UNIVERSIDAD DE ANTIOQUIA
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EVALUACIÓN DE CARACTERÍSTICAS DE IMPORTANCIA ECONÓMICA EN UN PROGRAMA DE MEJORA GENÉTICA DE BÚFALOS DOBLE PROPÓSITO EN COLOMBIA

DIVIER ANTONIO AGUDELO GÓMEZ

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DIRECTOR

MARIO FERNANDO CERÓN MUÑOZ, Zoot, PhD

COMITÉ TUTORIAL

DIANA MARÍA BOLIVAR VERGARA, Zoot, PhD
CARLOS EUGENIO SOLARTE PORTILLA, Zoot, PhD

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Resumen General

Se utilizó la información genealógica y productiva de 48621 animales, pertenecientes a 14 hatos bufalinos doble propósito de Colombia para realizar evaluaciones genéticas usando modelos unicaracterísticos, multicaracterísticos y de rango reducido, con los objetivos de estimar los parámetros genéticos y valores genéticos de los animales para las características: peso al destete (PD), peso a los doce meses (P12), peso a los 18 meses (P18), peso a los dos años (P24), producción de leche hasta los 270 días (PL270) y para edad al primer parto (EPP), determinar cuál modelo era el más adecuado para estimar el progreso genético de las características estudiadas y validar un índice de selección que permitiera optimizar el progreso genético de los búfalos en Colombia.

Los rangos de la heredabilidad (h^2) estimada en los diferentes modelos para PD, P12, P28, P24, EPP, y PL270 variaron ente 0,18 a 0.24, 0,20 a 0,26, 0,44 a 0,53, 0,21 a 0.30, 0,14 a 0,17 y 0,23 a 0,26, respectivamente. El rango de la h^2 para el efecto genético materno para PD (GMPD) y P12 (GMP12) varió entre 0.04 a 0.06 y 0.05 a 0.08, respectivamente. En todos los modelos evaluados P18 fue la característica que presentó la mayor h^2, indicando que sería la que tendría una mayor respuesta a procesos de selección. PD, P12, P24 y PL270 presentaron niveles medios a altos de h^2 y podrían responder en forma moderada a procesos de selección. GMPD, GMP12 y EPP son las características que tendrían una menor respuesta a procesos de selección.

Las correlaciones genéticas, estimadas en el modelo de rango reducido de tres componentes principales ($PC_{1:3}$) (que fue considerado como el mejor modelo), de AFC con las demás características fue negativa; la correlación genética entre las demás características fue positiva.

El progreso genético estimado en el periodo 2000 a 2014 de PD, P12, P18, P24, para machos y hembras fue de 0.43 y 0.36, 0.54 y 0.46, 0.77 y 0.59, y 0.54 y 0.46, kg/año, respectivamente. Para PL270 el progreso genético fue de 3.61 y 2.61 kg/año

para machos y hembras, respectivamente, y en EPP la el progreso genético fue nulo.

Se construyeron diferentes índices de selección (IS) usando los parámetros genéticos y los valores de cría estimados en los diferentes modelos, y se analizó el progreso genético alcanzado en cada uno de los IS con el objetivo de proponer un IS que pueda ser aplicado en la ganadería bufalina doble propósito en Colombia la para optimizar los procesos de selección.

El índice que, en general, permite alcanzar un progreso genético de acuerdo a los intereses económicos de los bufalistas, esto es, aumentar la el valor genético para PD, P12, P18, P24, y PL270, y disminuir EPP es el construido a partir de las correlaciones lineales del primer componente principal del modelo $PC_{1:3}$ y los valores de cría de los animales.

Introducción General

La población de búfalos en el mundo se estima en198,88 millones y se concentra en Asia en 97%. La producción de leche y de carne en 2012 con relación al 2007 crecieron en un 1.8% y 14%, respectivamente, presentando mayor crecimiento en países en vía de desarrollo donde son utilizados como animales doble propósito (FAO, 2013). La leche por el alto contenido grasa y proteína tiene mayores precios en el mercado que la del ganado vacuno (Heinz, 2001). En países como Italia ha tenido un especial crecimiento y desarrollo, promoviendo programas control productivo, genealógico y de mejoramiento genético, debido al posicionamiento en el mercado internacional de productos con denominación de origen (Borghese, 2010). En países de Sur América ha tenido especial desarrollo en los últimos 30 años, especialmente en Argentina, Brasil, Colombia y Venezuela, gracias a que los ganaderos han visto en la especie una alternativa de producción, debido a los mejores precios que recibe por litro de leche y a la mayor eficiencia en el crecimiento de los animales dedicados a la producción de carne, haciendo que la especie tenga cada día mayor participación en los mercados locales (Zava, 2013)

En Colombia los trabajos de mejoramiento genético en búfalos, fundamentados en evaluaciones genéticas, iniciaron en 2008 cuando se inició el programa nacional de control lechero en el que se controla la producción de leche y su calidad composicional (porcentaje de grasa y proteína) y se lleva control genealógico de los animales; también se controlan características asociadas a la producción de carne (pesos a diferentes edades) y recientemente se inició con la toma de medidas con ultrasonido para evaluar calidad de la canal.

Como resultado de los datos recolectados se han publicado los resultados de varias evaluaciones genéticas que han permitido identificar los parámetros genéticos y productivos de algunas características productivas relacionadas con la producción leche (Cerón-Muñoz et al., 2011; Cerón-Muñoz and Ramírez-Arias, 2015) con producción de carne (Agudelo-Gómez et al., 2009; Bolívar-Vergara et al., 2012; Barrera et al., 2014) y reproductivas (Bolívar-Vergara et al., 2010). Esto permite

realizar selección de animales para mejorar la producción de leche o sus componentes (porcentaje de grasa y proteína), o seleccionar animales para mejorar características relacionadas a la producción de carne (peso diferentes edades) o mejorar características reproductivas.

En los sistemas de producción doble propósito, se debe tener especial cuidado al momento de seleccionar los animales como reproductores pues se debe procurar que si se selecciona para mejorar una característica las otras no se vayan a ver afectadas negativamente, pues puede existir correlación genética negativa (Falconer and Mackay, 1996).

Las evaluaciones genéticas multicaracterísticas permiten identificar el tipo de relaciones genéticas existentes entre las características evaluadas lo que facilita establecer los criterios de selección en los sistemas productivos. La calidad de los resultados de cualquier evaluación genética (bien sean parámetros genéticos, o valores genéticos de los animales evaluados) dependen de la estructuración de los datos a analizar, de lo confiable del archivo de pedigree, de la cantidad de los datos, entre otros aspectos.

El presente trabajo se compone de tres capítulos:

El primer capítulo, titulado "**Genetic evaluation of dual-purpose buffaloes (*Bubalus bubalis*) in Colombia using principal component analysis"** (que ya fue aprobado para publicación en la Revista PLOS ONE, ver anexo 1). Se estiman los parámetros genéticos para las características peso al destete (PD), peso al año (P12), peso a los 18 meses (P18), peso a los dos años (P24), edad al primer parto (EPP) y producción de leche hasta los 270 días (PL 270), por medio de modelos unicaracterísticos.

Se realizó un análisis de componentes principales (PCA) con los valores genéticos de 133 machos reproductores que presentaron confiabilidad superior al 50% de los valores genéticos de todas las características, con el fin de definir el número de componentes principales (PC) que explicara la mayoría de la variación. Se estimaron las heredabilidades, el porcentaje de varianza retenida en cada uno de los

tres primeros PC y las correlaciones existentes entre cada característica y cada PC.

El APC permite abordar de forma diferente el análisis de características de interés económico en ganado bufalino doble propósito y disminuir la dimensión de características a analizar.

En el segundo capítulo, titulado **"Genetic principal components for reproductive and productive traits in dual-purpose buffaloes in Colombia"** (que ya fue aprobado para publicación en la Revista Journal of Animal Science, ver anexo 2). Se realiza la estimación de parámetros genéticos de las mismas características analizadas en el capítulo 1 pero se emplean un modelo multicaracterísitco (MC) y 5 modelos de rango reducido (con una estructura de componentes principales PC_1, $PC_{1:2}$, $PC_{1:3}$, $PC_{1:4}$, y $PC_{1:5}$), con el objetivo de determinar cuál era el modelo más apropiado para estimar los parámetros de las características analizadas y evaluar el progreso genético de búfalos doble propósito en Colombia.

De acuerdo al criterio de información de Akaike, el mejor modelo fue el de rango reducido de tres componentes principales ($PC_{1:3}$), además mantiene el 100% de la variación original y la estimación de los parámetros genéticos fue similar a la realizada en el MC pero con un menor error estándar.

En el tercer capítulo, titulado "**Comparación de índices de selección en búfalos doble propósito en Colombia**" se hace uso de la información obtenida en los dos primeros capítulos para construir diferentes índices de selección y definir cuál de los modelos utilizados y cuál índice permiten obtener el mayor progreso genético en las características evaluadas.

Se construyeron diferentes índices de selección aplicando la metodología de Hazel (1943), usando las matrices de (co)varianzas genéticas y fenotípicas estimadas en los modelo MC y $PC_{1:3}$, aplicando diferentes ponderaciones económicas, para estimar los regresores lineales, que fueron aplicados a cada uno de los valores genéticos estimados (BV) tanto en los modelos unicaracterísticos y en el modelo MC.

También se construyeron índices de selección a partir de las correlaciones lineales estimadas de cada una de las características con cada uno de los tres primeros PC

estimadas a partir de los modelos unicaracterísticos y a partir de las correlaciones lineales estimadas de cada una de las características estimadas en con cada uno de los tres primeros PC estimadas en el modelo de rango reducido $PC_{1:3}$.

Por medio de simulación de apareamientos se estimó el progreso genético obtenido en la progenie como la mitad de la suma del BV de las características obtenidas en los modelos unicaracterísticos.

De los índices evaluados, el que permitió obtener el mayor progreso genético, en forma integral, aumentando el valor genético de las características relacionadas con peso y producción de leche y disminuyendo el valor genético para la edad al primer parto), para todas las características fue el construido a partir de las correlaciones lineales entre las características evaluadas y las coordenadas del primer componente principal, estimadas en el modelo de rango reducido $PC_{1:3}$.

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Objetivos

Objetivo general:

Estimar parámetros genéticos para características relacionadas con crecimiento, producción de leche y edad al primer parto y construir un índice de selección que permita optimizar los procesos de selección en ganado bubalino doble propósito en Colombia.

Objetivos específicos

Estimar la relación existente entre los valores genéticos de características de crecimiento, producción de leche, y edad al primer parto de búfalos doble propósito usando un análisis de componentes principales, utilizando los valores genéticos estimados en modelos unicaracterísticos.

Identificar entre un modelo multicaracterístico y 5 modelos de rango reducido el que realice la mejor estimación de parámetros genéticos de características de crecimiento, producción de leche, y edad al primer parto y evaluar el progreso genético a partir del modelo seleccionado.

Construir un índice de selección que incluya características asociadas al crecimiento, producción de leche y edad al primer parto, que permita obtener el mayor progreso genético en el hato bufalino doble propósito en Colombia.

CAPÍTULO 1

Se presenta conforme a las normas de la revista PLOS ONE debido a que fue sometido a dicha revista y después de varias revisiones y ajustes fue aprobado para publicación, ver anexo 1)

Las normas para publicación de artículos en la revista PLOS ONE se presentan en el anexo 3.

Este artículo da respuesta al objetivo específico número uno

PLOS ONE

RESEARCH ARTICLE

Genetic Evaluation of Dual-Purpose Buffaloes (*Bubalus bubalis*) in Colombia Using Principal Component Analysis

Divier Agudelo-Gómez[1,2]*, Sebastian Pineda-Sierra[2], Mario Fernando Cerón-Muñoz[2]

1 Corporación Universitaria Lasallista, Facultad de Ciencias Administrativas y Agropecuarias, Grupo de Investigación Sobre Producción, Desarrollo y Transformación Agropecuaria, Caldas-Antioquia, Colombia, **2** Universidad de Antioquia, Facultad de Ciencias Agrarias, Grupo de investigación en Genética, Mejoramiento y Modelación Animal, (GaMMA), Medellín, Colombia

* diagudelo@lasallistadocentes.edu.co

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Abstract

Genealogy and productive information of 48621 dual-purpose buffaloes born in Colombia between years 1996 and 2014 was used. The following traits were assessed using one-trait models: milk yield at 270 days (MY270), age at first calving (AFC), weaning weight (WW), and weights at the following ages: first year (W12), 18 months (W18), and 2 years (W24). Direct additive genetic and residual random effects were included in all the traits. Maternal permanent environmental and maternal additive genetic effects were included for WW and W12. The fixed effects were: contemporary group (for all traits), sex (for WW, W12, W18, and W24), parity (for WW, W12, and MY270). Age was included as covariate for WW, W12, W18 and W24. Principal component analysis (PCA) was conducted using the genetic values of 133 breeding males whose breeding-value reliability was higher than 50% for all the traits in order to define the number of principal components (PC) which would explain most of the variation. The highest heritabilities were for W18 and MY270, and the lowest for AFC; with 0.53, 0.23, and 0.17, respectively. The first three PCs represented 66% of the total variance. Correlation of the first PC with meat production traits was higher than 0.73, and it was -0.38 with AFC. Correlations of the second PC with maternal genetic component traits for WW and W12 were above 0.75. The third PC had 0.84 correlation with MY270. PCA is an alternative approach for analyzing traits in dual-purpose buffaloes and reduces the dimension of the traits.

Introduction

Buffalo herds are managed under dual-purpose production systems in Colombia so farmers are interested in improving traits related with breeding, milk and meat production. A strategy to improve herd productivity is to select animals according to their breeding values (BV), which allow programming mating according to specific objectives. However, when BV are

available for various traits it can be difficult to select the animals, especially when the traits have negative genetic correlation.

The principal components analysis (PCA) is a multivariate technique that reduces the amount of originally-correlated variables into a smaller set of non-correlated variables, keeping most of the original variability, and reducing the dimensionality to a new set of variables named principal components (PC), under the assumption of losing the least possible amount of information. This technique creates orthogonal axes which are linear combinations of the original variables, based on the matrix eigenvalues of the variables considered. The eigenvalues are generated in order from highest to lowest and each eigenvalue is assigned a principal component allowing each PC to retain more variability than the following PC [1]. According to Meyer K [2], when the original variables are highly correlated the first PCs can explain most of the variation, thus allowing to eliminate redundant information.

Quantitative genetics has developed three uses for principal components (PCs): as a tool to visualize genetic variation patterns, to define the genetic parameters to be estimated, and to separate the original number of variables into a smaller set of principal components to estimate the genetic parameters of these PCs [3].

The PCA technique has been incorporated into genetic evaluations in beef cattle [4–6], dairy [7], and to analyze reproductive traits in different breeds [8–10]. Recently, PCA was used for genetic evaluations of nine traits of economic interest in buffalo cattle in Brazil, concluding that four PCs are sufficient to explain the covariance structure of the traits [11]. The reviewed literature concludes, among other things, that the PCA allows lowering dimensionality of the variables, facilitating the interpretation of data in a few PC, and identifying the type of relationship between the original variables.

The aim of this study was to explore the relationship between BV for growth, milk yield, and age at first calving in dual-purpose buffaloes by using PCA.

Materials and Methods

Materials

This study was approved by the Ethics Committee for Animal Experimentation of Universidad de Antioquia (approved on May, 2013, 83 minutes).

The Colombian Association of Buffalo Breeders (ACB) provided the database used in this study. The traits evaluated were: weaning weight (WW), yearling weight (W12), weight at 18 months of age (W18, view S1 Dataset), weight at 2 years of age (W24), milk yield at 270 days (MY270), and age at first calving (AFC). The age range allowed for WW, W12, W18, W24 and AFC was 180 to 300, 330 to 390, 450 to 510, 680 to 760, and 760 to 1500 days, respectively. MY270 was estimated following the guidelines of the International Committee of Animal Recording (ICAR) [12]. Animals were grazing on pastures and received mineral supplementation. The breeding system consisted in controlled natural mating. Records were taken between 1996 and 2014. All herds are located in Colombia's Caribbean region in a rainforest zone (height above sea level: 80 m, temperature: 28°C, and annual precipitation: 2000 mm) [13]. All herds were managed as dual-purpose systems. The database (S2 Dataset pedigree dataset available) included a relationship matrix with 48621 animals, predominantly Murrah crossbreds. An overview of the data is shown in Table 1.

Genetic parameters

One-trait models were used for estimating genetic parameters and breeding values with MTDFREML (Multiple trait Derivate-Free Restricted Maximum Likelihood) [14].

Table 1. Weights at weaning (WW), one year of age (W12), 18 months of age (W18), 2 years of age (W24), milk yield at 270 days (MY270), and age at first calving (AFC) for dual-purpose buffaloes in Colombia.

Trait	SX	n	Mean	CV
WW (kg)	M	12479	208.70	0.23
	F	11527	205.85	0.23
W12 (kg)	M	3045	213.27	0.21
	F	4184	208.92	0.20
W18 (kg)	M	1309	262.56	0.20
	F	2677	252.94	0.19
W24 (kg)	M	454	381.86	0.16
	F	2292	349.24	0.14
MY270 (kg)	F	15159	1044.00	0.23
AFC (days)	F	4244	1109.00	0.11

SX = sexo, (M = male, F = female), n = number of males or females, CV = coefficient of variation

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For WW and W12 the random effects were: direct additive genetic (a), maternal additive genetic (m), maternal permanent environmental (pe), and residual effect (ε). The fixed effects were: sex (male or female), number of calving (1 to 14) and contemporary group (farm, year, and birth time: January to April, May to August, or September to December). Age at weighing was used as a covariate (linear effect). The matrix representation of the model is:

$$y = X\beta + Z_1 a + Z_2 m + Wpe + \varepsilon. \text{ With } \quad Cov(Z_1 a,\ Z_2 m) = 0$$

Where y is a vector of observations, β is the vector of fixed effects, and ε is the random residual vector. X, Z_1, Z_2, and W are the incidence matrices relating the fixed effects, direct additive genetic effects, maternal additive genetic effects, and maternal permanent environmental effects, respectively.

The following formula

$$h_t^2 = (\sigma_a^2 + 0.5 * \sigma_m^2 + \sigma_{am})/\sigma_p^2,$$

by Willham RL [15], was used in the estimation of total heritability for WW and W12. Where

h^2_t = total heritability

σ^2_t = direct additive genetic variance

σ^2_m = maternal additive genetic variance

σ_{am} = genetic covariance between direct and maternal effects

σ^2_p = phenotypic variance

For W18 and W24 random effects were the additive genetic random (a) and the residual effect (ε). The fixed effects were sex (male or female), number of calving (1 to14), and contemporary group (defined as for WW and W12). The age at weighing was used as a covariate (linear effect).

For AFC the random effects were the same as for W18 and W24, and the fixed effect of contemporary group was included (farm, year, and time of first birth: January to April, May to August, or September to December).

The matrix representation of the model was:

$$y = XB + Z1a + Wpe + \varepsilon$$

For MY270 the random effects were: additive genetic (a), permanent environmental (pe), and residual effect (ε). The fixed effects were parity (1 to 14) and contemporary group (farm, year, and time of birth: January to April, May to August, or September to December).

The matrix representation of the model was:

$$y = XB + Z1a + Wpe + \varepsilon$$

Principal components

PCA was developed using the BV from 133 males, selected from 961 males with higher than 50% reliability for WW, W12, W18, W24, MY270, AFC, maternal genetic effect for weaning weight (MGWW), and maternal genetic effect for yearling weight (MGW12), data are also available in S3 Dataset. All BV were standardized to zero mean and unit variance. To select the number of principal components (PC) that explained the highest percentage of variance only those PC with greater than one eigenvalues were took into account [16]. The linear correlations of traits with each PC were estimated, and significant traits in each PC were defined. This analysis was conducted using command PCA, FactoMineR library [17] of r-project software [18].

Results

Genetic parameters

The estimated heritability of the studied traits is presented in Table 2. Traits with the highest and lowest heritability were W18 and AFC, with 0.53 and 0.17, respectively. Heritability of the other traits ranged between 0.18 and 0.23. Heritability of the maternal genetic component included in WW and W12 was 0.04 and 0.08, respectively, indicating the need to include this effect in genetic assessments to obtain more accurate heritabilities for these two traits. Heritabilities of the permanent environment for WW, W12, and MY270 were 0.11, 0.16, and 0.25, respectively.

Principal component analysis

PCA was performed using BV of WW, W12, W18, W24, MY270, AFC, MGWW and MGW12 from 133 breeding males chosen from 961 males. The first three PC had eigenvalues greater than one, and explained 65.78% of the original variance of the breeding values for the aforementioned traits, view Table 3. See PCA progam in S1 File.

Table 2. Direct heritability (h^2_a), maternal heritability (h^2m), permanent environment (c^2) and total heritability (h^2_t) of dual-purpose buffaloes in Colombia.

Trait	h^2_a	h^2_m	c^2	h^2_t
WW	0.16	0.04	0.11	0.18
W12	0.16	0.08	0.16	0.20
W18	0.53			
W24	0.21			
MY270	0.23		0.25	
AFC	0.17			

WW: weaning weight, W12: yearling weight, W18: weight at 18 months of age, W24: weight at two years of age, MY270: milk yield at 270 days AFC: age at first calving

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Table 3. Eigenvalues and variance proportions for the principal components (PC) of the genetic values.

PC	Eigenvalue	Variance proportion	Cumulative variance proportions
1	2.59	0.32	0.32
2	1.59	0.20	0.52
3	1.07	0.14	0.66
4	0.78	0.10	0.76
5	0.65	0.08	0.84
6	0.58	0.07	0.91
7	0.42	0.05	0.96
8	0.28	0.04	100.00

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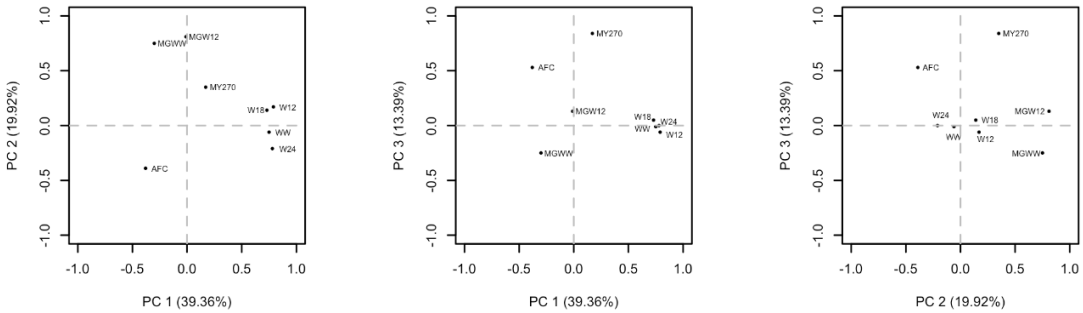

Fig 1. Distribution of the traits analyzed in each of the first three principal components (PC1 vs PC2, PC2 vs PC3 and PC2 vs PC3).

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Distribution of traits in each of the first three components (PC1, PC2 and PC2) is shown in Fig 1. The lines represent eigenvectors indicating the strength and direction in each PC [19]. Traits WW, W12, W18 and W24 showed greatest intensity in PC1, and related positively with this component. The MY270 behaved in similar way, but with less intensity. On the other hand, AFC and MGWW were negatively associated with PC1, while MGWW, MGW12 and MY270 related positively with PC2. The traits with greatest intensity in PC3 were MY270 and AFC, and they were positively related. The MGWW was negatively associated with this component, and had low intensity (Fig 1).

Table 4 shows the correlations of significant traits with each of the first three PC. The PC1 presented higher than 0.72 correlation with WW, W12, W18, and W24; and it was -0.38 and -0.30 with AFC and MGWW, respectively. Correlation of PC2 with WW and AFC was negative, while it was positive with MY270, MGWW and MGW12. Correlation of PC3 with MY270 and AFC was positive, and it was negative with MGWW.

Discussion

The values found in this study for WW and W12 were higher, and W18 and W24 were lower than those reported in Colombia for those traits: 182, 201, 278 and 363 kg, respectively [20]. Milk yield was lower to 2286.8 kg reported for buffaloes in Italy [21], and 1594 kg reported for Murrah buffaloes in Brazil [22]. AFC was higher to 1094 days reported for Murrah buffaloes in Brazil [22] and less than 1140 days reported for buffaloes in Colombia [23].

Table 4. Linear correlation of genetic values for the traits that were significant with principal components (PC1, PC2 and PC3).

Trait	PC1	PC2	PC3
WW	0.78	-0.21	
W12	0.75		
W18	0.78		
W24	0.73		
MY270	0.17	0.35	0.84
AFC	-0.38	-0.39	0.53
MGWW	-0.30	0.75	-0.25
MGW12		0.82	

PS weaning weight, W12: yearling weight, W18: weight at 18 months, W24: weight at 2 years, MY270: milk yield at 270 days AFC: age at first calving, MGWW: maternal genetic effect for weaning weight, MGW12: maternal genetic effect for weight at one year of age

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The performance parameters of buffaloes for WW, W12, W18, W24, MY270, and AFC were better than the data reported for the dual purpose cattle in Colombia [24], indicating that buffalo is a good livestock production alternative in this country.

The estimated WW, W12 and W24 heritability was lower than the figures reported in Colombia by Bolivar et al. [23]: 0.42, 0.42 and 0.41, respectively. Heritability of W18 was 0.42 in that report, which is lower than estimated in the present study.

In this study, the estimated heritability for milk yield was lower than previously reported for buffaloes in Brazil: 0.30, 0.25, and 0.28 [11,25,26], respectively, but was higher than that reported in Italy 0.14 [21], Brazil 0.22 [27] and Colombia 0.22 [28].

Table 5. Heritabilities (h^2) estimated for dual-purpose buffalo cattle in this study compared to other studies.

Trait	h^2, this study	h^2, other studies	Literature
WW	0.18	0.45	[20]
W12	0.20	0.42	[20]
W18	0.53	0.42	[20]
W24	0.21	0.41	[20]
MY270	0.23	0.25	[25]
	0.23	0.20	[26]
	0.23	0.30	[27]
	0.23	0.30	[11]
	0.23	0.14	[21]
	0.23	0.22	[28]
AFC	0.17	0.16	[29]
	0.17	0.47	[23]
MGWW	0.04	0.09	[31]
	0.04	0.01*	[30]
MGW12	0.08	0.08*	[30]

WW weaning weight, W12: yearling weight, W18: weight at 18 months, W24: weight at 2 years, MY270: milk yield at 270 days AFC: age at first calving, MGWW: maternal genetic effect for weaning weight, MGW12: maternal genetic effect for weight at one year of age.
*Ganado nelore Nelore cattle

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The estimated heritability for AFC was higher than that reported in Nellore heifers: between 0.08 and 0.16 [29]; but less than 0.47 estimated in buffaloes in Colombia [23].

The estimated maternal heritability for WW and W12 coincide with values reported by Albuquerque and Meyer [30] for Nellore cattle. They evaluated this trait from birth to 600 days of age, reporting values between 0.01 and 0.08 that were statistically significant at up to 390 days. In Brazil Malhado et al. [31] estimated maternal heritability as 0.09 for weight at 205 days of age in buffaloes. In Colombia Bolivar et al. [20] reported 0.28 for the same trait for weaning weight. These results suggest that inclusion of the maternal effect allows for a better estimation of heritability for WW and W12. In Table 5 shows the heritability estimates for the studied traits and those obtained by other researchers.

The PCA results in this study are consistent with other reports, evidencing the usefulness of PCA to reduce dimensionality. According to the report by Val and Ferraudo [8], the first two PCs comprised 70.33% of the total variation of six traits associated with meat production and one trait associated to breeding in Nellore cattle. Also in Nellore cattle, three PCs accounted for 100% of the additive genetic variance of nine traits associated with meat production [5]. Oliveira et al. [11] evaluated seven productive and two reproductive traits of buffaloes in Brazil concluding that a reduced rank model with 3 or 4 PCs was sufficient to explain the largest percentage of the additive genetic variance for all the traits.

Conclusions

According to the heritability figures obtained, W18 and MY270 would be the most responsive traits to the selection process, while AFC would be less responsive. PCA facilitates and improves efficiency of the animal selection process by using correlations between traits and components, hence reducing the range of the analysis. It is concluded that the traits studied in this work can be analyzed with the first three PCs.

Supporting Information

S1 Dataset. This file contains the information productive weight at 18 months W18, information of each of the columns corresponds to: animal (id), father (sire), mother (dam), sex (sx), contemporani group (cg), calving number (N), weight (W18), and age (age).
(XLSX)

S2 Dataset. This archive contains the genealogical information of animals tested, each of the three columns correspond to the renumbering of the animal, father and mother, respectively.
(XLS)

S3 Dataset. This archive contains breeding values (BVs) from 133 males used for the principal component analysis (PCA). Information of each column corresponds to BV for: milk yield at 270 days (MY270), weaning weight (WW), weight at one year (W12), weight at 18 months (W18), weight at two years (W24), age at first calving (AFC), maternal genetic effect for weaning weight (MGWW), and maternal genetic effect for yearling weight (MGW12).
(TXT)

S1 File. This file contains the program for principal components analysis (PCA) in r-project.
(DOCX)

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Author Contributions

Conceived and designed the experiments: DAG MFCM. Performed the experiments: DAG SPS MFCM. Analyzed the data: DAG SPS MFCM. Contributed reagents/materials/analysis tools: DAG SPS MFCM. Wrote the paper: DAG SPS MFCM.

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CAPÍTULO 2

Se presenta conforme a las normas de la revista Jorunal of Animal Science, debido a que fue sometido a dicha revista y después de varias revisiones y ajustes fue aprobado para publicación (Anexo 3).

La numeración de las páginas de este capítulo cambian debido a que tiene el formato exigido por la Revista Jorunal of Animal Science.

Las normas para publicación de artículos en la revista Jorunal of Animal Science se presentan en el anexo 4.

Este artículo da respuesta al objetivo específico número dos

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Genetic principal components for reproductive and productive traits in dual-purpose buffaloes in Colombia[1]

D. A. Agudelo-Gómez,*†[2] R. Pelicioni Savegnago,‡ M. E. Buzanskas,‡ A. S. Ferraudo,‡ D. Prado Munari,‡ and M. F. Cerón-Muñoz†

*Facultad de Ciencias Administrativas y Agropecuarias, Corporación Universitaria Lasallista, 055440 Caldas, Colombia; †Facultad de Ciencias Agrarias, Grupo de Investigación en Genética, Mejoramiento y Modelación Animal (GaMMA), Universidad de Antioquia, 050036 Medellín, Colombia; and ‡Departamento de Ciências Exatas, Faculdade de Ciências Agrárias e Veterinárias, UNESP, 14884-900 Jaboticabal, Brazil

ABSTRACT: A multitrait model (MC) and 5 reduced-rank models with principal component structure (components PC_1, $PC_{1:2}$, $PC_{1:3}$, $PC_{1:4}$, and $PC_{1:5}$) were compared. The objectives were to determine the most appropriate model for estimating genetic parameters and to evaluate the genetic progress of dual-purpose buffaloes in Colombia using that model. The traits evaluated were weaning weight (WW), yearling weight (W12), weight at 18 mo of age (W18), weight at 2 yr of age (W24), age at first calving (AFC), and milk yield at 270 d of first lactation (MY270). Genealogy and productive information from 34,326 buffaloes born in Colombia between 1997 and 2014 were used. Colombian Association of Buffalo Breeders (ACB) provided the data. Direct additive genetic and residual random effects were included for all the traits. In addition, the maternal additive genetic effect and permanent environmental random effect were included for WW, while a maternal additive genetic effect was included for W12. The fixed effects were contemporary group (farm, year, and calving season: January to April, May to August, or September to December; for all traits) and sex (for WW, W12, W18, and W24). Additionally, parity was included as a fixed effect for WW and W12. Age at weighing was used as a covariate for WW, W12, W18, and W24. Genetic progress of all traits was analyzed using a generalized smooth model (GAM). According to the Akaike information criteria (AIC), the best model was the one with reduced rank and first 3 principal components ($PC_{1:3}$). This model maintained 100% of the original variance. Genetic parameters estimated with this model were similar to those estimated by MC, but with smaller standard errors. Heritability for weight-related traits ranged between 0.23 and 0.44. Heritabilities for AFC and MY270 were 0.14 and 0.24, respectively. The genetic correlations obtained between all weights (WW, W12, W18, and W24) were positive and high. Correlations between all weights with AFC were negative and moderate. Correlations between all weights with MY270 were positive and moderate, and between MY270 with AFC were negative and low.

Key words: *Bubalus bubalis*, genetic evaluation, genetic progress, reduced-rank models

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INTRODUCTION

Buffalo herds in Colombia are managed as dual-purpose systems (Bolívar et al., 2012). It is important to know the genetic parameters and genetic correlations between traits associated with breeding and production of milk and meat because of their economic relevance. Traits associated with live weights can be measured several times over the life of the animals, and the associated milk yield can be assessed throughout several calving events. Multitrait

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[2]Corresponding author: diagudelo@lasallistadocentes.edu.co

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models (Arango et al. 2002; Boligon et al., 2009) and repeatability models are suitable for studying these traits (Boligon et al., 2009; Nephawe, 2004).

In multitrait models, the (co)variances and genetic correlations between measurements taken at different ages might vary, and overparameterization of the model occurs when the number of traits is very large (Nobre et al., 2003). In that context, the principal component analysis (**PCA**) is a statistical approach that allows decreasing the rank of the covariance matrix (Kirkpatrick and Meyer, 2004), reducing the dimensionality of a set of correlated traits, and generating a new reduced set of variables called principal components (**PC**). PC are orthogonal to each other and are linear combinations of the original traits, preserving the original maximum variability (Johnson and Wichern, 1992).

The PCA has been used to evaluate these models in genetic evaluation studies for beef cattle (Boligon et al., 2013) to estimate genetic parameters of BW and reproduction traits in female Canchim cattle and to explore the relationships among estimated breeding values (Buzanskas et al., 2013). It has also been used in Angus cattle to estimate genetic parameters (Meyer, 2005), as well as in poultry to estimate genetic parameters for traits associated with egg production and their relationships (Savegnago et al., 2011). It is also used in dairy cattle to estimate genetic parameters (Bignardi et al., 2012). In the aforementioned studies, PCA has allowed reduction of dimensionality, offering an appropriate estimate of genetic parameters.

The aims of this study were to select from a multitrait and 5 reduced-rank models the one that offers the best estimation of genetic parameters and to evaluate the genetic progress for the analyzed traits using that model.

MATERIALS AND METHODS

Data

The Colombian Association of Buffalo Breeders (**ACB**) provided the data used in this study. Information of 12 dual-purpose herds with once-a-day milking and weaning between 6 and 10 mo of age was included. The herds are located in the Colombian Caribbean region in a rainforest life-zone (height above sea level: 80 m, temperature: 28°C, precipitation: 2000 mm/year; Holdridge, 1996). The first mating occurs after females reached 330 kg. Males were kept whole and culled for slaughtered after reaching 430 kg (Ramírez Toro et al., 2011). The animals were managed on a pasture and received mineral supplementation. The breeding system consisted of controlled natural mating, except for few cases in which artificial insemination was used. Genetic connectivity between years and herds was verified using the Genetic Drift Variance methodology proposed by Kennedy and Trus (1993), who suggested that a small value would indicate a high degree of connectedness. Average connectivity between years was 0.01, and the maximum value was 0.06. Average connectivity between herds was 0.16, and the maximum value was 0.75. Genetic connectivity between herds occurs because herds exchange breeding males. Animals were predominantly crossbreds with a tendency toward high proportion of Murrah breed.

Records were obtained between 1997 and 2014. The relationship matrix included 34,326 animals with 8,572 mothers and 684 fathers. The number of animals between 1997 and 2014 was 42, 161, 297, 725, 1,042, 1,490, 1,937, 2,041, 2,619, 1,989, 4,148, 4,558, 4,855, 5,417, 5,371, 4,194, 1,897, and 347, respectively.

The traits evaluated were weaning weight (**WW**) from 12,429 males and 11,518 females, yearling weight (**W12**) from 3,040 males and 4,154 females, weight at 18 mo of age (**W18**) from 1,305 males and 2,624 females, weight at 24 mo of age (**W24**) from 451 males and 2,282 females, age at first calving (**AFC**) from 4,138 records, and milk yield from first calving to 270 d in milk (**MY270**) from 2,229 females. The age ranges (in days) for each trait were WW (180 to 300), W12 (330 to 390), W18 (450 to 510), W24 (680 to 760), and AFC (760 to 1500). MY270 was estimated following the guidelines of the International Committee of Animal Recording (ICAR, 2012). Analyses performed by means of the generalized linear model helped to define the fixed effects that were considered in the contemporary groups. Observations with standardized residuals of 3.5 standard deviations above and below the mean were excluded. Additionally, contemporary groups with fewer than 3 observations were also excluded. The general structure of the data is presented in Table 1.

Models

A multitrait model was fitted for the traits. Several fixed and random effects were fitted for the different traits. An overview is provided in Table 2. The contemporary group for WW, W12, W18, and W24 was defined as farm, year, and calving season (January to April, May to August, and September to December). The contemporary group for AFC and MY270 was farm, year, and first calving season (January to April, May to August and September to December).

A multitrait model (**MC**) and 5 reduced-rank models were analyzed, considering a structure of principal components from 1 to 5 components (PC_1, $PC_{1:2}$, $PC_{1:3}$, $PC_{1:4}$, and $PC_{1:5}$).

Table 1. Description of data for weaning weight (WW), yearling weight (W12), weight at 18 mo (W18), weight at 2 yr (W24), age at first calving (AFC), and milk yield at 270 d of first lactation (MY270)[1]

Trait	SX	No. Observations	Mean	No. Observations Total	Mean	CV	Min	Max	NCG
WW (kg)	M	12429	208.70	23937	207.35	0.23	80	384	216
	H	11508	205.89						
W12 (kg)	M	3040	213.00	7194	210.75	0.21	100	490	192
	H	4154	209.88						
W18 (kg)	M	1305	263.48	3929	256.09	0.20	130	500	155
	H	2624	253.25						
W24 (kg)	M	451	385.34	2733	358.48	0.15	250	759	143
	H	2282	353.65						
AFC (days)	H			4138	1110.35	0.11	761	1499	162
MY270 (kg)	H			2229	993.69	0.23	401	2192	149

[1]SX = sex, CV = coefficient of variation, Min = minimum value, Max = maximum value, NCG = number of contemporary groups.

The matrix representation of the MC model was

$$y = X\beta + Z_1a + Z_2m + Wpe + \varepsilon.$$

The model used for PC analysis was obtained by reparametrizing MC, generating an equivalent model that fits the principal components rather than conforming to the original traits (Meyer, 2005).

The matrix representation of the PC model is

$$y = X\beta + Z_1^*a^* + Z_2m + Wpe + \varepsilon,$$

where y is vector of observations, β is vector of fixed effects, a is vector of direct additive genetic random effects, m is vector of maternal genetic effect, pe is vector of maternal permanent environmental effect, and ε is random residual vector. X, Z_1, Z_2, and W are incidence matrices relating the fixed effects, direct additive genetic effects, maternal genetic effects, and permanent environmental effects, respectively.

Where $Z_1^* = Z_1(E \otimes I)$, $a^* = (E' \otimes I)$, $Var(a^*) = (I \otimes A)$, and $\sum_a = E\Lambda E'$. E = matrix of the eigenvectors e_i, Λ = diagonal matrix of eigenvalues λ_i and $\otimes$ = direct product. Then, the direct additive genetic (co)variance matrix (Σ_a) can be decomposed in terms of E and Λ, with $EE' = I$, and λ_i and e_i are ordered from highest to lowest. Considering only the largest mPC and replacing E by Em, the matrix comprises only the first m columns of $E(e_1, \ldots, e_m)$, and Z_1 has a number of columns proportional to the range of m to 6. The number of equations is correspondingly smaller (replacing Λ by submatrix Λ_m formed by the first m rows and columns), and a^* contains m elements for each individual (Meyer and Kirkpatrick, 2005).

Wombat software (Meyer, 2007a) was used, applying the restricted maximum likelihood (**REML**) information criterion. The convergence criterion was set at 10^{-9}.

The best model was selected by comparing the Akaike information criterion (**AIC**), which allows comparisons between nonhierarchical models, penalizing those with more parameters (Schwarz, 1978), and can be represented as

$$AIC = -2logL + 2p,$$

where p is the number of model parameters and log L is the logarithm of restricted maximum likelihood. The best model is the one with the lowest AIC.

Genetic Progress

A generalized model with smoothed estimates (**GAM**) was used to describe the genetic progress of WW, W12, W18, W24, AFC, and MY270. The model included year of birth as a smoothed variable. Statistical analyses were performed separately for males and females. The "gam" library (Wood, 2011) of R Project software was used for models and graphic construction (R Core Team, 2014).

Table 2. Fixed, random, and covariate effects for weaning weight (WW), yearling weight (W12), weight at 18 mo (W18), weight at 2 yr (W24), age at first calving (AFC), and milk yield at 270 d of first lactation (MY270) included in the models[1]

	Random effects				Fixed effects			Covariable
Trait	a	m	pe	ε	SX	NC	CG	(age)
WW	X	X	X	X	X	X	X	X
W12	X	X		X	X	X	X	X
W18	X			X	X	X	X	X
W24	X			X	X	X	X	X
AFC	X			X			X	
MY270	X			X			X	

[1]a = additive genetic effect, m = maternal genetic effect, pe = maternal permanent environmental effect, ε = residual effect, SX = sex (male, female), CN = number of calving (1 to 14), and CG = contemporary group.

Table 3. Number of estimated parameters (NP), Akaike information criterion (AIC), and percentage of direct additive genetic variance explained by each of the eigenvalues in each model

Model[1]	NP	AIC	λ_1	λ_2	λ_3	λ_4	λ_5	λ_6
PC_1	30	354077,96	100.00					
$PC_{1:2}$	36	354036,87	79.82	20.18				
$PC_{1:3}$	40	354033,18	74.77	22.31	2.92			
$PC_{1:4}$	43	354142,18	76.66	19.63	3.19	0.52		
$PC_{1:5}$	45	354045,87	77.60	18.30	3.33	0.16	0.16	
MC	46	354143,17	77.56	17.59	3.82	0.65	0.37	0.01

[1]PCn = reduced-analysis model for n principal components, MC = multi-trait model.

The model was as follows:

$$Y_i = \beta_0 + s(y_i) + \varepsilon_i,$$

where Y_i is the *i*th estimated breeding value (**EBV**) record of the animal in the *i*th year of birth (y_i), b0 is the intercept, $s(y_i)$ is the nonparameterized smooth function of the *i*th year of birth, and ε_i is the residual effect. GAM models allow data analysis without assuming a functional form known (Wood, 2006).

RESULTS AND DISCUSSION

According to the AIC, the best model was the $PC_{1:3}$ because of the following reasons: it kept all the original variance in the 3 eigenvalues, was more parsimonious because it estimated 40 parameters instead of the 46 estimated with MC (Table 3), achieved the convergence criterion faster-decreasing computational requirements, and adequately described the covariance structure between 6 traits, keeping 100% of the genetic variance of the traits. Several studies indicate that PCA is efficient enough to decrease the range of the model, maintaining a high percentage of the variation of the original traits in several production systems.

Similar results to those found in this study were reported by Meyer (2005), who found that the first 3 or 4 PC summarize most of the genetic variation of 8 traits measured in Angus cattle. The author also concluded that 7 PC can explain most of the variations of the 14 traits associated with beef production (Meyer, 2007a,b). Similarly, Boligon et al. (2013) reported that 3 PC are sufficient to explain 100% of the variation in 8 traits related to body weight in Nellore cattle and found genetic correlations of 0.47 to 0.86, which allow for reducing the analysis range to a few PC, thus avoiding redundant information of highly correlated traits.

In Brazil, Savegnago et al. (2011) reported that 4 PC were sufficient to account for 80.04% of the variation of 13 traits associated with egg production of laying hens. Buzanskas et al. (2013) evaluated 4 reproductive traits in Canchim Cattle and reported that the first 2 PC explained 73.37% of the total variation.

A Holstein study in Brazil analyzed 10 traits associated with milk production. According to the authors, a 2-PC model kept 94.25% of the genetic variation of all the traits, having to estimate 74 instead of the 110 parameters required by the complete range model. The authors concluded that the low number of PC required to estimate most of the variance was due to the high genetic correlations between the analyzed traits (Bignardi et al., 2012).

The PCA technique was used to estimate genetic parameters of 9 traits (6 associated with milk production, 2 with reproduction, and 1 with health status) in buffaloes, concluding that a 3-PC model kept 94.25% of the total variation, without losing estimation efficiency (Oliveira et al., 2014).

Live weights of animals for WW, W12, W18, and W24 are presented in Table 1. Males were heavier than females (2.81, 4.35, 9.65, and 30.18 kg, respectively). The study by Bolívar-Vergara et al. (2012) in Colombia reported 182 ± 42.46, 201.8 ± 38.70, 50.89 ± 278, and 363.4 ± 54.32 live weights for the aforementioned traits, respectively. Their WW and W12 were lower, while W18 and W24 were higher than those observed in this work.

The MY270 estimated in this work is lower than that reported in Brazil by Tonhati et al. (2008) for Murrah buffaloes at 305 d of lactation (993.69 vs. 1,495.08 ± 617.08 kg, respectively; Table 1). It is also lower than that reported in Italy by Rosati and Van Vleck (2002) for buffaloes up to 270 d of lactation (2,286.8 ± 492.1 kg). In Colombia, Hurtado-Lugo et al. (2006) reported 1,064.59 kg yield at 270 d. These 3 mentioned studies measured yield of animals with several parities.

The estimated AFC in this work (1,110.35 d; Table 1) was higher than that reported for buffaloes in Brazil and Colombia, which were 1064.59 ± 171.83 d, n = 2,436; and 1,140 ± 283.5 d, n = 216 (Bolívar Vergara et al., 2010; Oliveira et al. (2014), respectively). This difference may be due to lower number of records in relation to the amount analyzed in the present study.

Heritabilities of the direct additive genetic component for W12, W18, W24, and MY270 estimated by model $PC_{1:3}$ were similar to heritabilities estimated by the MC model. Heritabilities for WW and AFC were the same in both models (Table 4).

Heritabilities estimated by model $PC_{1:3}$ were lower for WW, W12, and W24, and they were higher for W18 when compared with values reported for the same traits in Colombia, which were 0.33, 0.42, 0.42, and 0.41, respectively (Bolívar-Vergara et al., 2012).

Table 4. Heritabilities (on the diagonal bold), genetic correlations (below the diagonal) and phenotypic correlations (above the diagonal) estimated for dual-purpose buffaloes in Colombia using a reduced model with three principal components ($PC_{1:3}$) and a complete multi-trait model (MC; standard errors are in parentheses)

Trait[1]	WW	W12	W18	W24	AFC	MY270
$PC_{1:3}$ model						
WW	**0.24 (0.02)**	0.78 (0.02)	0.72 (0.03)	0.39 (0.04)	-0.19 (0.03)	0.09 (0.93)
W12	0.99 (0.02)	**0.26 (0.02)**	0.81 (0.01)	0.49 (0.01)	-0.23 (0.10)	0.05 (0.04)
W18	0.94 (0.01)	0.95 (0.01)	**0.44 (0.03)**	0.66 (0.03)	-0.33 (0.02)	0.15 (0.10)
W24	0.80 (0.04)	0.79 (0.04)	0.89 (0.03)	**0.30 (0.04)**	-0.32 (0.08)	0.29 (0.04)
AFC	-0.51 (0.09)	-0.52 (0.10)	-0.51 (0.09)	-0.76 (0.08)	**0.14 (0.03)**	0.11 (0.03)
MY270	0.86 (0.10)	0.88 (0.11)	0.76 (0.09)	0.41(0.12)	-0.13 (0.08)	**0.24 (0.05)**
MC model						
WW	**0.24 (0.01)**	0.75 (0.00)	0.72 (0.00)	0.40 (0.01)	-0.19 (0.01)	0.08 (0.03)
W12	0.91 (0.02)	**0.27 (0.02)**	0.79 (0.00)	0.49 (0.02)	-0.22 (0.02)	0.56 (0.04)
W18	0.95 (0.02)	0.86 (0.03)	**0.45 (0.03)**	0.66 (0.01)	-0.33 (0.02)	0.12 (0.04)
W24	0.78 (0.06)	0.75 (0.07)	0.85 (0.05)	**0.30 (0.04)**	-0.33 (0.02)	0.17 (0.05)
AFC	-0.57 (0.09)	-0.44 (0.11)	-0.53 (0.09)	-0.76 (0.11)	**0.14 (0.03)**	0.12 (0.03)
MY270	0.43 (0.22)	0.60 (0.12)	0.53 (0.10)	0.51 (0.12)	-0.14 (0.9)	**0.26 (0.06)**

[1]WW = weaning weight, W12 = yearling weigh, W18 = weight at 18 mo of age, W24 = weight at 24 mo, AFC = age at first calving, MY270 = milk yield at 270 d of first lactation.

Bold values indicate heritabilities.

The heritability estimate for AFC was 0.14. Other researchers reported that heritability was between 0.08 and 0.16 for the same trait in Nellore heifers (Dias et al., 2004). These values are considered low to moderate, suggesting that AFC would respond better to environmental improvement programs than to selection processes.

The heritability for MY270 estimated in this study was similar to that reported in Murrah buffaloes in Brazil by Aspilcueta-Borquis et al. (2010), Mendes Malhado et al. (2013), and Tonhati et al. (2008), 0.26, 0.25, and 0.28, respectively. A heritability estimate equal to 0.22 was obtained for the same trait in Colombia by other researchers (Hurtado-Lugo et al., 2006), while 0.24 was reported for milk production in Italy (Rosati and Van Vleck, 2002).

Heritability of the maternal genetic component for W12 was 0.05 and 0.06 in models $PC_{1:3}$ and MC, respectively, and it was 0.05 for WW in both models. Those values indicate that no major changes would be expected in the short term for the maternal genetic effect as a result of selection based on WW or W12. Boligon et al. (2013) reported similar estimates for these traits in the Nellore breed. Also in Nellore, the maternal genetic effect was low, increasing from 0.03 at birth to 0.14 at 240 d, and then it decreased to zero at 600 d (Galvão de Albuquerque and Meyer, 2001).

The genetic correlation between AFC and body weight traits was negative in both models. This correlation was between -0.76 and -0.44 in model $PC_{1:3}$ and between -0.76 and -0.51 in model MC (Table 4), indicating that selected animals at heavier weights and earlier age will be more precocious, starting to breed earlier. Caetano et al. (2013) reported a genetic correlation of -0.34 between age at first calving and weight gain in Nellore between 210 and 365 d, while Buzanskas et al. (2013) reported -0.15 between AFC and weight at 420 d in Canchim cattle; both correlations are also negative but less intense than those estimated in this work.

The genetic correlations between AFC and MY270 were low in $PC_{1:3}$ and MC (-0.13 and -0.14, respectively). In Brazil, Seno et al. (2010) reported a similar genetic correlation of -0.12 between AFC and MY270, suggesting that selection of animals with less AFC may slightly increase milk yield in the first lactation.

Genetic correlations between WW, W12, W18, and W24 were positive and high in the $PC_{1:3}$ and MC models (Table 4). This can be explained by the existing part-whole component because the first weight records are correlated with weight data taken in subsequent periods. In model $PC_{1:3}$, the highest genetic correlation was in W12 with W18, with a value of 0.99, and the lowest was between WW and W12 with W24, with a value of 0.79. This lower value may be because they are the most distant measurements over time.

Another study in buffaloes estimated 0.85, 0.54, and 0.91 genetic correlations between W12-W18, W12-W24, and W18-W24, respectively (Bolívar-Vergara et al., 2012). Genetic correlations in Bosmara cattle were 1.00, 0.97, and 0.97 between WW-W12, WW-W18, and W12-W18, respectively (Bignardi et al., 2014). Similar data were reported in Nellore (Boligon et al., 2009). The genetic correlation values estimated in this work suggest that the genes responsible for WW are also highly responsible for later weights, which would allow for conducting the selection process at an early age.

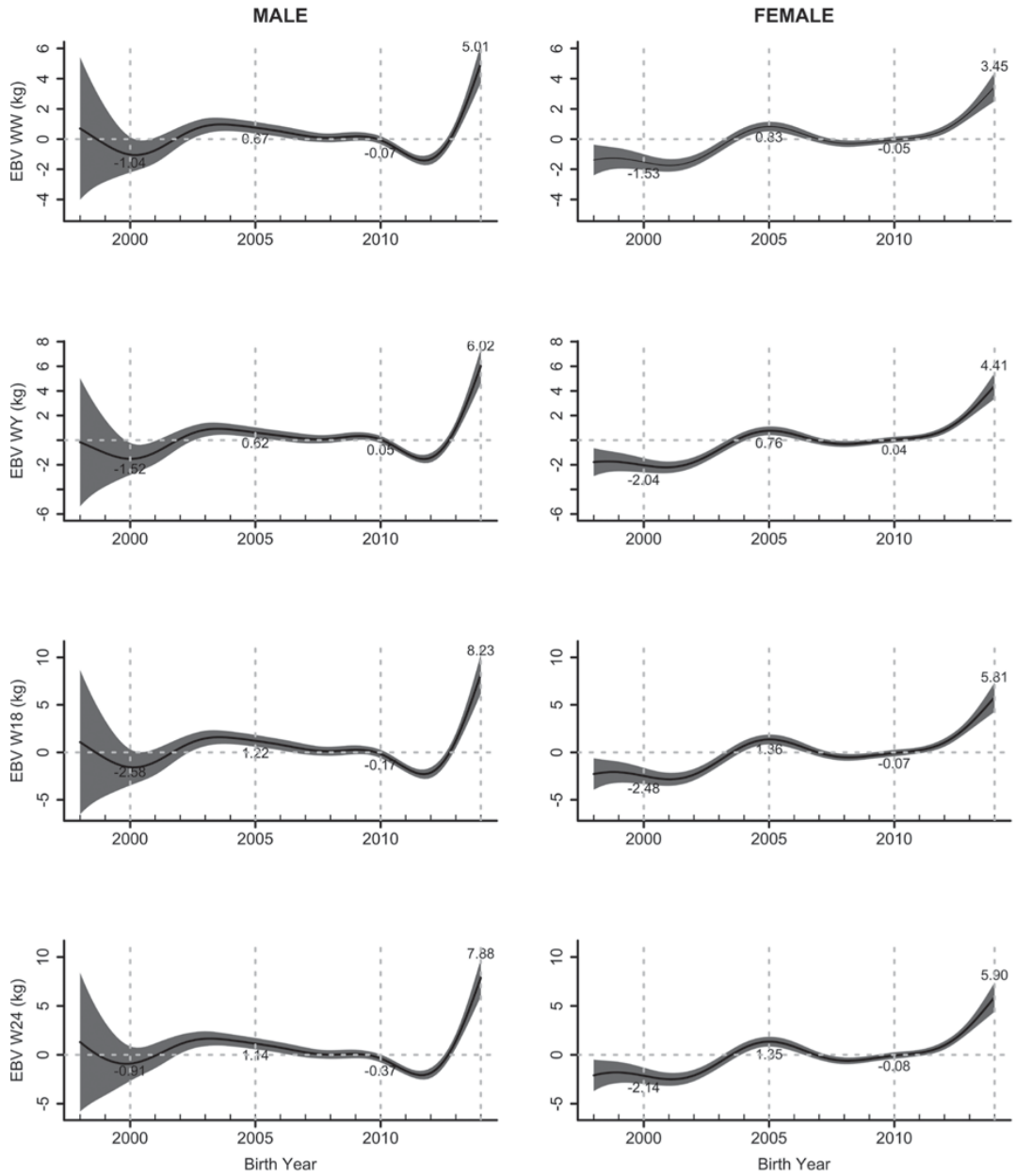

Figure 1. Genetic trend of estimated breeding values (EBV) for WW, W12, W18, and W24 in dual-purpose buffalo cattle in Colombia by year of calving.

The genetic correlations of MY270 with WW, W12, W18, and W24 estimated by the $PC_{1:3}$ model were greater than 0.41 (Table 4), suggesting that animals selected at high weight and early age may have increased milk production during first lactation. Some studies have reported negative genetic correlations between live-weight traits and milk yield (Vercesi Filho et al., 2007). Other studies have reported positive genetic correlations, in agreement with those reported in this work (Moore et al., 1991; Van der Waaij, Galesloot, and Garrick, 1997). According to the data obtained in this work, selection of heavier animals at weaning would increase weight at 18 and 24 mo, increase milk production in first lactation, and lower the age at first calving.

Genetic Progress

The genetic trend of EBV and the standard error (indicated by the shaded area) for traits associated with meat production, WW, W12, W18, and W24 are

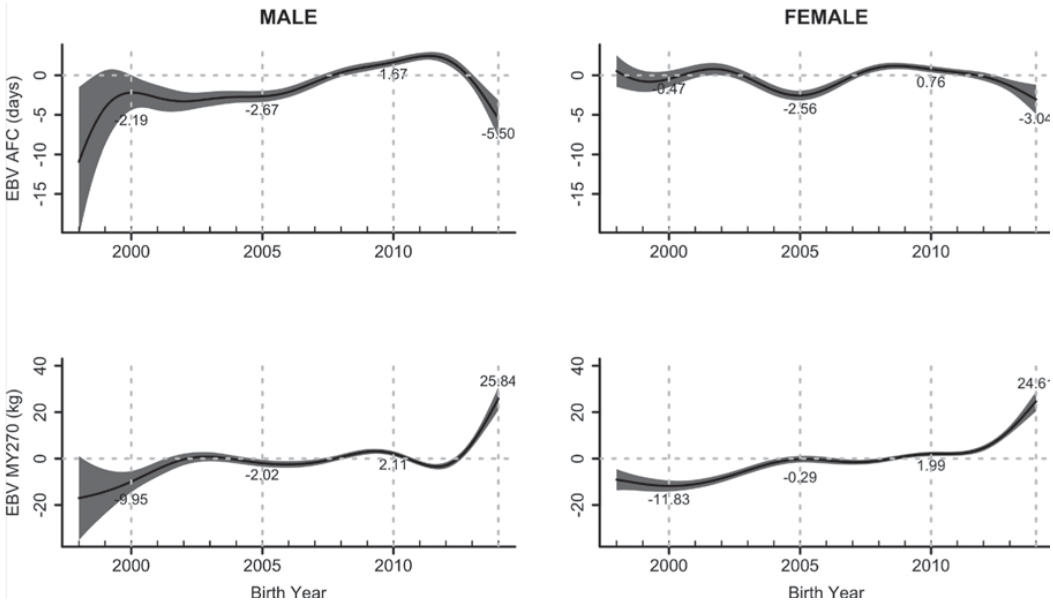

Figure 2. Genetic trend of estimated breeding values (EBV) for AFC and MY270 by year of calving in dual-purpose buffaloes in Colombia

presented in Fig. 1. Genetic progress in males and females was nonexistent until 2010, possibly because of a lack of clear selection criteria. Between 2010 and 2012, males showed a decrease in EBV and females showed a slight increase. During 2000 to 2014, W18 was the trait with the greatest increase: 0.77 and 0.59 kg/yr for males and females, respectively, while WW had the lowest genetic progress: 0.43 and 0.36 kg/yr for males and females, respectively. The greatest standard error occurred during the 1998–2000 period because of fewer production records and pedigree information.

Genetic progress of males and females for W12 was 0.54 and 0.46 kg/yr, and for W24 it was 0.63 and 0.57 kg/yr, respectively. In Creole cattle, the genetic trend for WW was reported in Thailand as 0.32 kg/yr (Intaratham et al., 2008). In Nellore, the tendency for weight at 205, 365, and 505 d was 0.27, 0.45, and 0.74 kg/yr, respectively, over a 26 yr period (de Assunção Sousa et al., 2013).

The genetic trend for AFC and MY270 is shown in Fig. 2. In the 2012–2014 period, the genetic trend for AFC was -0.24 and -0.18 d/yr for males and females, respectively. MY270 showed a genetic tendency of 3.27 and 2.61 kg/yr in males and females, respectively. In Chile, 1.91 kg/yr genetic trend increase for milk yield was reported for Overo Colorado cattle during 1978–1999 (Uribe and Smulders, 2004). In the United States, genetic trend increases for milk production in Holstein were 79, 102, and 116 kg/yr in the 1970s, 1980s, and 1990s, respectively (Hansen, 2000).

During 2012 to 2014, an increasing tendency for EBV of genetic traits associated with meat production and MY270 and a decrease for EBV associated with AFC were observed (Fig. 1 and 2). This coincides with the estimated genetic correlations among all traits. There are young animals in this period that had not yet been used for reproduction, suggesting that if selection is conducted according to EBV, major changes in the genetic trend might be expected for future generations, resulting in further progress and increased productivity of buffalo herds in Colombia.

Conclusions

The trait that could have a greater response to the selection process is W18. Nevertheless, MY270 was the trait with the greatest genetic progress during the evaluation period, probably due to the empirical selection conducted for this trait. The maternal genetic component for WW, W12, and AFC would have a lower response to the selection process due to low heritabilities. Reduced range models allow for a good estimation of both genetic parameters and genetic evaluation for economically important traits in Colombian buffaloes.

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Capítulo 3

Este artículo da respuesta al objetivo específico número tres

En este capítulo se retoma la paginación, como si el capítulo 2 se hubiese enumerado en forma continua.

Comparación de índices de selección en búfalos doble propósito en Colombia

Divier Antonio Agudelo-Gómez*‡1, Mario Fernando Cerón-Muñoz‡,

*Corporación Universitaria Lasallista, Facultad de Ciencias Administrativas y Agropecuarias, Grupo de investigación en Producción Desarrollo y Transformación Agropecuaria,055440, Caldas, Colombia; ‡Universidad de Antioquia, Facultad de Ciencias Agrarias, Grupo de investigación en Genética, Mejoramiento y Modelación Animal, (GaMMA), 050036, Medellín, Colombia

RESUMEN:

Se usaron los parámetros genéticos y valores genéticos estimados en modelos unicaracterísticos, multicaracterísticos y de rango reducido de tres componentes principales ($PC_{1:3}$) de las características peso al destete (PD), peso al año (P12), peso a los 18 meses (P18), peso a los dos años (P24), edad al primer parto (EPP), producción de leche hasta los 270 días (PL270), el efecto genético materno para peso al destete GMPD), y del efecto genético materno para peso al año (GMP12), estimados en una población bufalina doble propósito en Colombia, para construir índices de selección y estimar el progreso genético por medio de modelación de apareamientos aplicando diferentes criterios de selección y diferentes ponderaciones económicas a cada una de las características evaluadas. La selección por una sola característica permite el mayor progreso genético de ella, sin embargo no hay claridad en la tendencia de las demás características lo que podría tener consecuencias no deseadas en el rebaño bufalino. El índice que en general permitió mejorar los parámetros productivos para todas las características estudiadas es el construido a partir de las correlaciones lineales entre el primer componente principal del modelo de rango reducido $PC_{1:3}$ y los valores genéticos estimados de las características estudiadas.

1 Corresponding author: diagudelo@lasallistadocentes.edu.co

Palabras claves: modelación, progreso genético

INTRODUCCIÓN

Para establecer un programa de mejoramiento genético es necesario tener claro varios aspectos: 1) definir las características que se desean mejorar, en el caso de la ganadería bufalina colombiana las más importantes, por su impacto en la economía de los productores, son las relacionadas con la producción de leche, carne y la reproducción, 2) conocer los parámetros genéticos (heredabilidad de cada una de las características y las correlaciones genéticas existentes entre las ellas), 3) estimar los valores genéticos, para cada característica, de cada uno de los animales que hacen parte de la población objetivo, y 4) establecer la estrategia a implementar, para realizar la selección de los animales y programar los apareamientos, todo esto, con el objetivo último de obtener progreso genético y aumento en la productividad de los hatos que implementen un programa de mejoramiento.

En Colombia desde el año 2006 se han realizado evaluaciones genéticas en el hato bufalino, para producción de leche (Cerón-Muñoz et al., 2006; Hurtado-Lugo et al., 2006), producción de carne desde 2008 (Agudelo-Gómez et al., 2009) y características reproductivas desde 2010 (Bolívar-Vergara et al., 2010), pero hasta la fecha no se había realizado en forma paralela una evaluación genética que integrara: peso al destete (PD), peso al año (P12), peso a los 18 meses (P18), peso a los dos años (P24), edad al primer parto (EPP) y producción de leche hasta los 270 días (PL 270).

Los bufalistas, en Colombia, tradicionalmente han realizado una selección fenotípica basada principalmente en la producción de leche, pues es la característica que representa mayores ingresos económicos. Sin embargo, dado que los búfalos machos después del destete son destinados al engorde y a la posterior producción de carne, es importante que se preste atención a las características asociadas al

peso vivo de los animales para poder realizar una selección que permita aumentar en forma paralela las características asociadas a la producción de leche y carne, sin dejar de lado las características reproductivas.

Como alternativa a la selección tradicional, en la que se seleccionan los animales por una sola característica, los índices de selección (IS) permiten integrar en un solo valor toda la información disponible (genética, fenotípica, además de poder incorporar información económica), de tal manera que la falta de mérito en una característica puede ser equilibra por la superioridad en otras, permitiendo al final obtener un solo valor, denominado genotipo agregado.

Los índices utilizados en los programas de mejoramiento por selección fueron definidos por Smith, (1936) como una combinación lineal de los valores fenotípicos de los caracteres de interés y se desarrollaron inicialmente para la selección multicarácter en plantas. Según Hazel (1943) el índice de selección mide el mérito neto de mejoramiento de las unidades de selección, en la especie que se utilice. En resumen, un índice de selección mide la ganancia económica por efecto de la utilización de los animales escogidos como reproductores. Para Falconer and Mackay (1996) el índice de selección es el mejor predictor lineal del valor de mejoramiento por unidad de selección y toma la forma de la regresión múltiple del valor de mejoramiento, sobre todas las fuentes de información. Otro aspecto importante que tiene este tipo de índices, es que dependiendo de las condiciones del mercado, o de los intereses de los productores, se le puede dar mayor o menor importancia a determinada característica.

Por su parte el Análisis de Componentes Principales (PCA), es una técnica multivariada que permite examinar la relación existente entre diferentes características cuantitativas y puede ser usado para disminuir el número de variables a analizar, agrupándolas en un nuevo conjunto de variables denominado componentes principales (PC) (Kaiser, 1960), que pueden ser usados para construir índices de selección dependiendo el tipo de relación existente entre las características analizadas con cada PC (Buzanskas et al., 2013).

El objetivo de este trabajo fue construir diferentes índices de selección a partir de

evaluaciones genéticas realizadas con modelos unicaracterísticos, multicaracterísticos y multicaracterísticos de rango reducido (PCA), y estimar el progreso genético para cada característica, para definir cuál metodología de evaluación permite construir el índice de selección que genere el mayor progreso genético para las características evaluadas en la población de búfalos doble propósito en Colombia.

MATERIALES Y MÉTODOS

Datos

Se utilizaron los valores genéticos (BV) de machos y hembras estimados en los modelos unicaracterístico, multicaracterístico y multicaracterísticos de rango reducido. Las características tenidas en cuenta para la construcción de los índices fueron peso al destete (PD), peso al año (P12), peso a los 18 meses (P18), peso a los dos años (P24), edad al primer parto (EPP), producción de leche hasta los 270 días (PL270), el efecto genético materno para peso al destete (GMPD), y el efecto genético materno para peso al año (GMP12).

Metodologías de índices empleadas:

El progreso genético fue estimado por el promedio de valores genéticos de la primera generación (G1) obtenida por apareamientos al azar (utilizando pseudo-simulación con distribución uniforme) de los individuos que se incluyeron en los análisis descritos por Agudelo-Gómez et al., (2015) y Agudelo-Gómez et al., (2015b)

Los índices construidos fueron:

Inicialmente se realizaron apareamientos al azar de animales escogidos aleatoriamente de la población utilizando ensayos de Bernoulli del 70% de hembras con el 5% de machos (**IS_0**). También se aparearon (distribución uniforme) el 70% de las mejores hembras y el 5% de los mejores machos según el valor genético para

producción de leche obtenido en análisis unicaracterístico (**IPL270**).

Posteriormente se escogió el 70% de las mejores hembras y el 5% de los mejores machos según los valores de los índices de selección con base en la metodología propuesta Hazel (1943), (**IS_1, IS_2,…,IS_7**), a partir de los valores de cría de las características obtenidos en los modelos unicaracterísticos y variando la ponderación económica como se muestra en la Tabla 1.

Posteriormente se escogió el 70% de las mejores hembras y el 5% de los mejores machos según los valores de los índices de selección con base en la metodología propuesta Hazel (1943), (**IS_8, IS_9,…,IS_{14}**), a partir de los valores de cría de las características obtenidos en los modelos multicaracterísticos y variando la ponderación económica como se muestra en la Tabla 1.

La construcción del índice de selección a partir de la metodología propuesta por Hazel, (1943) es como se describe a continuación:

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

donde:

h_i = coeficiente de regresión para *i-ésima* características, usados para la construcción del índice, P^{-1} = es la matriz de (co)varianzas fenotípicas, G = es la matriz de (co)varianzas genéticas, y v = son las ponderaciones económicas para cada una de las características estudiadas.

Las matrices de varianzas *P* y *G* fueron obtenidas del modelo multicaracterístico, descrito por Agudelo-Gómez et al., (2015b).

Las matrices *P* y *G* se presentan a continuación:

$$\begin{bmatrix} h_{PD} \\ h_{P12} \\ h_{P18} \\ h_{P24} \\ h_{EPP} \\ h_{PL270} \\ h_{GMPD} \\ h_{GMP12} \end{bmatrix} = \begin{bmatrix} 1107,5 & 891,3 & 960,0 & 582,0 & -679,4 & 479,3 & 0,0 & 0,0 \\ 891,3 & 1277,7 & 1124,2 & 762,0 & -830,7 & 382,2 & 0,0 & 0,0 \\ 960,0 & 1124,2 & 1605,2 & 1158,4 & -1410,4 & 922,9 & 0,0 & 0,0 \\ 582,0 & 762,0 & 1158,4 & 1930,0 & -1529,5 & 1491,9 & 0,0 & 0,0 \\ -679,4 & -830,7 & -1410,4 & -1529,5 & 11174,0 & 2475,9 & 0,0 & 0,0 \\ 479,3 & 382,2 & 922,9 & 1491,9 & 2475,9 & 36831,0 & 0,0 & 0,0 \\ 0,0 & 0,0 & 0,0 & 0,0 & 0,0 & 0,0 & 1107,5 & 0,0 \\ 0,0 & 0,0 & 0,0 & 0,0 & 0,0 & 0,0 & 0,0 & 1277,7 \end{bmatrix}^{-1} \times \begin{bmatrix} 270,0 & 282,2 & 418,8 & 310,3 & -389,1 & 699,9 & 0,0 & 0,0 \\ 282,2 & 349,3 & 432,1 & 340,7 & -340,1 & 1091,1 & 0,0 & 0,0 \\ 418,8 & 432,1 & 717,4 & 554,2 & -591,5 & 1372,2 & 0,0 & 0,0 \\ 310,3 & 340,7 & 554,2 & 588,7 & -763,4 & 1218,2 & 0,0 & 0,0 \\ -389,1 & -340,1 & -591,5 & -763,4 & 1699,9 & -571,3 & 0,0 & 0,0 \\ 699,9 & 1091,1 & 1372,2 & 1218,2 & -571,3 & 9482,0 & 0,0 & 0,0 \\ 0,0 & 0,0 & 0,0 & 0,0 & 0,0 & 0,0 & 270,0 & 0,0 \\ 0,0 & 0,0 & 0,0 & 0,0 & 0,0 & 0,0 & & 349,3 \end{bmatrix} \times \begin{bmatrix} V_{PD} \\ V_{P12} \\ V_{P18} \\ V_{P24} \\ V_{EPP} \\ V_{PL270} \\ V_{GMPD} \\ V_{GMP12} \end{bmatrix}$$

Con los regresores: h_{PD}, h_{P12}, h_{P18}, h_{P24}, h_{EPP}, h_{PL270}, h_{GMPD}, y h_{GMP12}, se construye el

índice para cada animal de la siguiente forma:

$$IS=h_{PD}Y_{PD}+h_{P12}Y_{P12}+h_{P18}Y_{P18}+h_{P24}Y_{P24}+h_{EPP}Y_{EPP}+h_{PL270}Y_{PL270}+h_{GMPD}Y_{GMPD}+h_{GMP12}Y_{GMP12}$$

Donde, *IS* es el índice se selección, Y_{PD}, Y_{P12}, Y_{P18}, Y_{P24}, Y_{EPP}, Y_{PL270}, Y_{GMPD}, y Y_{GMP12}, son los BV de las características evaluadas en los modelos unicaracterísticos.

Tabla 1. Ponderaciones económicas para cada una de las características evaluadas, usadas para la construcción de cada uno de los índices de selección IS_n

Característica	**Ponderación económica (*v*), para los diferentes índices analizados**													
	IS_1	**IS_2**	**IS_3**	**IS_4**	**IS_5**	**IS_6**	**IS_7**	**IS_8**	**IS_9**	**IS_{10}**	**IS_{11}**	**IS_{12}**	**IS_{13}**	**IS_{14}**
PD	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
P12	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
P18	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
P24	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
EPP	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
PL270	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
GMPD	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
GMP12	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

PD: peso al destete, P12: peso al año, P18: peso a los 18 meses, P24: peso a los 2 años, PL270: producción de leche hasta los 270 días, EPP: edad al primer parto, GMPD: efecto genético materno para peso al destete, GMP12: efecto genético materno al año

También se construyeron índices de selección a partir de las correlaciones lineales de las características evaluadas con cada uno de los tres primeros compontes principales estimadas por Agudelo-Gómez et al., (2015ª) y Agudelo-Gómez et al., (2015b). La construcción de los índices $IPCA_{1l}$, $IPCA_{2l}$, e $IPCA_{3l}$ $IPCA_{4l}$, $IPCA_{5l}$, e $IPC6_{6l}$ se realizó de la siguiente forma:

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

Dónde $IPCA_{jl}$ es el índice correspondiente al l-*ésimo* animal, en el *j-ésimo* componente principal, eig_{ij} es el eigenvector (correlación lineal) de la *i-ésima* característica en el *j-ésimo* componente principal, y BV_{il} es el valor de cría de la *i-ésima* característica del *j-ésimo* l-*ésimo* animal.

Los índices $IPCA_{1l}$, $IPCA_{2l}$, e $IPCA_{3l}$, se construyeron a partir de los BV estimados en los modelos unicaracterísticos y las coordenadas (correlaciones lineales) de cada una de las características en cada uno de los tres primeros PC, estimados por Agudelo-Gómez et al., (2015a), (ver Tabla 2).

Tabla 2. Correlación lineal de los valores genéticos de las características con los componentes principales (PC1), (PC2) y (PC3)

Característica	PC1	PC2	PC3
PD	0.78	-0.21	0.83
P12	0.75	-0.05	-0.00
P18	0.78	0.16	-0.00
P24	0.73	0.13	-0.05
PL270	0.17	0.35	0.84
EPP	-0.38	-0.39	0.53
GMPD	-0.30	0.75	-0.25
GMP12	-0.00	0.82	0.13

PD: peso al destete, P12: peso al año, P18: peso a los 18 meses, P24: peso a los 2 años, PL270: producción de leche hasta los 270 días, EPP: edad al primer parto, GMPD: efecto genético materno para peso al destete, GMP12: efecto genético materno al año

Los índices $IPCA_{4l}$, $IPCA_{5l}$, e $IPC6_{6l}$, se construyeron a partir de los BV estimados en los modelos unicaracterísticos y las coordenadas (correlaciones lineales) de cada una de las características en cada uno de los tres primeros PC, estimados por Agudelo-Gómez et al., (2015b), (ver Tabla 3).

Tabla 3. Correlación lineal de los valores genéticos de las características con los componentes principales (PC1), (PC2) y (PC3) estimados en el modelo $PC_{1:3}$

Característica	PC1	PC2	PC3
PD	0.45	0.11	0.05
P12	0.65	0.10	0.11
P18	0.77	0.20	0.58
P24	0.60	0.37	0.56
PL270	0.79	-0.31	-0.23
EPP	-0.32	-0.83	0.51
GMPD	0.01	0.25	-0.05
GMP12	0.01	0.13	-0.08

PD: peso al destete, P12: peso al año, P18: peso a los 18 meses, P24: peso a los 2 años, PL270: producción de leche hasta los 270 días, EPP: edad al primer parto, GMPD: efecto genético materno para peso al destete, GMP12: efecto genético materno al año

El progreso genético fue evaluado en la generación 1; en la construcción de cada índice se realizaron 200 simulaciones de los apareamientos, para luego obtener la estadística descriptiva del progreso genético de cada una de las características en cada uno de los índices desarrollados; también se estimó el intervalo de confianza al 95%

RESULTADOS Y DISCUCIÓN

Los regresores h_i para cada uno de los IS_n (IS_1, $IS_{2.....}$, IS_{14}) son presentados en la Tabla 4.

Tabla 4. Regresores h_i aplicados para la construcción de cada uno de los índices de selección económicas para cada una de las características evaluadas, en cada uno de los índices

Característica	Los regresores h_i, para los diferentes índices analizados													
	IS_1	IS_2	IS_3	IS_4	IS_5	IS_6	IS_7	IS_8	IS_9	IS_{10}	IS_{11}	IS_{12}	IS_{13}	IS_{14}
PD	-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
P12	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
P18	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
P24	-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
EPP	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
PL270	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
GMPD	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
GMP12	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

PD: peso al destete, P12: peso al año, P18: peso a los 18 meses, P24: peso a los 2 años, PL270: producción de leche hasta los 270 días, EPP: edad al primer parto, GMPD: efecto genético materno para peso al destete, GMP12: efecto genético materno al año

Los valores promedio de BV en la población estudiada, para las características PD, P12, P18, P24, PL270, GMPD, GMP12, y EPP, fueron de 0.96, 1.11, 2.22, 0.96, 10.53, 0.41 -0.13 kg y 1.40, días, respectivamente.

El progreso genético alcanzado al aplicar cada uno de los índices para PD, P12, P18, P28, EPP, PL270, GMPD y GMP12, se presentan en las tablas 5 a 12, respectivamente.

Dependiendo el interés que tenga cada criador podría seleccionar un índice que permita cumplir con los objetivos planteados en el sistema de producción. Si se selecciona teniendo en cuenta una sola característica, se obtendrá el mayor progreso genético para la característica en cuestión. Sin embargo, si no se tiene en cuenta el tipo de relaciones genéticas existentes con otras, puede existir el riesgo de

que no se obtenga progreso genético en las otras características que no fueron tenidas en cuenta, o peor aún, que exista un efecto no deseado sobre otra característica (Falconer and Mackay, 1996).

Para dar sustento al párrafo anterior se presenta en este trabajo el índice en el que se seleccionó por PL270, pues esta característica en los sistemas de producción bufalino doble propósito en Colombia es, sin duda alguna, a la que los bufalistas dan mayor importancia económica; además la leche de búfalas es reconocida por su calidad, en cuanto al alto porcentaje de grasa y proteína, lo que la hace especial para la elaboración de productos especializados, como el queso mozzarella (Rosati and Van Vleck, 2002). El mayor progreso genético para PL270 se obtuvo cuando se seleccionó por PL270 con un valor de 59.95 kg y el menor progreso genético fue de 14.62 kg, el cual ocurrió cuando no se realizó ningún tipo de selección (IS_0), (ver Tabla 10).

Al analizar el efecto que tiene la selección por PL270 sobre las demás características se puede observar que no permite un progreso genético importante al compararlo con el progreso genético alcanzado por otros índices cuyos resultados se presentan más adelante. Se puede resaltar que si se selecciona únicamente por PL270 también aumentan la EPP en 11.37 días, (ver Tabla 9), y se disminuye el GMPD y GMP12 (ver Tablas 11 y 12 respectivamente), aspectos que no son deseados en los hatos bufalinos.

Entre los índices desarrollados bajo la metodología de Hazel (1943), el mayor progreso genético para PL270 fue de 44.90 kg, obtenido en el IS_8, en el que las ponderaciones económicas para todas las características fue uno. Este mismo índice presentó progresos genéticos positivos con todas las demás características y es el que aumenta en mayor cantidad de días la EPP (24 d), (ver Tabla 9), este último aspecto no es deseado entre los productores debido al interés que los animales inicien una vida productiva lo más pronto posible (Rosati and Van Vleck, 2002; Bolívar-Vergara et al., 2010; Oliveira et al., 2014).

Entre los IS desarrollados a partir de las correlaciones lineales de las características con los PC el que presentó el mayor progreso genético para PL270 fue $IPCA_3$ con

46.49 kg, lo que coincide con la alta correlación lineal que tuvo PL270 con PC3 (0.84) (ver Tabla 2). El mismo índice presentó progresos genéticos positivos par PD, P12, P18, P24, y EPP, (ver Tablas 5 a 9). EPP presentó el menor progreso genético en el IPCA3 (24.00 días), esto se explica debido a la mayor correlación lineal de esta característica (0.53); en el PC3, (ver Tabla 2). GMPD y GMP12 presentaron progreso genético negativo en este índice.

Otra de las característica a la que los bufalistas dan mucha importancia es P18, debido a que a esta edad en muchos hatos bufalinos se realizan procesos de selección de hembras reproductoras (Barrera et al., 2014), y lo s machos inician el proceso de finalización para la ceba (Ramírez Toro et al., 2011); además de acuerdo a los valores de heredabilidad estimados en los dos trabajos anteriores (capítulo 1, 0.53, en el modelo unicaracterístico y capítulo 2, 0.44 y 0.45 en los modelos de rango reducido y multicaracterístico, respectivamente) es una característica que respondería muy bien a los procesos de selección, además de presentar correlaciones genéticas altas y positivas con PD, P12, P24 y PL270, y alta y negativa con EPP.

El mayor progreso genético para P18 entre los índices desarrollados con la metodología de Hazel (1943) se obtuvo en el IS_{10} (ver Tabla 7). Este índice también permite obtener un progreso genético en todas las demás características, excepto con EPP que aumenta en 4.42 días, (ver Tablas 5, 6, y 8 a 12).

Dentro de los índices desarrollados a partir de las correlaciones lineales con los PC, el modelo que permitió alcanzar el mayor progreso genéticos para P18 fue $IPCA_1$, que también es el índice que permite obtener el mayor progreso genético para PD y P12, con valores de 14.08 y 10.94 kg, (ver Tablas 5 y 6), respectivamente. Este índice también permite obtener progresos genéticos positivos para P24, PL270, GMPD y GMP12, con valores de 7.09, 31.77, 1.18, 3.67 kg, (ver Tablas 8, y 10 a 12), respectivamente; y obtener un progreso genético negativo para EPP con -3.66 días, (ver Tabla 9). Los progresos genéticos obtenidos con este índice coinciden con las correlaciones lineales de las características evaluadas con el primer PC (ver Tabla 2), obtenido a partir de las estimaciones de los valores genéticos de las

características de los animales evaluados en los modelos unicaracterísticos.

Algunos criadores de búfalos dan importancia al P24 debido a que en muchos sistemas de producción se tiene esta edad como referencia para realizar la programación de las bubillas para primer servicio o en el caso de los machos para ser destinados al sacrificio (Ramírez Toro et al., 2011). El menor y mayor progreso genético para P24, en los índices evaluados fue de -0-09 y 11.99, en IS_0 e $IPCA_4$, respectivamente, (ver Tabla 8). Entre los índices en que se empleó la metodología de Hazel, (1943) el mayor progreso fue de 8.59 kg, obtenido en el IS_{11}, (ver Tabla 8). El IS_{11} también permitió obtener progresos genéticos positivos para todas las características, incluso para EPP con 4.64 días, que como se mencionó en párrafos anteriores no es deseado por parte de los criadores.

Dentro de los índices desarrollados con las correlaciones lineales de las características y los PC, el índice que permitió obtener un mayor progreso genético para P24 fue el $IPCA_4$, con 11.99 kg, (ver Tabla 8), también fue el que presentó el mayor progreso genético para P12 con 10.53 kg, (ver Tabla 6). Además fue el índice que presentó el menor progreso genético para EPP con -13.13 días. Con las demás características: PD, P18, PL270, GMPD, y GMP12, presentó progresos genéticos de 9.62, 18.80, 41.33, 0.62, y 0.17 kg, (ver Tablas 5, 7 y 10 a 12), respectivamente. El efecto de este índice sobre todas las características se explica por las correlaciones que tiene este componente con todas las características, (ver Tabla 3).

Con respecto a la construcción de índices de selección usando los BV estimados con los modelos unicaracterísticos (IS_1, IS_2,…,IS_7) y a los construido con los BV en el modelo multicaracterístico (IS_8, IS_9,…,IS_{14}), se observa, en general, un mayor aumento en la tendencia genética de las características en los últimos índices. También se puede identificar que el progreso genético fue similar dentro de los índices creados a partir de los modelos unicaracterísticos, e igualmente el progreso genético de las diferentes características fue similar dentro de los índices creados a partir del modelo multicacterístico, (ver Tablas 5 a 14).

Tabla 5. Progreso genético alcanzado para peso al destete (PD), medido en kg, en cada uno de los índices de selección (IS) utilizados

IS	Media	SD	Min	Max	I C inf	I C Sup
IS_0	1,12	0,07	0,99	1,33	1,10	1,13
IPL270	3,89	0,12	3,58	4,15	3,87	3,92
IS_1	5,02	0,06	4,85	5,16	5,01	5,04
IS_2	5,61	0,06	5,45	5,74	5,60	5,62
IS_3	6,28	0,05	6,17	6,40	6,27	6,29
IS_4	5,89	0,04	5,78	6,02	5,88	5,9
IS_5	4,06	0,06	3,87	4,20	4,05	4,07
IS_6	6,66	0,05	6,50	6,75	6,65	6,67
IS_7	6,96	0,05	6,81	7,12	6,95	6,97
IS_8	10,67	0,23	10,23	11,17	10,63	10,72
IS_9	15,67	0,25	15,05	16,35	15,62	15,72
IS_{10}	15,72	0,20	15,28	16,26	15,68	15,76
IS_{11}	15,69	0,21	15,21	16,05	15,65	15,73
IS_{12}	10,77	0,13	10,39	11,07	10,74	10,79
IS_{13}	16,22	0,22	15,72	16,80	16,18	16,27
IS_{14}	16,00	0,22	15,48	16,57	15,96	16,05
$IPCA_1$	14,08	0,07	13,90	14,29	14,07	14,09
$IPCA_2$	2,36	0,12	2,14	2,70	2,34	2,39
$IPCA_3$	1,22	0,13	0,93	1,54	1,19	1,24
$IPCA_4$	9,62	0,11	9,33	9,91	9,60	9,64
$IPCA_5$	-0,12	0,11	-0,39	0,14	-0,14	-0,10
$IPCA_6$	-0,05	0,08	-0,26	0,18	-0,07	-0,04

IS=índice de selección, SD=desviación estándar, Min=mínimo, Max=máximo, IC inf=intervalo de confianza inferior, IC sup=intervalo de confianza superior

Tabla 6. Progreso genético alcanzado para peso al año (P12), medido en kg en cada uno de los índices de selección (IS) utilizados

IS	Media	SD	Min	Max	I C inf	I C Sup
IS_0	2,51	0,04	2,38	2,59	2,50	2,52
IPL270	5,06	0,06	4,94	5,18	5,05	5,07
IS_1	6,79	0,05	6,69	6,89	6,78	6,79
IS_2	7,21	0,04	7,11	7,29	7,20	7,22
IS_3	7,21	0,04	7,10	7,31	7,20	7,21
IS_4	7,10	0,04	6,97	7,19	7,09	7,11
IS_5	5,34	0,04	5,26	5,43	5,33	5,35
IS_6	6,60	0,05	6,46	6,71	6,59	6,61
IS_7	6,56	0,04	6,44	6,65	6,55	6,57
IS_8	9,98	0,03	9,90	10,07	9,97	9,99
IS_9	10,64	0,07	10,42	10,83	10,62	10,65
IS_{10}	10,46	0,07	10,31	10,60	10,45	10,47
IS_{11}	10,56	0,07	10,43	10,73	10,54	10,57
IS_{12}	8,38	0,06	8,25	8,53	8,37	8,40
IS_{13}	9,89	0,09	9,66	10,12	9,87	9,91
IS_{14}	9,76	0,09	9,50	10,00	9,74	9,77
$IPCA_1$	10,94	0,03	10,85	11,00	10,93	10,95
$IPCA_2$	4,72	0,06	4,56	4,86	4,71	4,73
$IPCA_3$	4,12	0,05	3,99	4,26	4,11	4,13
$IPCA_4$	10,53	0,13	10,23	10,80	10,50	10,55
$IPCA_5$	0,44	0,11	0,19	0,75	0,42	0,46
$IPCA_6$	1,17	0,09	0,94	1,40	1,15	1,18

S=índice de selección, SD=desviación estándar, Min=mínimo, Max=máximo, ICinf=intervalo de confianza inferior, ICsup=intervalo de confianza superior

Tabla 7. Progreso genético alcanzado para peso a los 18 meses (P18) , medido en kg, en cada uno de los índices de selección (IS) utilizados

IS	Media	SD	Min	Max	I C inf	I C Sup
IS_0	7,72	0,10	7,51	7,99	7,70	7,74
IPL270	13,08	0,13	12,74	13,31	13,06	13,11
IS_1	27,04	0,08	26,83	27,20	27,03	27,06
IS_2	25,47	0,09	25,22	25,67	25,46	25,49
IS_3	26,32	0,08	26,13	26,53	26,30	26,33
IS_4	25,84	0,09	25,6	26,1	25,83	25,86
IS_5	19,80	0,09	19,57	20,03	19,78	19,82
IS_6	27,93	0,07	27,77	28,10	27,92	27,94
IS_7	27,70	0,08	27,52	27,92	27,69	27,72
IS_8	22,06	0,12	21,70	22,36	22,04	22,09
IS_9	24,88	0,21	24,41	25,32	24,83	24,92
IS_{10}	25,30	0,18	24,86	25,81	25,27	25,34
IS_{11}	25,12	0,20	24,61	25,57	25,08	25,16
IS_{12}	20,92	0,17	20,57	21,41	20,89	20,95
IS_{13}	25,12	0,22	24,57	25,52	25,08	25,17
IS_{14}	25,13	0,21	24,52	25,70	25,08	25,17
$IPCA_1$	26,56	0,09	26,36	26,79	26,54	26,58
$IPCA_2$	17,13	0,14	16,75	17,56	17,10	17,16
$IPCA_3$	9,42	0,12	9,13	9,73	9,40	9,45
$IPCA_4$	15,80	0,16	15,38	16,28	15,77	15,83
$IPCA_5$	1,89	0,17	1,48	2,33	1,86	1,93
$IPCA_6$	2,10	0,12	1,78	2,47	2,08	2,13

IS=índice de selección, SD=desviación estándar, Min=mínimo, Max=máximo, ICinf=intervalo de confianza inferior, ICsup=intervalo de confianza superior

Tabla 8. Progreso genético alcanzado para peso a los dos años (P24) , medido en kg, en cada uno de los índices de selección (IS) utilizados

IS	Media	SD	Min	Max	I C inf	I C Sup
IS_0	-0,09	0,06	-0,23	0,06	-0,10	-0,08
IPL270	2,23	0,08	2,07	2,43	2,22	2,25
IS_1	2,76	0,06	2,55	2,87	2,75	2,77
IS_2	4,16	0,06	3,99	4,35	4,15	4,18
IS_3	4,71	0,05	4,58	4,89	4,70	4,72
IS_4	4,60	0,06	4,47	4,73	4,59	4,61
IS_5	2,22	0,05	2,07	2,34	2,21	2,23
IS_6	3,95	0,06	3,79	4,13	3,94	3,97
IS_7	4,78	0,06	4,64	4,93	4,76	4,79
IS_8	6,89	0,09	6,72	7,09	6,87	6,91
IS_9	8,18	0,12	7,91	8,48	8,16	8,20
IS_{10}	8,47	0,14	8,16	8,82	8,44	8,49
IS_{11}	8,59	0,13	8,27	9,02	8,57	8,62
IS_{12}	5,04	0,10	4,79	5,29	5,02	5,06
IS_{13}	7,63	0,13	7,31	7,92	7,60	7,65
IS_{14}	8,21	0,14	7,84	8,58	8,18	8,24
$IPCA_1$	7,09	0,05	6,94	7,21	7,08	7,10
$IPCA_2$	3,46	0,08	3,28	3,67	3,45	3,48
$IPCA_3$	0,34	0,09	0,02	0,55	0,32	0,36
$IPCA_4$	11,99	0,13	11,61	12,36	11,97	12,02
$IPCA_5$	2,74	0,14	2,42	3,11	2,71	2,77
$IPCA_6$	0,00	0,11	-0,28	0,33	-0,02	0,02

IS=índice de selección, SD=desviación estándar, Min=mínimo, Max=máximo, ICinf=intervalo de confianza inferior, ICsup=intervalo de confianza superior

Tabla 9. Progreso genético alcanzado para edad al primer parto (EPP), medido en días, en cada uno de los índices de selección (IS) utilizados

IS	Media	SD	Min	Max	I C inf	I C Sup
IS_0	7,80	0,10	7,53	8,04	7,78	7,82
IPL270	11,37	0,12	11,11	11,61	11,34	11,39
IS_1	5,57	0,14	5,23	5,87	5,54	5,60
IS_2	3,53	0,13	3,19	3,81	3,50	3,55
IS_3	3,11	0,12	2,85	3,37	3,09	3,13
IS_4	3,23	0,13	2,79	3,54	3,21	3,26
IS_5	4,10	0,12	3,84	4,40	4,08	4,13
IS_6	3,53	0,12	3,23	3,83	3,51	3,56
IS_7	2,89	0,12	2,59	3,19	2,87	2,92
IS_8	8,25	0,12	7,98	8,60	8,23	8,27
IS_9	5,18	0,21	4,68	5,65	5,14	5,23
IS_{10}	4,42	0,21	3,93	4,94	4,38	4,46
IS_{11}	4,64	0,20	4,15	5,12	4,60	4,68
IS_{12}	4,81	0,19	4,31	5,28	4,78	4,85
IS_{13}	4,16	0,20	3,67	4,73	4,12	4,20
IS_{14}	3,28	0,21	2,69	3,73	3,24	3,32
$IPCA_1$	-3,66	0,08	-3,85	-3,44	-3,68	-3,65
$IPCA_2$	-7,53	0,13	-7,88	-7,19	-7,56	-7,51
$IPCA_3$	24,00	0,15	23,58	24,35	23,97	24,03
$IPCA_4$	-13,23	0,18	-13,67	-12,61	-13,27	-13,20
$IPCA_5$	-1,07	0,19	-1,46	-0,47	-1,11	-1,03
$IPCA_6$	9,04	0,16	8,51	9,43	9,01	9,07

IS=índice de selección, SD=desviación estándar, Min=mínimo, Max=máximo, ICinf=intervalo de confianza inferior, ICsup=intervalo de confianza superior

Tabla 10. Progreso genético alcanzado para producción de leche hasta los 270 días (PL270) , medido en kg, en cada uno de los índices de selección (IS) utilizados

IS	Media	SD	Min	Max	I C inf	I C Sup
IS_0	14,62	0,18	14,09	14,98	14,59	14,65
IPL270	59,95	0,08	59,76	60,13	59,93	59,96
IS_1	23,83	0,19	23,33	24,32	23,79	23,87
IS_2	28,51	0,18	28,06	28,94	28,48	28,55
IS_3	26,14	0,20	25,63	26,63	26,11	26,18
IS_4	27,65	0,21	27,16	28,1	27,61	27,69
IS_5	22,95	0,18	22,55	23,43	22,91	22,98
IS_6	19,04	0,20	18,55	19,53	19,00	19,08
IS_7	19,23	0,18	18,75	19,61	19,19	19,26
IS_8	44,90	0,17	44,45	45,27	44,87	44,94
IS_9	37,63	0,36	36,73	38,49	37,56	37,70
IS_{10}	36,23	0,35	35,20	36,95	36,16	36,30
IS_{11}	37,33	0,31	36,46	37,99	37,26	37,39
IS_{12}	32,70	0,38	31,74	33,84	32,62	32,77
IS_{13}	30,18	0,44	29,28	31,26	30,09	30,26
IS_{14}	30,58	0,38	29,59	31,45	30,50	30,65
$IPCA_1$	31,77	0,16	31,33	32,13	31,74	31,80
$IPCA_2$	43,00	0,21	42,44	43,48	42,96	43,04
$IPCA_3$	46,49	0,18	46,11	46,97	46,46	46,53
$IPCA_4$	41,33	0,48	40,14	42,67	41,24	41,43
$IPCA_5$	31,00	0,39	30,33	32,02	30,92	31,08
$IPCA_6$	37,65	0,31	36,87	38,45	37,59	37,71

IS=índice de selección, SD=desviación estándar, Min=mínimo, Max=máximo, ICinf=intervalo de confianza inferior, ICsup=intervalo de confianza superior

Tabla 11. Progreso genético alcanzado para el efecto genético materno al destete (GMPD)en cada uno de los índices de selección (IS) utilizados

IS	Media	SD	Min	Max	I C inf	I C Sup
IS_0	0,84	0,03	0,77	0,89	0,83	0,84
IPL270	-0,52	0,05	-0,63	-0,42	-0,53	-0,51
IS_1	1,66	0,03	1,58	1,73	1,65	1,66
IS_2	1,16	0,03	1,09	1,24	1,15	1,16
IS_3	1,39	0,03	1,32	1,48	1,38	1,39
IS_4	1,25	0,03	1,16	1,32	1,24	1,26
IS_5	1,35	0,02	1,30	1,42	1,34	1,35
IS_6	1,96	0,03	1,87	2,03	1,95	1,96
IS_7	1,93	0,03	1,87	2,02	1,93	1,94
IS_8	0,38	0,09	0,17	0,56	0,36	0,40
IS_9	1,16	0,11	0,87	1,40	1,14	1,18
IS_{10}	1,36	0,10	1,00	1,57	1,34	1,38
IS_{11}	1,33	0,10	1,09	1,53	1,31	1,35
IS_{12}	1,90	0,05	1,76	2,04	1,89	1,91
IS_{13}	1,40	0,09	1,17	1,63	1,39	1,42
IS_{14}	1,39	0,10	1,15	1,61	1,37	1,41
$IPCA_1$	1,18	0,04	1,08	1,27	1,17	1,19
$IPCA_2$	1,31	0,05	1,20	1,42	1,30	1,32
$IPCA_3$	-0,91	0,05	-1,06	-0,77	-0,92	-0,90
$IPCA_4$	0,62	0,06	0,44	0,78	0,60	0,63
$IPCA_5$	0,15	0,05	0,05	0,27	0,14	0,16
$IPCA_6$	0,22	0,04	0,13	0,33	0,21	0,23

IS=índice de selección, SD=desviación estándar, Min=mínimo, Max=máximo, ICinf=intervalo de confianza inferior, ICsup=intervalo de confianza superior

Tabla 12. Progreso genético alcanzado para el efecto genético materno al año (GMP12) en cada uno de los índices de selección (IS) utilizados

IS	Media	SD	Min	Max	I C inf	I C Sup
IS_0	-0,09	0,05	-0,25	0,02	-0,10	-0,08
IPL270	-0,87	0,06	-1,00	-0,71	-0,88	-0,86
IS_1	3,75	0,06	3,56	3,87	3,74	3,76
IS_2	3,71	0,05	3,59	3,82	3,70	3,72
IS_3	3,77	0,06	3,65	3,93	3,76	3,78
IS_4	3,7	0,06	3,57	3,82	3,69	3,71
IS_5	3,82	0,05	3,72	3,93	3,81	3,83
IS_6	3,97	0,06	3,86	4,09	3,96	3,98
IS_7	4,02	0,05	3,88	4,12	4,01	4,03
IS_8	0,46	0,05	0,34	0,57	0,46	0,47
IS_9	1,89	0,09	1,65	2,08	1,88	1,91
IS_{10}	2,05	0,09	1,88	2,28	2,04	2,07
IS_{11}	1,91	0,09	1,67	2,13	1,89	1,93
IS_{12}	3,59	0,09	3,31	3,83	3,57	3,61
IS_{13}	2,34	0,10	2,05	2,58	2,32	2,36
IS_{14}	2,25	0,10	2,00	2,54	2,23	2,27
$IPCA_1$	3,67	0,05	3,53	3,78	3,66	3,68
$IPCA_2$	1,59	0,07	1,42	1,75	1,58	1,61
$IPCA_3$	-1,90	0,06	-2,10	-1,76	-1,91	-1,89
$IPCA_4$	0,17	0,06	0,02	0,34	0,16	0,18
$IPCA_5$	-0,97	0,04	-1,09	-0,88	-0,97	-0,96
$IPCA_6$	-0,92	0,04	-1,01	-0,82	-0,92	-0,91

IS=índice de selección, SD=desviación estándar, Min=mínimo, Max=máximo, ICinf=intervalo de confianza inferior, ICsup=intervalo de confianza superior

La Asociación de Criadores de Ganado Holstein de los Estados Unidos, dentro de su programa de mejoramiento genético tiene incorporado el Total Performance Index (TPI) o en español el Índice de desempeño total. En la actualidad el TPI cuenta con 12 características dentro de las que hay algunas relacionadas con la producción de leche y su calidad composicional y sanitaria, aspectos anatómicos, aspectos sanitarios, otras relacionadas con la eficiencia alimentaria, longevidad, por mencionar algunas. Los criadores de Ganado Holstein reconocen en el TPI, una herramienta importante para realizar los procesos de selección, pues se puede utilizar para hacer mejoras en varios rasgos al mismo tiempo. Esto está bien ilustrado cuando se mira en dos rasgos antagónicos, como la producción y la fertilidad. (Holstein Asosiation, 2015)

Otros índices que se aplican en diferentes partes del mundo y que son reconocidos por los criadores por su aporte a los programas de selección y de mejoramiento genético son: el APR en Australia, LPI en Canadá, RZG en Alemania, S.Index en Dinamarca, ICO en España, ISU en Francia, PLI en Inglaterra, EBI en Irlanda, PPD01 en Israel, PFT en Italia, NTP en Japón, BW en Nueva Zelanda y el Net Merit en USA(Miglior et al., 2005). Algunos de ellos tiene características en común, pero quizás el aspecto más importante es que cada uno incluye las características que son consideradas de relevancia económica en cada uno de los países en que se desarrolla; además no son estáticos en el tiempo, variando las características que los conforman así como la ponderación económica de cada una de ellas.

En Colombia, en ganado de lechería especializada, en el trópico alto de Nariño Betancur-Zambrano et al, (2012) propusieron dos índices de selección, uno en el que incluían características productivas asociadas a la producción de leche, porcentaje de grasa y proteína y otro al que además de las características productivas, incluyeron tres medidas anatómicas de importancia en el comportamiento productivo; concluyendo que los animales seleccionados con valores superiores del índice son los que mostraron superioridad genética para las características analizadas en el estudio; también recomiendan el uso de los índices construidos a los animales propios de la región en la que se desarrolló la investigación.

En Colombia Ruales-España and Manrique (2007) usaron la técnica de componentes principales para proponer un índice de selección para ganado criollo, para características asociadas a producción de carne, concluyendo que la técnica de PCA es una técnica eficiente para la selección de animales.

En Italia la Asociación Nacional de Criadores de Especies Bufalina desarrolló el índice Mozarella, en el que combinan la producción de leche y el porcentaje de proteína y grasa (Rosati and Van Vleck, 2002); este índice es de gran importancia por que permite identificar los animales que tienen la capacidad de producir más kg de queso mozarella por lactancia.

En Brasil usaron la metodología de análisis de componentes principales para proponer un índice en ganado Nellore (Buzanskas et al., 2013), en el que, dependiendo de los intereses de los criadores, se pueden seleccionar animales para mejorar los parámetros reproductivos usando las coordenadas estimadas en el primer componentes principal, o las coordenadas del segundo componente principal para seleccionar individuos con un mejor mérito genético para peso a los 420 días.

En Brasil la construcción de un índice de selección para un rebaño doble propósito de la raza Caracu, concluyeron que la implementación del índice, que incluyó la producción de leche, el peso al destete, el perímetro escrotal, la edad al primer parto, y la vida productiva, permite obtener una respuesta adecuada de acuerdo a los intereses de los criadores (De Queiroz et al., 2005)

Conclusiones

El mayor progreso genético para una característica se obtiene cuando se realiza la selección de los animales que tienen el mayor mérito genético para ella; sin embargo puede haber efectos no deseados sobre otras características asociadas a la primera, que también pueden ser de interés económico para los productores.

El modelo que permite hacer una mejor estimación de parámetros genéticos, es el modelo de rango reducido $PC_{1:3}$, debido a que permite aumentar el progreso genético de las características PD, P12, P18, P24, PL270, GMPD, y GMP12 y disminuir la EPP.

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CONCLUSIONES GENERALES

En la población bufalina doble propósito existe variabilidad genética para las características estudiadas, lo que permite establecer programas de mejoramiento genético animal para aumentar el progreso genético y la productividad del hato.

La implementación de diferentes metodologías para realizar evaluaciones genéticas puede llevar a resultados similares, sin embargo, de las metodologías analizadas en este estudio la más adecuada, porque permite hacer una mejor estimación de los parámetros genéticos y de los valores de cría de las características analizadas, es la evaluación genética realizada con el modelo de rango reducido de tres componentes principales $PC_{1:3}$, que además permite la construcción de un índice de selección que facilita un mejoramiento genético de las características de interés económico.

Se debe dar continuidad al presente trabajo, implementando, en campo, en la medida de lo posible los resultados expuestos en él, para estudiar el efecto de la selección sobre los parámetros productivos y sobre el progreso genético alcanzado. Se deben incluyendo otras características de interés económico a las evaluaciones genéticas.

ANEXOS

ANEXO 1. Correo electrónico en el que certifican la aceptación del artículo "Genetic evaluation of dual-purpose buffaloes (*Bubalus bubalis*) in Colombia using principal component analysis"

PLOS ONE <em@editorialmanager.com>
Para: Divier AGUDELO-GÓMEZ <diagudelo@lasallistadocentes.edu.co>
Responder a: PLOS ONE
PONE-D-15-04175R2: Final Decision Being Processed - [EMID:761bf03bdc3c0820]

23 de junio de 2015 9:06
Ocultar detalles

Genetic evaluation of dual-purpose buffaloes (Bubalus bubalis) in Colombia using principal component analysis
PONE-D-15-04175R2

Dear Dr. AGUDELO-GÓMEZ,

We are pleased to inform you that your manuscript has been judged scientifically suitable for publication and will be formally accepted for publication once it complies with all outstanding technical requirements.

Within one week, you will receive an e-mail containing information on the amendments required prior to publication. When all required modifications have been addressed, you will receive a formal acceptance letter and your manuscript will proceed to our production department and be scheduled for publication.

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With kind regards,

William Barendse
Academic Editor
PLOS ONE

Additional Editor Comments (optional):

Reviewers' comments:

Anexo 2. Correo electrónico en el que certifican la aceptación del artículo "Genetic principal components for reproductive and productive traits in dual-purpose buffaloes in Colombia"

paul.arthur@dpi.nsw.gov.au
Para: diagudelo@lasallistadocentes.edu.co
Cc: diagudelo@lasallistadocentes.edu.co , rodrigopsa@yahoo.com.br , marcosbuz@yahoo.com.br , fsajago@gmail.com , danisio@fcav.unesp.br , cerongamma@gmail.com Muñoz , glewis@asas.org
Journal of Animal Science - Decision on Manuscript ID E-2015-8940.R2

17 de junio de 2015 18:45
Ocultar detalles

17-Jun-2015

Dear Prof. Agudelo-Gómez:

It is a pleasure to accept your manuscript entitled "Genetic principal components for reproductive and productive traits in dual-purpose buffaloes in Colombia" for publication in the Journal of Animal Science (JAS). Thank you for the timely manner in which you responded to the request(s) for corrections to your manuscript.

To facilitate earlier dissemination, accepted manuscripts will be assigned a digital object identifier (DOI) and posted to the JAS publish-ahead-of-print site in the form in which they are accepted; because this does not represent the final, published form of the manuscript, the authors bear the primary responsibility for the content of manuscripts posted to the publish-ahead-of-print site.

You should anticipate receiving a PDF proof of your final manuscript within approximately 3 months. If you have any questions, please contact the editorial office (emueller@sciencesocieties.org).

On behalf of the editors of the Journal of Animal Science, we look forward to your continued contributions to the journal.

Sincerely,
Dr. Paul Arthur
Section Editor, Journal of Animal Science
paul.arthur@dpi.nsw.gov.au

Anexo 3. Normas para someter artículos en al revista PLOS ONE

Las normas de la revista PLS ONE pueden ser consultadas en el link
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Anexo 4. Normas para someter artículos a la revista Journal of Animal Science.

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Journal of Animal Science

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- For SI units, the National Institute of Standards and Technology provides a comprehensive guide. http://physics.nist.gov/cuu/Units/index.html
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Abstract. ABSTRACT consists of no more than 2,500 keystrokes (characters and spaces) in one paragraph and contains a summary of the pertinent results, with statistical evidence (i.e., *P*-values), in a brief but understandable form, beginning with a clear statement of the objective and ending with the conclusions, with no references cited. Abbreviations in the abstract that are not in **Standard *JAS* Abbreviations** must be defined at first use.

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Commercial Products. The use of names of commercial products should be minimized. When a commercial product is used as part of an experiment, the manufacturer name and location (city and state if in the US; city, administrative region or district [e.g., province], and country if outside the US) or a website address must be given parenthetically at first mention in text, tables, and figures. The generic name should be used subsequently. No ™, ®, or © symbols should be used.

General Usage.

- Abbreviations are not used to begin sentences. Words must be spelled out
- Note that "and/or" is allowed but not preferred; we ask that authors choose the more appropriate meaning or use "x or y or both" if possible.
- "Sex" should be used, rather than "gender." Gender is more appropriate for describing a role in society than for describing biological sex.
- State total sample size (e.g., the study included a total of 600 animals), rather than using "N" to represent total sample size.
- In math, the hierarchy for brackets and parentheses is [( )]. For example, $[(2 + 3) \times (12 \div 2)] \times 2 = 60$.
- In writing, however, a parenthetical remark within a parenthetical is punctuated as brackets within parentheses, ([ ]). For example, "The title page includes a running head (no more than 45 keystrokes [i.e., characters plus spaces]); the title…"

- Meat shear force should be expressed in kilograms (kg), although newtons (N) may also be acceptable.
- Report time using the 24-h system (e.g., 1410 h rather than 2:10 p.m.).
- Use italics to designate genus and species (e.g., *Bos taurus*) and botanical varieties (e.g., *Medicago sativa* var. Potomac). Designations for botanical cultivars should be preceded by "cv." or enclosed in single quotes (e.g., *Festuca arundinacea* cv. Kentucky 31 or *Festuca arundinacea* 'Kentucky 31').
- Names of muscles are not italicized.
- Specify the basis (i.e., as-fed or dry matter) for dietary ingredient and chemical composition data listed in text or in tables. Similarly, specify the basis for tissue composition data (e.g., wet or dry basis).
- Calculations of efficiency should be expressed as output divided by input (i.e., gain:feed, not feed:gain). This avoids the spurious positive and negative infinity values when body weight gain is zero or negative. It also avoids the confusion associated with discussing an improvement as being a decrease.
- A diet is a feedstuff or a mixture of feedstuffs; a ration is the daily allotment of the diet.
- Restrict the use of "while" and "since" to meanings related to time. Appropriate substitutes include "and," "but," or "whereas" for "while," and "because," "even though," or "although" for "since."
- The word "Table" is capitalized and never abbreviated.
- Except to begin a sentence, the word "Figure" should be abbreviated to "Fig."
- Except to begin a sentence, experiment and equation should be abbreviated to Exp. and Eq., respectively, when preceding a numeral (e.g., Exp. 1).
- Avoid jargon unfamiliar to scientists from other disciplines. Do not use the term "head" to refer to an animal or group of animals. Instead, use animal, sow, ewe, steer, heifer, cattle, etc.
- Avoid bi- as a prefix because of its ambiguity; biweekly means twice per week and once every 2 weeks.
- Breed and variety names should be capitalized (e.g., Landrace and Hereford).
- Trademarked or registered names should be capitalized, but no ™ or ® symbols should be used.

II. POLICIES AND PROCEDURES OF *JAS*

The mission of the American Society of Animal Science (ASAS) is to "***foster the discovery, sharing, and application of scientific knowledge concerning the responsible use of animals to enhance human life and well-being***" (https://asas.org/about-asas/history-and-mission). The *Journal of Animal Science*, which is published monthly by ASAS, accepts manuscripts presenting information for publication with this mission in mind.

The *JAS* is divided into the following Sections: Animal Genetics; Animal Nutrition: Nonruminant Nutrition; Animal Nutrition: Ruminant Nutrition; Animal Physiology; Animal Production; Animal Products; Special Topics; and Symposia, which contains invited manuscripts from symposia at ASAS meetings. Manuscripts that do not fit one of the *JAS* Sections will not be considered for publication.

The Editor-in-Chief, Managing Editor, and Section Editors establish the editorial policies of *JAS*, subject to review by the publications committee and ASAS Board of Directors. The views expressed in articles published in *JAS* represent the opinions of the author(s) and do not necessarily reflect the official policy of the institution with which an author is affiliated, the ASAS, or the *JAS* Editor-in-Chief. Authors are responsible for ensuring the accuracy of collection, analysis, and interpretation of data in manuscripts and ultimately for guaranteeing the veracity of the contents of articles published in *JAS*.

The *JAS* is one of the most frequently cited, peer-reviewed, agriculturally oriented research journals in the world, based on statistics published by Thomson Reuters (formerly ISI Inc.; Philadelphia, PA). Its high ranking in several categories attests to the quality standards of the *JAS* editors, editorial board, and staff and the authors who submit manuscripts for publication.

Contact Information

For information on the scientific content of the journal, contact the Editor-in-Chief, Dr. Gregory S. Lewis, American Society of Animal Science, P.O. Box 7410, Champaign, Illinois 61826-7410; e-mail: glewis@asas.org.

For questions about submitting a manuscript and ScholarOne Manuscripts, contact Mr. Brett Holte, Submission Services Manager; e-mail: bholte@sciencesocieties.org.

For assistance with author proofs, contact Ms. Emily Mueller, Managing Editor; e-mail: emueller@sciencesocieties.org.

Care and Use of Animals

All authors submitting to *JAS* must complete the Care and Use of Animals form certifying that any research that involves animals has followed established standards for the humane care and use of animals and must specify which standards were used. Only investigations that have followed high standards for the humane care and use of animals in research will be reported in *JAS*.

Also, the manuscript must include a statement of institutional animal care and use committee (IACUC), or equivalent, approval of all animal procedures. The IACUC statement should appear as the first item in MATERIALS AND METHODS and should specify which publically available animal care and use standards were followed (e.g., FASS Guide for the Care and Use of Agricultural Animals in Research and Teaching; Primary Industries Ministerial Council, Model code of practice for the welfare of animals: the sheep). The manuscript should describe anesthetics, analgesics, tranquilizers, and care taken to minimize pain and discomfort during preoperative, operative, and postoperative procedures. If research requires discomfort to the animals or stress-

ful conditions, justification for these conditions must be evident in papers published in *JAS*.

Protection of Human Subjects

In the United States, federally funded or regulated research involving human subjects must comply with Code of Federal Regulations (CFR), Title 45 Public Welfare, Part 46 Protection of Human Subjects. However, CFR 45 Part 46.101(b) exempts some research from these regulations. For all exempted research and other details, see http://www.hhs.gov/ohrp/humansubjects/guidance/45cfr46.html. Exempted research includes that in which the only involvement of human subjects is for "taste and food quality evaluation and consumer acceptance if 1) wholesome foods without additives are consumed or 2) a food is consumed that contains a food ingredient at or below the level and for a use found to be safe, or agricultural chemical or environmental contaminant at or below the level found to be safe, by the Food and Drug Administration or approved by the Environmental Protection Agency or the Food Safety and Inspection Service of the U.S. Department of Agriculture." If human subjects were used in exempted research and the research was in compliance with CFR 45 Part 46, or equivalent regulations where the research was conducted, authors must state in **MATERIALS AND METHODS** or acknowledgements that they were in full compliance. If human subjects were used in research that was not exempted in CFR 45 Part 46, or equivalent regulations where the research was conducted, authors must certify that the research received a priori approval from an appropriate Institutional Review Board.

Conflict of Interest

All *JAS* editors, ASAS staff, ASAS Board of Directors, and submitting authors must disclose any actual or potential conflicts of interest that may affect their ability to objectively present or review research or data. This generally includes any relevant professional, personal, political, intellectual, religious, or financial interest in, or relationship with, an individual or business that could have an actual or perceived influence, positive or negative, on the conduct and publication of the research or data. Financial relationships generally refer to financial benefits accrued to authors through avenues such as salary, consulting fees, honoraria (including paid holidays, use of vacation property, country club privileges, and other nonmonetary rewards for service), intellectual property rights, royalties, business ownership, and investments, other than diversified mutual funds or the equivalent.

Disclosures for *JAS* authors are to be provided as an acknowledgement on the title page of a manuscript (for instructions, see ***Title Page***). The *JAS* may use such information as a basis for editorial and publication decisions, and may publish such disclosures if that is deemed relevant and sufficient. The *JAS* editors, ASAS staff, and ASAS Board of Directors with actual or potential conflicts of interest that may affect their ability to objectively evaluate or manage a manuscript will be prevented from gaining access to the manuscript and associated documents, unless they are an author or coauthor, in which case ScholarOne Manuscripts will limit their access to the Corresponding Author Center. When the current Editor-in-Chief, for example, has an actual or potential conflict of interest with a manuscript, a former Editor-in-Chief will assume the responsibilities of the Editor-in-Chief for that manuscript.

Types of Articles

Articles published in *JAS* encompass a broad range of research topics in animal production and fundamental aspects of genetics, nutrition, physiology, and preparation and utilization of animal products. Many articles are multidisciplinary and cannot be conveniently categorized. Articles typically report research with cattle, goats, pigs, and sheep. However, studies involving other farm animals (e.g., poultry and meat and working horses) and companion animals, including performance and recreational horses, aquatic, and wildlife species will be considered for publication. Studies with laboratory animal species that address fundamental questions related to the biology of livestock, companion animals, and other managed animals may be considered. Manuscripts that report research on production issues in animals other than those constituting the main focus of *JAS* should be submitted to other journals.

The preceding paragraph is not meant to exclude manuscripts but, rather, is a clarification of the focus of *JAS*. Authors may contact the Editor-in-Chief if there are questions about whether the topic of a manuscript is appropriate for *JAS*.

Research Articles. Results of research contained in manuscripts submitted to *JAS* must not have been published in or submitted previously to a peer-reviewed scientific journal. Previous presentation at a scientific meeting or the use of data in field-day reports or similar documents, including press publications or postings to personal or departmental websites, do not preclude the publication of such data in *JAS*. However, abstracts, proceedings papers, field-day reports, or similar presentations that are expanded to produce full-length manuscripts should be referenced and cited in *JAS* manuscripts. Articles simultaneously posted to websites and submitted to *JAS* should carry a disclaimer on the website that this version of the paper has not undergone *JAS* peer-review and is not to be considered the final published form of the article. If the article has been published in *JAS*, the author should include the complete *JAS* citation so that proper credit can be given to *JAS* as the publisher of the article. Because *JAS* holds the copyright to articles it publishes, posting altered *JAS* articles that are represented as exact duplicates of the published version constitutes copyright violation.

Review Articles. The journal publishes invited review articles. The Editor-in-Chief, in consultation with Section Editors and the ASAS Board of Directors, identifies invited reviews. Section Editors may solicit proposals for review articles to be published in *JAS*, after consultation with and approval by the Editor-in-Chief; the authors may be responsible for a portion of the publication charges for invited reviews. Unsolicited review

articles will not be considered.

Special Topics. This Section includes Biographical or Historical Sketches and Contemporary Issues in the animal sciences. Even though Biographical or Historical Sketches are part of the Special Topics Section, they will be published on the ASAS website and in the Association News section of *JAS*. The frequency of publication depends on the availability of the prepared sketches. For more information, see http://www.animalsciencepublications.org/publications/jas/infora..

Contemporary Issues include topics such as environmental concerns, legislative proposals, systems analysis, and various "newsworthy" scientific issues. Even though Contemporary Issues manuscripts do not have to include original data, authors' assertions should be substantiated with references to established information from credible published sources.

Special Topics papers will be subject to peer review in a manner similar to other *JAS* submissions. Because of the nature of these manuscripts, their format may vary from that of standard scientific articles, although ABSTRACT and INTRODUCTION must be consistent with keystroke (characters and spaces) limitations defined earlier in this document.

Teaching articles should be submitted to *Natural Sciences Education*, which is a joint venture of several professional societies, including the ASAS. Articles in *Natural Sciences Education* are "written by and for educators in extension, universities, industry, administration, and grades K–12" and highlight teaching techniques, concepts, ideas, and other teaching-related issues. The goal is build a portfolio of teaching-related articles that can be accessed at a single location. For detailed information about *Natural Sciences Education*, see https://www.agronomy.org/publications/nse.

Technical Notes. A technical note is used to report a new method, technique, or procedure of interest to *JAS* readers. When possible, a technical note should include a comparison of results from the new method with those from previous methods, using appropriate statistical tests. The advantages and disadvantages of the new procedure should be discussed. When typeset for publication, a technical note shall not exceed 8 pages (approximately 12 Microsoft Word document pages), including tables and figures. "Technical note:" shall be the first portion of the title of such manuscripts. The review process for a technical note will be the same as that for other manuscripts. Information that is more extensive or detailed than necessary for a Technical note may be presented in an e-supplement (see ***E-Supplements***). Short communications, brief communications, and similar types of articles will not be considered for publication in *JAS*.

Letters to the Editor. A letter judged suitable for publication will be printed in a "Letters to the Editor" section of *JAS*. The purpose of this section is to provide a forum for scientific exchange relating to articles published in *JAS*. To be acceptable for publication, a letter must adhere to the following guidelines. 1) Only a letter that addresses matters of science and relates to information published in *JAS* will be considered. In general, a letter should not exceed 5,000 keystrokes and should contain no more than 5 citations. 2) A letter should provide supporting evidence based on published data for the points made or must develop logical scientific hypotheses. A letter based on conjecture or unsubstantiated claims will not normally be published. No new data may be presented in a letter. 3) The Editor-in-Chief will evaluate each letter and determine whether a letter is appropriate for publication. If a letter is considered appropriate, the author(s) of original *JAS* article(s) will be invited to write a letter of response. Normally both letters will be published together. 4) All letters will be subject to acceptance and editing by the Editor-in-Chief and editing by a technical editor.

SUBMISSION OF MANUSCRIPTS

Manuscripts should be submitted electronically through ScholarOne Manuscripts at http://mc.manuscriptcentral.com/jas. Authors with questions about using the electronic manuscript submission system or, for technological reasons, are unable to submit manuscripts electronically may contact Mr. Brett Holte (bholte@sciencesocieties.org).

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REVIEW OF MANUSCRIPTS

General Procedures. The Editor-in-Chief and Section Editors determine whether manuscripts are suitable for publication in *JAS*. All communications about a submitted manuscript should maintain confidentiality. Section Editors handle correspondence with the peer re-

viewers and corresponding author and promptly decide whether a manuscript should be accepted, revised, or rejected. A Section Editor's decision to accept, invite revision, or reject a manuscript after peer review is based on peer-reviewer comments and recommendations and the Section Editor's own review of the manuscript. Section Editors forward document files for accepted and rejected manuscripts to the Editor-in-Chief. After acceptance, manuscript files are forwarded to the technical editors. The Editor-in-Chief is the final arbiter concerning acceptance or rejection of manuscripts submitted for publication.

Rejections. Manuscripts are rejected for 3 general reasons. 1) The substance of the manuscript may not meet *JAS* standards; the work may be incomplete, the evidence may not support the conclusions, the experimental approach may be poorly conceived, or the work may repeat established fact or represent no advancement of the existing knowledge. 2) Even though the work may be sound and the results valid, the paper may be better suited for publication elsewhere. 3) Manuscripts are not written clearly, concisely, and coherently, or they are not consistent with guidelines in the 2015 Instructions for Authors, *Journal of Animal Science*. These manuscripts may be rejected without review. Authors whose first language is not English are urged to have an editing service review their manuscripts before they are submitted to *JAS*. However, *JAS* considers the authors, and not an editing service, responsible for the content of manuscripts.

Appeals. If a manuscript is rejected, as a first course of action the author should discuss the matter with the Section Editor responsible for the manuscript. Decisions must be appealed to the Editor-in-Chief if the author(s) believe(s) that the judgment was erroneous or biased. A letter presenting the reasons for the appeal should be sent to the Editor-in-Chief. The Editor-in-Chief will review the author's reasons, all documents related to the manuscript, and, if necessary, consult with the Section Editor responsible for the manuscript. The Editor-in-Chief will then decide whether to accept or deny the appeal. A rejected manuscript may be resubmitted for publication in another Section of *JAS* only if the Editor-in-Chief recommends this action or if the Section Editor originally assigned to the manuscript has specifically recommended this action and the Editor-in-Chief has approved the transfer.

Revisions. Most manuscripts that are eventually accepted for publication are returned to the author(s) at least once for revision. All revised manuscripts must be returned to Section Editors via *JAS* ScholarOne Manuscripts. Authors will be permitted 15 days to revise and return manuscripts classified as Minor Revision and permitted 35 days to revise and return manuscripts classified as Major Revision. ScholarOne Manuscripts prompts reviewers to classify manuscripts as Minor Revision or Major Revision. Section Editors will use the reviewers' classifications and their own evaluations to estimate the time required for authors to respond to reviews and use that estimate during the process of classifying manuscripts. A manuscript that will clearly require more than 35 days for revisions may be rejected. However, the author will be invited to revise the manuscript, create a new submission, and reference the original manuscript tracking number (e.g., Manuscript ID E-2015-1234) in the submission letter that accompanies the new submission. Section Editors will use the original reviews and the author's responses to the original reviews to evaluate the submission. Unless the new submission contains a significant amount of new data, there should be no reason to seek new reviews.

Manuscripts that exceed the revision-option deadline will be withdrawn. Extenuating circumstances may justify the need to extend the revision-option deadline. Requests for extensions must be communicated to the Section Editor responsible for the manuscript before the revision-option expires. The Editor-in-Chief must approve extensions. As a general rule, only one short extension will be approved. The Revision Checklist for Authors is sent with requests for revision (http://www.animalsciencepublications.org/files/publications/jas/jas-revision-checklist.pdf). Authors should closely follow the Checklist.

PAPERS IN PRESS, AUTHOR PROOFS, AND PUBLICATION CHARGES

Papers in Press. To facilitate earlier disclosure of research results, accepted manuscripts will be assigned a digital object identifier (doi) and posted to the *JAS* First Look site (http://www.animalsciencepublications.org/publications/jas/first-look) in the form in which they are accepted. The authors bear the primary responsibility for the content of manuscripts posted to the Papers in Press site. Because articles posted to this site have not been professionally edited and typeset, and are frequently changed in response to questions from editors, they do not represent the final, published form of the manuscript. The date a complete monthly issue of *JAS* is posted online is the official publication date for *JAS* articles. However, the date on which a manuscript is posted to the *JAS*-Papers in Press website may represent the official public disclosure date for the contents of the article. Authors concerned about intellectual property issues, such as patents and disclosure dates, should seek legal counsel before submitting manuscripts to a scientific journal.

Author Proofs. Accepted manuscripts are forwarded to the editorial office for technical editing and typesetting. During this process, the technical editor may contact the authors for missing information or figure revisions. The manuscript is then typeset, figures reproduced, and author proofs (also called galley proofs) prepared. Correspondence concerning the accepted manuscript should be directed to the technical editor.

Proofs of all manuscripts will be provided to the corresponding author and should be read carefully and checked against the typed manuscript. Accuracy of the author proof is the sole responsibility of the author(s). Corrections may be returned by e-mail (preferred), fax, or overnight mail. For faxed or mailed corrections, changes to the proof should be made neatly and clearly in the margins of the proof. If extensive correction is required, changes should be provided on a separate sheet of paper with a symbol indicating location on the proof.

Changes e-mailed to the technical editor must indicate page, column, and line numbers for each correction to be made on the proof. Notes created with Adobe editing tools and pointing to specific locations for corrections may also be used. Editor queries should be answered on the galley proofs; failure to do so may delay or prevent publication. Excessive author changes made at the proof stage may result in a $250 surcharge for additional typesetting, and they may be deemed so excessive that the manuscript will be returned to the Section Editor for additional scientific review.

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Professional membership in ASAS is available to any person who has research, educational, commercial, or administrative responsibilities or interests in the broad disciplines within animal science. Annual professional membership is $135, and the complete details are available at the following website. https://www.asas.org/membership-services/member-information

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STANDARD *JAS* ABBREVIATIONS

The following abbreviations should be used without definition in *JAS*. Plural abbreviations do not contain a final "s" because the context of an abbreviation implies whether it is singular or plural. Use of the standard 3-letter abbreviations for amino acids (e.g., Ala) is acceptable in *JAS*. Use of the internationally recognized chemical symbols for chemical elements (e.g., P and S) is acceptable in *JAS*. Except for N (not italicized), which is the recognized abbreviation for nitrogen and newton (unit of force), chemical symbols for elements are reserved for elements (e.g., C is for carbon and never for control). For chemical units and abbreviations, refer to the ACS Style Guide (published by the American Chemical Society, Washington, DC).

Physical units

Item	Unit
Bq	becquerel
°C	degree Celsius
cal	calorie
Ci	curie
cM	centimorgan (spell out morgan if used without a prefix)
Da	dalton
Eq	equivalent (only can be used with a prefix; e.g., mEq)
g	gram
ha	hectare
Hz	hertz
IU	international unit
J	joule
L	liter
lx	lux
m	meter
M	molar (concentration; preferred over mol/L)
mol	mole
N	newton (N not italicized)
N	normal (concentration)
Pa	pascal
rpm	revolutions/minute (not to be used to indicate centrifugal force)
t	metric ton (1,000 kg)
V	volt
W	watt

Units of time

Item	Unit
s	second
min	minute
h	hour
d	day
wk	week
mo	month
yr	year

Statistical symbols and abbreviations

Item	Term
ANOVA	analysis of variance
CI	confidence interval
CV	coefficient of variation

df	degree(s) of freedom (spell out if used without units)
F	*F*-distribution (variance ratio)
LSD	least significant difference
n	sample size (used parenthetically or in footnotes; note italics)
P	probability
r	simple correlation coefficient
r^2	simple coefficient of determination
R	multiple correlation coefficient
R^2	multiple coefficient of determination
s^2	variance (sample)
SD	standard deviation (sample)
SE	standard error
SED	standard error of the differences of means
SEM	standard error of the mean
t	*t*-(or Student) distribution
α	probability of Type I error
ß	probability of Type II error
μ	mean (population)
σ	standard deviation (population)
σ^2	variance (population)
χ^2	chi-squared distribution

Others

Item	Term
AA	amino acid(s)
ACTH	adrenocorticotropic hormone
ADF	acid detergent fiber (assumed sequential unless designated otherwise)
ADFI	average daily feed intake (not to be confused with DMI)
ADG	average daily gain
ADIN	acid detergent insoluble nitrogen
ADL	acid detergent lignin
ADP	adenosine diphosphate
AI	artificial insemination
AIA	acid insoluble ash
ARS	Agricultural Research Service
ATP	adenosine triphosphate
avg	average (use only in tables, not in the text)
BCS	body condition score
BLUE	best linear unbiased estimate
BLUP	best linear unbiased prediction
bp	base pair
BSA	bovine serum albumin
BTA	*Bos taurus* chromosome
BW	body weight (used for live weight)
cDNA	complementary deoxyribonucleic acid
C/EBP	CAAT-enhancer binding protein
cfu	colony-forming unit
CIE	International Commission on Illumination (Commission Internationale d'Eclairage)
CLA	conjugated linoleic acid
CoA	coenzyme A
Co-EDTA	cobalt ethylenediaminetetraacetate
CP	crude protein (N × 6.25)
D	dextro-
diam.	diameter
DE	digestible energy
DEAE	(dimethylamino)ethyl (as in DEAE-cellulose)
DFD	dark, firm, and dry (meat)
DM	dry matter
DMI	dry matter intake
DNA	deoxyribonucleic acid
EBV	estimated breeding value(s)
eCG	equine chorionic gonadotropin
EDTA	ethylenediaminetetraacetic acid
EFA	essential fatty acid
EIA	enzymeimmunoassay
ELISA	enzyme-linked immunosorbent assay
EPD	expected progeny difference(s)
Eq.	Equation(s)
Exp.	experiment (always followed by a numeral)
FFA	free fatty acid(s)
FSH	follicle-stimulating hormone
GEBV	genomic estimated breeding value(s)
g	gravity
GE	gross energy
G:F	gain-to-feed ratio
GLC	gas-liquid chromatography
GLM	general linear model
GnRH	gonadotropin-releasing hormone
GH	growth hormone
GHRH	growth hormone-releasing hormone
h^2	heritability
i.m.	intramuscular
i.p.	intraperitoneal
i.v.	intravenous
hCG	human chorionic gonadotropin
HCW	hot carcass weight

HEPES	*N*-(2-hydroxyethyl)piperazine-*N*′-2-ethanesulfonic acid
HPLC	high-performance (pressure) liquid chromatography
i.d.	inside diameter
Ig	immunoglobulin (when used to identify a specific immunoglobulin)
IGF	insulin-like growth factor
IGFBP	insulin-like growth factor-binding protein(s)
IL	interleukin
IVDMD	in vitro dry matter disappearance
kb	kilobase(s)
KPH	kidney, pelvic, heart fat
L	levo-
LD_{50}	lethal dose 50%
LH	luteinizing hormone
LHRH	luteinizing hormone-releasing hormone
LM	longissimus muscle
ME	metabolizable energy
MP	metabolizable protein
mRNA	messenger ribonucleic acid
MUFA	monounsaturated fatty acid
NAD	nicotinamide adenine dinucleotide
NADH	reduced form of NAD
NDF	neutral detergent fiber
NDIN	neutral detergent insoluble nitrogen
NE	net energy
NE_g	net energy for gain
NE_l	net energy for lactation
NE_m	net energy for maintenance
NEFA	nonesterified fatty acid
No.	number (use only in tables, not in the text)
NPN	nonprotein nitrogen
NRC	National Research Council
o.d.	outside diameter
OIE	World Organisation for Animal Health (Office International des Epizooties)
OM	organic matter
PAGE	polyacrylamide gel electrophoresis
PBS	phosphate-buffered saline
PCR	polymerase chain reaction
PG	prostaglandin
$PGF_{2\alpha}$	prostaglandin $F_{2\alpha}$
PMSG	pregnant mare's serum gonadotropin
PPAR	peroxisome proliferator-activated receptor
PSE	pale, soft, and exudative (meat)
PUFA	polyunsaturated fatty acid(s)
QTL	quantitative trait locus (loci)
RDP	ruminally degradable protein
REML	restricted maximum likelihood
RFLP	restriction fragment length polymorphism
RIA	radioimmunoassay
RNA	ribonucleic acid
RQ	respiratory quotient
RUP	ruminally undegradable protein
rRNA	ribosomal ribonucleic acid
SAS	SAS Institute Inc. (no longer stands for Statistical Analysis System)
s.c.	subcutaneous
SDS	sodium dodecyl sulfate
SFA	saturated fatty acid
SNP	single nucleotide polymorphism
spp.	species
ssp.	subspecies
SSC	*Sus scrofa* chromosome
ST	somatotropin
TDN	total digestible nutrients
TLC	thin layer chromatography
Tris	tris(hydroxymethyl)aminomethane
tRNA	transfer ribonucleic acid
TSAA	total sulfur amino acids
USDA	US Department of Agriculture
UV	ultraviolet
VFA	volatile fatty acid(s)
vol	volume
vol/vol	volume/volume (used only in parentheses)
vs.	versus
wt	weight (use only in tables, not in the text)
wt/vol	weight/volume (used only in parentheses)
wt/wt	weight/weight (used only in parentheses)

LITERATURE CITED GUIDELINES FOR *JOURNAL OF ANIMAL SCIENCE*

References in the Text. In the body of the manuscript, refer to authors as follows: Smith and Jones (1992) or Smith and Jones (1990, 1992). If the sentence structure requires the authors' names to be included in parentheses, the proper format is (Smith and Jones, 1982; Jones, 1988a,b; Jones et al., 1992, 1993). When there are more than 2 authors of an article, the first author's name is

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Sample references are as follows:

1. Books and articles within edited books:

AOAC. 1990. Official methods of analysis. 15th ed. Assoc. Off. Anal. Chem., Arlington, VA.

NRC. 2000. Nutrient requirements of beef cattle. 7th rev. ed. Natl. Acad. Press, Washington, DC.

Robinson, P. H., E. K. Okine, and J. J. Kennelly. 1992. Measurement of protein digestion in ruminants. In: S. Nissen, editor, Modern methods in protein nutrition and metabolism. Academic Press, San Diego, CA. p. 121–127.

2. Handbooks, technical bulletins, theses, and dissertations

Goering, H. K., and P. J. Van Soest. 1970. Forage fiber analyses (apparatus, reagents, procedures, and some applications). Agric. Handbook No. 379. ARS-USDA, Washington, DC.

Shreck, A. L., C. D. Buckner, G. E. Erickson, and T. J. Klopfenstein. 2011. Digestibility of crop residues after chemical treatment and anaerobic storage. In: 2011 Nebraska Beef Cattle Report. Rep. No. MP94. Univ. of Nebraska, Lincoln. p. 35–36.

Sigma. 1984. Total hemoglobin: Quantitative, colorimetric determination in whole blood at 530–550 nm. Tech. Bull. No. 525. rev. ed. Sigma Chemical, St. Louis, MO.

Ward, J. D. 1995. Effects of copper deficiency on performance and immune function of cattle. PhD Diss. North Carolina State Univ., Raleigh.

3. Journal articles and abstracts

Centon, J. R., G. E. Erickson, T. J. Klopfenstein, K. J. Vander Pol, and M. A. Greenquist. 2007. Effects of roughage source and level in finishing diets containing wet distillers grains on feedlot performance. J. Anim. Sci. 85(Suppl. 2):76. (Abstr.) doi:10.2527/ jas.2006-354 (**NOTE**: The doi is now considered part of a citation.)

Cleale, R. M., IV, R. A. Britton, T. J. Klopfenstein, M. L. Bauer, D. L. Harmon, and L. D. Satterlee. 1987a. Induced non-enzymatic browning of soybean meal. II. Ruminal escape and net portal absorption of soybean protein treated with xylose. J. Anim. Sci. 65:1319–1326. (**NOTE**: Articles published before circa 2005 may not have a doi.)

Perez, V. G., A. M. Waguespark, T. D. Bidner, L. L. Southern, T. M. Fakler, T. L. Ward, M. Steidinger, and J. E. Pettigrew. 2011. Additivity of effects from dietary copper and zinc on growth performance and fecal microbiotia of pigs after weaning. J. Anim. Sci. 89:414–425. doi:10.2527/jas.2010-2839

Revidatti, M. A., J. V. Delgado Bermejo, L. T. Gama, V. Landi Periati, C. Ginja, L. A. Alvarez, J. L. Vega-Pla, A. M. Martínez, and BioPig Consortium. 2014. Genetic characterization of local Criollo pig breeds from the Americas using microsatellite markers. J. Anim. Sci. 92:4823-4832. doi: 10.2527/jas.2014-7848

The Bovine Hap Map Consortium. 2009. Genome-wide survey of SNP variation uncovers the genetic structure of cattle breeds. Science. 324:528-532. doi 10.1126/science.1167936

4. Conference proceedings

Bailey, E. A., J. R. Jaeger, J. W. Waggoner, G. W. Preedy, L. A. Pacheco, and K. C. Olson. 2012. Effect of weaning method on welfare and performance of beef calves during receiving. Proc. West. Sec. Amer. Soc. Anim. Sci. 63:25-29.

NMC. 1995. Summary of peer-reviewed publications on efficacy of premilking and postmilking teat disinfections published since 1980. In: Natl. Mastitis Counc. Reg. Meet. Proc., Harrisburg, PA. Natl. Mastitis Counc., Arlington, VA. p. 82–92.

Talmant, A., X. Fernandez, P. Sellier, and G. Monin. 1989. Glycolytic potential in longissimus dorsi

muscle of Large White pigs as measured after in vivo sampling. In: Proc. 35th Int. Congr. Meat Sci. Technol., Copenhagen, Denmark. p. 1129.

Van der Werf, J. H. J. 1990. A note on the use of conditional models to estimate additive genetic variance in selected populations. Proc. 4th World Congr. Genet. Appl. Livest. Prod., Edinburgh, Scotland XIII:476–479.

5. Electronic Publications

FDA. 2014. Approved animal drug products online (Green Book). http://www.fda.gov/AnimalVeterinary/Products/ApprovedAnimalDrugProducts/default.htm (Accessed 26 December 2014.)

Galyean, M. L. and P. J. Defoor. 2003. Effects of roughage source and level on intake by feedlot cattle. J. Anim. Sci. 81(E. Suppl. 2):E8–E16.

Heaton, M. P., T. S. Kalbfleisch, D. T. Petrik, B. Simpson, J. W. Kijas, M. L. Clawson, C. G. Chitko-McKown, G. P. Harhay, K. A. Leymaster, and the International Sheep Genomics Consortium. 2013. Genetic testing for TMEM154 mutations associated with lentivirus susceptibility in sheep. PLoS ONE 8(2): e55490. doi:10.1371/journal.pone.0055490

POLICIES REGARDING NUMBER USAGE FOR *JOURNAL OF ANIMAL SCIENCE*

Number usage in *JAS* is consistent with the *Scientific Style and Format: The CSE Manual for Authors, Editors, and Publishers*.

- All cardinal numbers are written as numerals except when they begin a sentence or appear in a title, when 2 numerals are adjacent in a sentence (spell out the number most easily expressed in words; e.g., two 10-kg samples), or when a number is used as a figure of speech.
- Numbers less than 1 are written with a preceding (leading) zero (e.g., 0.75).
- A comma separator is used in numbers greater than 999 (e.g., 1,234 and 1,234,567).
- Numerals should be used to designate ratios and multiplication factors (e.g., 2:1 and 3-fold increase).
- Statements such as "5 times less" should be avoided because "times" means multiplied by, and the product of a positive number (multiplicand) multiplied by 5, for example, is greater, not less, than the multiplicand. The opposite is true for a negative multiplicand, but the notion of "5 times less than –5," for example, may be not be clear to readers.
- If a number is spelled out at the beginning of a sentence, its associated unit is also spelled out (e.g., Ten microliters of fluid . . ., not Ten µL of fluid . . .).
- Units of measurement not associated with a number should be spelled out rather than abbreviated (e.g., lysine content was measured in milligrams per kilogram of diet) unless used parenthetically, as "lysine content (mg/kg of diet) was measured," or in tables and figures.
- Single-digit ordinals are spelled out (i.e., first through ninth); larger ordinals are expressed in numeric form. Single-digit ordinals may be expressed numerically when they form part of a series (e.g., 1st, 3rd, 10th, 20th, not first, third, 10th, and 20th).
- Measures must be presented in the metric system (SI or Système International d'Unités; see http://physics.nist.gov/cuu/Units/introduction.html.
- When a term must be expressed in nonmetric units for clarity (e.g., bushel weight), show the nonmetric value in parentheses immediately after the metric value.
- Use "to" instead of a hyphen to indicate a numerical range in text (e.g., 1 to 10).
- Avoid the use of multiplying factors (e.g., $\times 10^{-6}$) in table columns or rows, or in figure axis labels because of the uncertainty about whether the data are to be, or already have been, multiplied by the factor.
- Avoid ambiguity by stating units (e.g., numbers of spermatozoa, millions/mL).
- Do not use more than one slant line (for "per") in a single expression; for example, use 5 mg/(g · d) or 5 mg · g^{-1} · d^{-1} instead of 5 mg/g/d. Mathematically, "per" implies division; when 2 "per" occur consecutively, it is unclear precisely what is being divided by what.
- Dietary energy may be expressed in calories or in joules, although joule is the standard SI unit for energy.
- Hyphenate units of measure used as preceding adjectives (e.g., 5-kg sample). Hyphens are not used with percent or degree signs.
- Insert spaces around all signs (except slant lines) of operation when these signs occur between 2 values (e.g., 10 ± 1; $5 < 10$; $2 + 2 = 4$).
- Convert "mg %" to other units, such as mg/L or mg/mL.
- Use "mol/100 mol" rather than "molar percent.".