 4.02 (SI7) for MGW12, and from 14.62 (S0) to 59.95 (IMY) for MY (Table 5). The average breeding value (days) varied from 9.04 (IPC3) to −13.23 (IPCR1) for AFC. The duality diagram between traits and the SI relationship analysis are presented in Fig. 1.

Table 3
Eigenvalues of economically important traits in buffaloes, reduced to the first three principal components (PC) described by Agudelo-Gomez et al. (2015a).

Trait	PC_1	PC_2	PC_3
WW, kg	0.78	−0.21	0.83
W12, kg	0.75	−0.05	−0.00
W18, kg	0.78	0.16	−0.00
W24, kg	0.73	0.13	−0.05
MY, kg	0.17	0.35	0.84
AFC, days	−0.38	−0.39	0.53
MGWW, kg	−0.30	0.75	−0.25
MGW12, kg	−0.00	0.82	0.13

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.

Table 4
Eigenvalues of economically important traits in buffaloes, reduced to the first three principal components in the multitrait reduced range models (PCR) described by Agudelo-Gomez et al. (2015b).

Trait	PCR_1	PCR_2	PCR_3
WW, kg	0.45	0.11	0.05
W12, kg	0.65	0.10	0.11
W18, kg	0.77	0.20	0.58
W24, kg	0.60	0.37	0.56
MY, kg	0.79	−0.31	−0.23
AFC, days	−0.32	−0.83	0.51
MGWW, kg	0.01	0.25	−0.05
MGW12, kg	0.01	0.13	−0.08

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.

4. Discussion

The greatest genetic progress for WW, W12, W18, W24, MY, AFC, MGWW, and MGW12 was obtained with indexes SI13, SI9, SI1, SI14, IMY, RPC1, SI6 and SI7, respectively (Table 5), indicating that none SI was the best for two or more traits.

Among the indexes developed with the Hazel (1943) methodology, the greatest genetic progress was 44.90 kg for MY, obtained in SI8 when the weighted values were equal to 1. The same index showed positive genetic progress for all other traits, although AFC (24 days) increased, which is not desired by breeders due to their interest in an early beginning of productive life (Rosati and Van Vleck, 2002; Bolívar-Vergara et al., 2010; Oliveira et al., 2014).

Buffalo breeders regard W12 as another trait of considerable importance because at this age many herds conduct selection processes for breeding females (Barrera et al., 2014) and males begin the fattening process (Ramírez Toro et al., 2011). Additionally, according to heritability values described by Agudelo-

Table 5
Average breeding values ± Standard Deviations for traits of economic importance obtained by buffalo pairing pseudo simulations chosen from selection indexes.

Trait Index	WW (kg)	W12 (kg)	W18 (kg)	W24 (kg)	MY (kg)	MGWW (kg)	MGW12 (kg)	AFC (days)
G0	0.96 ± 12.6	1.11 ± 9.0	2.22 ± 23.0	0.96 ± 11.5	10.53 ± 37.6	0.41 ± 4.8	−0.13 ± 11.7	1.4 ± 2.83
S0	1.12 ± 0.1	2.51 ± 0.0	7.72 ± 0.1	−0.09 ± 0.1	14.62 ± 0.2	0.84 ± 0.0	−0.09 ± 0.1	7.8 ± 0.1
IMY	3.89 ± 0.1	5.06 ± 0.1	13.08 ± 0.1	2.23 ± 0.1	**59.95 ± 0.1**	−0.52 ± 0.1	−0.87 ± 0.1	11.37 ± 012
SI1	5.02 ± 0.1	6.79 ± 0.1	**27.04 ± 0.1**	2.76 ± 0.1	23.83 ± 0.2	1.66 ± 0.0	3.75 ± 0.1	5.57 ± 0.1
SI2	5.61 ± 0.1	7.21 ± 0.0	25.47 ± 0.1	4.16 ± 0.1	28.51 ± 0.2	1.16 ± 0.0	3.71 ± 0.1	3.53 ± 0.1
SI3	6.28 ± 0.1	7.21 ± 0.0	26.32 ± 0.1	4.71 ± 0.1	26.14 ± 0.2	1.39 ± 0.0	3.77 ± 0.1	3.11 ± 0.1
SI4	5.89 ± 0.0	7.1 ± 0.0	25.84 ± 0.1	4.6 ± 0.1	27.65 ± 0.2	1.25 ± 0.0	3.7 ± 0.1	3.23 ± 0.1
SI5	4.06 ± 0.1	5.34 ± 0.0	19.8 ± 0.1	2.22 ± 0.1	22.95 ± 0.2	1.35 ± 0.0	3.82 ± 0.1	4.1 ± 0.1
SI6	6.66 ± 0.1	6.6 ± 0.1	27.93 ± 0.1	3.95 ± 0.1	19.04 ± 0.2	**1.96 ± 0.0**	3.97 ± 0.1	3.53 ± 0.2
SI7	6.96 ± 0.1	6.56 ± 0.0	27.7 ± 0.1	4.78 ± 0.1	19.23 ± 0.2	1.93 ± 0.0	**4.02 ± 0.1**	2.89 ± 0.12
SI8	10.67 ± 0.2	9.98 ± 0.0	22.06 ± 0.1	6.89 ± 0.1	44.9 ± 0.2	0.38 ± 0.1	0.46 ± 0.1	8.25 ± 0.12
SI9	15.67 ± 0.3	**10.64 ± 0.1**	24.88 ± 0.2	8.18 ± 0.1	37.63 ± 0.4	1.16 ± 0.1	1.89 ± 0.1	5.18 ± 0.
SI10	15.72 ± 0.2	10.46 ± 0.1	25.3 ± 0.2	8.47 ± 0.1	36.23 ± 0.4	1.36 ± 0.1	2.05 ± 0.1	4.42 ± 0.1
SI11	15.69 ± 0.2	10.56 ± 0.1	25.12 ± 0.2	8.59 ± 0.1	37.33 ± 0.3	1.33 ± 0.1	1.91 ± 0.1	4.64 ± 0.2
SI12	10.77 ± 0.1	8.38 ± 0.1	20.92 ± 0.2	5.04 ± 0.1	32.7 ± 0.4	1.9 ± 0.1	3.59 ± 0.1	4.81 ± 0.2
SI13	**16.22 ± 0.2**	9.89 ± 0.1	25.12 ± 0.2	7.63 ± 0.1	30.18 ± 0.4	1.4 ± 0.1	2.34 ± 0.1	4.16 ± 0.2
SI14	16 ± 0.2	9.76 ± 0.1	25.13 ± 0.2	**8.21 ± 0.1**	30.58 ± 0.4	1.39 ± 0.1	2.25 ± 0.1	3.28 ± 0
PCI1	14.08 ± 0.3	10.94 ± 0.0	26.56 ± 0.1	7.09 ± 0.1	31.77 ± 0.2	1.18 ± 0.0	3.67 ± 0.1	−3.66 ± 0.1
PCI2	2.36 ± 0.1	4.72 ± 0.1	17.13 ± 0.1	3.46 ± 0.1	43 ± 0.2	1.31 ± 0.1	1.59 ± 0.1	−7.53 ± 0.1
PCI3	1.22 ± 0.1	4.12 ± 0.1	9.42 ± 0.1	0.34 ± 0.1	46.49 ± 0.2	−0.91 ± 0.1	−1.9 ± 0.1	24.00 ± 2
RPCI1	9.62 ± 0.1	10.53 ± 0.1	15.8 ± 0.2	11.99 ± 0.1	41.33 ± 0.5	0.62 ± 0.1	0.17 ± 0.1	−**13.23 ± 0.2**
RPCI2	−0.12 ± 0.1	0.44 ± 0.1	1.89 ± 0.2	2.74 ± 0.1	31 ± 0.4	0.15 ± 0.0	−0.97 ± 0.0	−1.07 ± 0.2
RPCI3	−0.05 ± 0.1	1.17 ± 0.1	2.1 ± 0.1	0 ± 0.1	37.65 ± 0.3	0.22 ± 0.0	−0.92 ± 0.0	9.04 ± 0.2

WW: weaning weight (kg); W12 (kg): yearling weight (kg); W12: weight at 18 months (kg); W24: weight at 2 years (kg); MY: milk yield to 270 days (kg); AFC: age at first calving (days); MGWW: maternal genetic effects for weaning weight (kg); MGW12: maternal genetic effect at one year of age (kg); G0: parental generation; S0, without selection; SI1 to SI7: Hazel (1943) indexes with unitrait analysis (Agudelo-Gómez et al., 2015a); Si8 to SI14: Hazel (1943) indexes with multitrait analysis (Agudelo-Gómez et al., 2015b); PCI1 to PCI3: principal components indexes (Agudelo-Gómez et al., 2015a); and RPCI1 to RPCI3 principal components indexes in multitrait reduced analysis (Agudelo-Gómez et al., 2015b). The highest value into each column is bolded.

Gómez et al. (2015a) and Agudelo-Gomez et al. (2015b) this trait responds very well to the selection process and has high positive genetic correlations with WW, W18, W24, and MY; but high negative correlation with AFC.

Among the indexes developed with the Hazel (1943) methodology, the greatest genetic progress for W12 were obtained in SI8 to SI10, and with principal components PCI1 and RPCI1, although they did not allow the greatest genetic progress for MGWW and MGW12. For highly correlated traits, the first few principal components explain most of the data variation and those with the smallest contribution on the variance can be excluded without notably altering the accuracy of the estimates (Meyer, 2007b; Tyrisevä et al., 2011). The best SI for MY were PCI3 and IMY, but they were not adequate for weight traits. The greatest SI genetic progress for weight and MY corresponded to SI8 and RPCI1, although SI8 also increased AFC.

Brazilian researchers used principal component analysis to propose an index for Nellore cattle (Buzanskas et al., 2013) in which, depending on the breeder interests, animals can be selected to improve reproductive parameters using the coordinates estimated in the first principal component. The coordinates of the second principal component can be used to select individuals with a better genetic merit for weight at 420 days.

While constructing a selection index for the Caracu breed Brazilian researchers concluded that the index implementation (which included milk yield, weaning weight, scrotal circumference, age at first calving, and productive life) allows for an appropriate response in accordance with the interests of the breeders (Queiroz et al., 2005). If the interest of Colombian producers was only milk quality, they should use the so-called “Mozzarella Index”, which combines milk yield with milk protein and fat percentage (Rosati and Van Vleck, 2002).

5. Conclusions

The RPC1 reduced-range model best estimates genetic parameters because it allows increasing the genetic progress of traits such as WW, W12, W18, W24, MY, MGWW, and MGW12 while decreasing AFC. Reducing multivariate statistical complexity by using PC is an attractive option since it simplifies the problem to a series of non-correlated new traits that can conceptually be useful as a “simpler” selection strategy. However, to establish whether this approach is better or worse than a conventional SI and its practical consequences would require further evaluations.

Conflict of interest statement

There are no known conflicts of interest associated with this publication and there has been no significant financial support for this work that could have influenced its outcome.

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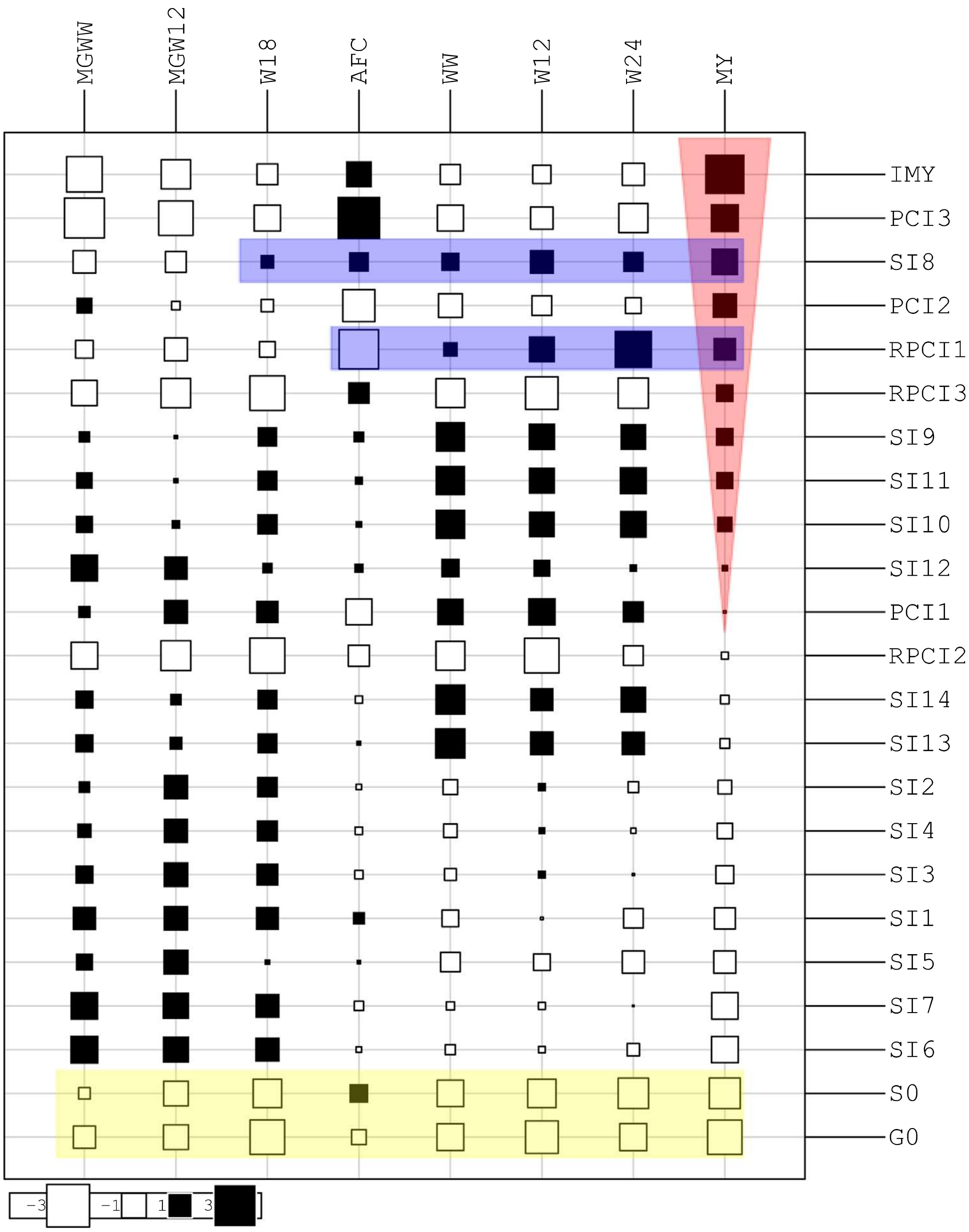

Fig. 1. Duality diagram (−3 to 3 standard deviations) between weaning (WW), yearling (W12), 18 months (W18) and 24 months (W24) weight, milk yield (MY), age at first calving (AFC), and maternal genetic effect of WW (MGWW) and W12 (MGW12) with average genetic values of parental generation (G0) and progeny obtained by not selection (S0), milk yield only (IMY), Hazel selection (SI1 to SI14), principal components (PCI1 to PCI3), and reduced components (RPCI1 to RPCI3) index in Colombian buffaloes.

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