Original

Genetic parameters for growth and reproduction in Simmental cattle from pedigree and genomic relationship

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ABSTRACT

Objective. To estimate genetic parameters for weight at eight months of age (W8M), age at first calving (AFC) and first calving interval (FCI) using pedigree and genomic relationship. **Materials and methods.** Phenotypic data on 481, 3063 and 1098 animals for W8M, AFC and FCI were used, respectively. The genomic information came from a population of 718 genotyped animals with a density chip of 30,106 single nucleotide polymorphism markers (SNP). Univariate and bivariate models were used under the conventional (BLUP) and single step genomic best linear unbiased predictor (ssGBLUP) methodologies. **Results.** The heritabilities for W8M, AFC and FCI ranged from 0.25 to 0.26, from 0.20 to 0.22 and from 0.04 to 0.08, respectively. The AFC and FCI models under ssGBLUP slightly decreased the error and increased the additive genetic variance, respectively. **Conclusions.** The inclusion of genomic information slightly increases the accuracy of the genetic estimates in this population. However, a larger amount of genotyped animals and with a higher genetic relationship connectivity would allow breeders to increase the potential of the ssGBLUP methodology in Colombian Simmental cattle.

Keywords: best linear unbiased predictor, genetic parameters, genomic selection, variance components (*Source*: Agrovoc, MeSH).

RESUMEN

Objetivo. Estimar parámetros genéticos para peso a los ocho meses de edad (W8M), edad al primer parto (AFC) y primer intervalo entre partos (FCI) usando parentesco genómico y por pedigrí. **Materiales y métodos.** Se utilizaron 481, 3063 y 1098 registros fenotípicos para W8M, AFC y FCI, respectivamente. La información genómica estuvo compuesta por una población de 718 animales genotipados con un chip que incluyó 30106 marcadores genéticos tipo polimorfismo de nucleótido simple (SNP). Modelos univariado y bivariado fueron construidos bajo la metodología del mejor predictor lineal insesgado convencional (BLUP) y genómico en una etapa (ssGBLUP). **Resultados.** Las heredabilidades para W8M, AFC y FCI variaron desde 0.25 a 0.26, 0.20 a 0.22 y 0.04 a 0.08, respectivamente. Los modelos de AFC y FCI con la metodología ssGBLUP disminuyeron ligeramente

el error y aumentaron la varianza genética aditiva, respectivamente. **Conclusiones.** La inclusión de información genómica mejora levemente la precisión de las estimaciones genéticas en esta población. Sin embargo, una población de animales genotipados más grande y con mayor conectividad genética por parentesco permitiría aumentar para los criadores el potencial de la metodología ssGBLUP en ganado Simmental de Colombia.

Palabras clave: Componentes de varianza, mejor predictor lineal insesgado, parámetros genéticos, selección genómica (Fuente: Agrovoc, MeSH).

INTRODUCTION

Traditionally, genetic evaluations are based on the analysis of pedigree and phenotypic information through the mixed model equation system (1). However, in recent decades the availability of genetic markers such as single nucleotide polymorphism (SNP) has also allowed researchers identifying genes of productive importance, measuring genetic variability and estimating genomic breeding values. That has been recommended especially for traits with low heritability or those difficult to measure (2).

Weight at eight months of age (W8M), age at first calving (AFC) and first calving interval (FCI) have been used as selection criteria to increase productivity and evaluate reproductive efficiency in cattle production systems (2,3). The decrease in AFC and FCI reduces production costs of replacing females and production costs per calf per year (4). Likewise, the selection by growth traits allows animals to stay a shorter time in pastures, decreasing the production cycle time and obtaining a higher profit.

Genetic parameters estimates with genomic information have been discrepant according to the strategy used to genotype animals and the evaluated trait, especially for reproductive traits (5). Nonetheless, the inclusion of genomic information has shown more reliable estimates, which could be important for traits with variable results and low heritability (6). Therefore, the use of genomic information could allow breeders to achieve greater genetic progress through increases in accuracy and reduction of generation interval (7).

In Colombia, the Simmental breed is used as a dual-purpose system and is currently distributed throughout the Colombian territory. However, there are no estimates of genetic parameters, which have limited the design and implementation of a breeding program.

Therefore, the aim of this study was to estimate genetic parameters for W8M, AFC and FCI in Colombian Simmental cattle using univariate and bivariate animal models under conventional best linear unbiased predictor (BLUP) and single-step genomic BLUP (ssGBLUP).

MATERIALS Y METHODS

Approval by an ethics committee was not necessary in this study as all the records used in the analyses came from an existing database and did not involve experiments or procedures with animals.

Pedigree and phenotypic data. Pedigree information from the Colombian Simmental Breeders Association (Asosimmental) was used in this study. The pedigree file included 27.986 animals born from 1975 to 2017 with 15 generations traced. The number of W8M (animals between 210 and 270 days of age), AFC and FCI records were 481, 3063 and 1098, respectively. The final pedigree file used to compute the numerator relationship matrix had 26376, 27037 and 26650 animals for W8M, AFC and FCI, respectively.

Genotyping and quality control. The genotyped population consisted of 718 animals using the GeenSeek Genomic Profiler-LD chip (GGP Bovine LD v4) with 30106 SNP. For the quality control, SNP with a miss rate of >10%, a minor allele frequency of <0.05 and a Hardy-Weinberg equilibrium test p-value of <0.001 were excluded and animals with call rate lower than 90% were also excluded using PLINK (8). After quality control, 661 animals and 22395 SNPs were used to genetic parameter estimates. The number of animals with genotypes and phenotypic records were 372 and 162 for AFC and FCI, respectively. Animals with phenotypic records for W8M did not have genomic information, but they were related with the genotyped population.

Ecological and management conditions. According to the Colombian farmer practices, the milking cows and calves are kept on pasture during the whole year. The diet consisted of roughage, concentrates and mineral supplementation. Artificial insemination is used instead of natural mating and there is no a fixed breeding season for the Colombian Simmental cows, which means that cows are allowed to be inseminated in any month.

Genetic analysis. Variance components were estimated using univariate (W8M, AFC, FCI) and bivariate (W8M x AFC and AFC x FCI) animal models. The fixed effects for W8M were contemporary group (sex, year of birth from 2010 to 2015 and month of birth from January to December) and the covariate age. The W8M did not include the maternal effect because the animals evaluated were removed from the dam and artificially fed. The fixed effect for AFC was year of birth from 1999 to 2014 and the fixed effects for FCI were year of calving from 2003 to 2015 and herd. The effect of region was not included for all the traits because that was not significant or available. Random effects included in all the animal models were the animal and the residual.

In matrix notation the animal model used was as follows:

$$y = X\beta + Za + e,$$

where y is the vector of observations; β is the vector of fixed effects; a is the vector of solutions for the coefficients of direct animal (additive) genetic random effects; e is the vector of residual effects; X and Z, are the correspondent incidence matrices of the fixed effects and additive genetic. The model assumed that $E[y] = X\beta; Var(a) = AG_a; Var(e) = I \otimes R$, where A is the numerator relationship matrix, $\otimes$ is the Kronecker product, G_a is a (co)variance matrix of direct additive genetic effects, I is an identity matrix and R is a (co)variance matrix of residual effects.

Genomic analyses. Variance components were estimated using the ssGBLUP methodology. The same univariate and bivariate animal models described in genetic analysis section were performed, but the numerator relationship matrix (A) was replaced by a matrix H, as follows:

$$H = \begin{bmatrix} A_{11} + A_{12}A_{22}^{-1}(G - A_{22})A_{22}^{-1}A_{21} & A_{12}A_{22}^{-1}G \\ GA_{22}^{-1}A_{21} & G \end{bmatrix}$$

where, A_{11} is the numerator relationship matrix for ungenotyped animals, A_{22} is the relationship matrix for the genotyped animals, A_{12} which is equal to A_{21} are matrices that contain relationship among genotyped and ungenotyped animals, G is the genomic relationship matrix. Hence, matrix H includes relationships based on pedigree and differences between pedigree and genomic relationship (9).

Variance components estimations from genetic and genomic analysis were performed using the procedure of the average information restricted maximum likelihood (AIREML) included in the BLUPF90 family software (10).

RESULTS

Means for W8M, AFC and FCI were 247±37 kg, 1080±269 d and 464±106 d, respectively. Heritabilities for W8M, AFC and FCI from genetic and genomic analysis are shown in table 1.

Table 1. Heritabilities for weight at eight months of age (W8M), age at first calving (AFC) and first calving interval (FCI) from genetic and genomic analysis in Colombian Simmental cattle.

Trait	Model	Heritabilities	
		Genetic analysis	Genomic analysis
W8M	Univariate	0.26±0.15	0.26±0.15
	Bivariate with AFC	0.25±0.15	0.25±0.15
AFC	Univariate	0.22±0.04	0.20±0.04
	Bivariate with W8M	0.21±0.04	0.20±0.04
	Bivariate with FCI	0.21±0.04	0.20±0.04
FCI	Univariate	0.04±0.05	0.07±0.06
	Bivariate with AFC	0.05±0.05	0.08±0.06

All the models used to estimate heritabilities of AFC that included genomic information slightly improved (from third decimal) the accuracy of the heritability. There were not increases in accuracy when using genomic information for W8M and FCI, but heritabilities for those traits were slightly higher with genomic information (from third decimal) than those estimated without genomic information. The genetic correlations estimates between W8M and AFC showed medium and negative values of -0.34 and -0.27 with and

without genomic relationship, respectively. Regarding genetic correlations between AFC and FCI, they were positive with values of 0.23 and 0.25 with and without genomic relationship, respectively.

DISCUSSION

The average W8M was higher than reported in a Colombian Brahman population, which had lighter weights (237±36 kg) at an older age (270 days) (11). The Colombian Simmental production systems use grain supplements and high-quality forages, which could partially explain the heavier weights found in this population. Brown Swiss dual-purpose production systems in Mexico with similar environmental conditions and management practices showed a 240-day weight of 235±44 kg (12), which was similar to the average reported in this study.

The average AFC was always longer compared to other studies reported in taurine dairy breeds. For example, a Colombian Holstein population showed the most similar value with an average of 962 days of age at first calving (13). Although dairy farming has become more intensive in Colombia, culling animals from the breeding stock based on AFC is not yet implemented by the Colombian Simmental farmers. That could contribute to a longer AFC. Furthermore, the criteria for the first insemination in Simmental cattle has been the body weight, which could be another factor to increase AFC if average daily gain from weaning weight to AFC is low.

The average FCI was higher compared to a Holstein population that had a 385 days FCI (14). Although productive and reproductive management practices in Simmental systems are favourable and intensive, the Colombian Simmental farmers keep animals with reproductive problems due to the scarcity of females. In the previous context, calving interval may have longer periods.

Heritabilities for W8M coincided with those reported by other authors with values from 0.11 to 0.35 (15,16). Direct heritabilities estimated for W8M were higher than those reported by Guillen et al. (15) in a Zebu population in tropical conditions, but very similar to the

results reported by Kebede & Komlosi (17) who estimated a direct heritability of 0.26 in another Simmental cattle population. The consulted Zebu population had a high selection intensity for weaning weight (25%), which could partially explain a lower additive genetic variance due to selection processes. In Colombia, W8M results indicate that an important improvement for that trait could be achieved by genetic selection. However, a higher amount of phenotypic records and genotyped animals are still necessary to increase accuracy in estimates and, consequently genetic progress.

Although heritability differences for W8M between univariate and bivariate models including or not genomic relationship were small (<0.006), a lower heritability in bivariate models could be due to a few animals in the database with phenotypic information for all the traits (16). The increase in the heritability was slight (0.0024) in models that included genomic relationship. That was in agreement to what has been reported in other studies for growth traits (2). The slight differences found could suggest that the genomic and pedigree relationship matrix for the genotyped animals is similar, which would not alter much the genetic parameter estimates. Besides, the fact that there were no animals with genomic and phenotypic information for W8M could explain the slight changes in estimates.

Heritabilities for AFC have varied considerably between taurus and indicus populations, ranging from 0.08 to 0.47 (18,19,20). A Colombian Creole population presented a value of 0.15 (21) and populations of Colombian and Brazilian Holstein cattle had lower values, ranging from 0.13 to 0.19 (13). The differences in estimates may be related to the size of the databases, the effects included in the models and even environmental factors that were not recorded (22). Marques et al (18) found a heritability for AFC from 0.16 to 0.18 and suggested that a decrease in that trait could be made by genetic selection. Then, genetic progress for AFC in the Colombian Simmental cattle may be possible.

Heritability differences for AFC according to the models were different from that reported by Buzanskas et al (23), who observed higher

heritability for AFC in univariate versus bivariate models. The lower genetic variances could be due to the use of SNP, which could identify a lower degree of relationship among some animals, and thereby, decreased the proportion of the known genetic variance (9). On the other hand, the effect of genomic relationship on standard errors was in agreement with the results reported by Haile-Mariam et al (24), who reported lower standard errors for estimates with genomic information compared to models that included only the pedigree relationship.

The heritabilities reported for FCI were lower compared to W8M and AFC. Estimates of heritability for FCI in the Colombian Simmental cattle were consistent with heritabilities found in other studies, which ranged from 0.01 to 0.11 in taurine dairy breeds (3, 14, 19, 25). Those variations could be mainly due to differences in the environment, which may be related to feeding systems and decisions on the breeding season programs. On the other hand, taurine breeds have been more selected by reproductive performance, which reduce the additive genetic variance over time. Although farmers have not yet implemented a breeding program in Colombia, that Simmental cattle population comes from intensively selected European and North American populations, which can explain the low heritabilities.

The heritabilities variations for FCI were in agreement with the reported by Haile & Price (26), where the heritability varied from 0.03 to 0.06. The increases in heritability observed in the bivariate models including or not genomic relationship may be due to the positive genetic correlation between AFC and FCI, leading to a greater explanation of the additive genetic variance. Likewise, the simultaneous use of bivariate models and genomic relationship is favourable for traits with fewer records and generally allows researchers to explain a higher amount of genetic variance (27).

Higher degree of relationship between pedigree and genomic relationship could lead to more precise estimates and capture a higher additive genetic variance. The correlation between those matrices was high (>0.8), which indicates a good pedigree quality. This could partially explain the discrepancies in estimations for the additive genetic variance of AFC and FCI when including genomic information. However, the low number of genotyped animals in this study, and the density of the genotyping chip must also be considered among the differences of the estimates, which could affect the variance of the evaluated traits (24).

The genetic correlation between W8M and AFC was equal to the reported by Chin-Collin et al (3), who reported a negative value of -0.34. However, other studies have reported values close to zero and slightly negative values of -0.02 (12). The heritabilities and genetic correlation indicate an opportunity for those traits to be included in a breeding program. That would optimise the genetic progress because animals with higher W8M would have a shorter AFC. The higher genetic correlation including genomic relationship could be associated with a greater relationship of the polygenic effects of ungenotyped and genotyped animals, which contributes to the construction of the genomic relationship and differences found (28).

The genetic correlation between AFC and FCI coincided with the reported by Gutiérrez et al (22) in beef breeds. However, Rocha et al (21) and Chin-Colli et al (3) reported negative genetic correlation between those traits with values of -0.43 and -0.26, respectively. The differences respect to those populations are possibly associated with different selection criteria that changes the genetic structure over time and the magnitude of the heritabilities and the genetic correlations. In Colombia, the simultaneous availability and use of beef and dairy type bulls from Europe and North America can be currently affecting that breed structure and genetic parameter estimates.

Although the heritabilities and genetic correlations for AFC and FCI were low, their inclusion in breeding programs could be a reliable strategy to increase productivity due to its economic effect (29). In addition, these results in the Colombian Simmental population suggest that selection of animals with higher breeding value for W8M and lower breeding value for AFC would represent a greater reproductive efficiency. On the other hand, the inclusion of AFC in genetic selection

schemes could be considered to increase genetic progress for traits associated with fertility (30).

In conclusion, using genomic information through ssGBLUP methodology could optimise genetic improvement for the traits evaluated due to increases in accuracy and the heritabilities. Although differences in the standard errors and heritabilities between pedigree and genomic relationship estimates are very small in this population, strategies such as genotyping a larger number of animals that are most closely related to the ungenotyped animals could significantly improve the estimations. Likewise, increasing phenotypic record keeping is crucial to obtain a greater benefit from the potential offered by genomic selection in local breeding programs.

Conflict of interests.

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