

## ANIMAL GENETICS AND GENOMICS

# Estimating dominance genetic variances for growth traits in American Angus males using genomic models

Carolina A. Garcia-Baccino,<sup>\*1</sup> Daniela A. L. Lourenco,<sup>†</sup> Stephen Miller,<sup>‡</sup> Rodolfo J. C. Cantet,<sup>\*,§</sup> and Zulma G. Vitezica<sup>#</sup>

<sup>\*</sup>Departamento de Producción Animal, Facultad de Agronomía, Universidad de Buenos Aires, C1417DSQ Buenos Aires, Argentina, <sup>†</sup>Department of Animal and Dairy Science, University of Georgia, Athens, GA 30602, <sup>‡</sup>Angus Genetics Inc., St. Joseph, MO 64506, <sup>§</sup>INPA, UBA-CONICET, C1427CWO Buenos Aires, Argentina, <sup>#</sup>INP ENSAT, UMR 1388 GenPhySE, 31326 Castanet-Tolosan, France

<sup>1</sup>Corresponding author: [bcagarci@agro.uba.ar](mailto:bcagarci@agro.uba.ar)

ORCID number: 0000-0002-1465-5708 (C. A. Garcia-Baccino); 0000-0003-3140-1002 (D. A. L. Lourenco); 0000-0001-6282-146X (R. J. C. Cantet); 0000-0002-3162-7258 (Z. G. Vitezica).

## Abstract

Estimates of dominance variance for growth traits in beef cattle based on pedigree data vary considerably across studies, and the proportion of genetic variance explained by dominance deviations remains largely unknown. The potential benefits of including nonadditive genetic effects in the genomic model combined with the increasing availability of large genomic data sets have recently renewed the interest in including nonadditive genetic effects in genomic evaluation models. The availability of genomic information enables the computation of covariance matrices of dominant genomic relationships among animals, similar to matrices of additive genomic relationships, and in a more straightforward manner than the pedigree-based dominance relationship matrix. Data from 19,357 genotyped American Angus males were used to estimate additive and dominant variance components for 3 growth traits: birth weight, weaning weight, and postweaning gain, and to evaluate the benefit of including dominance effects in beef cattle genomic evaluations. Variance components were estimated using 2 models: the first one included only additive effects (**MG**) and the second one included both additive and dominance effects (**MGD**). The dominance deviation variance ranged from 3% to 8% of the additive variance for all 3 traits. Gibbs sampling and REML estimates showed good concordance. Goodness of fit of the models was assessed by a likelihood ratio test. For all traits, MG fitted the data as well as MGD as assessed either by the likelihood ratio test or by the Akaike information criterion. Predictive ability of both models was assessed by cross-validation and did not improve when including dominance effects in the model. There was little evidence of nonadditive genetic variation for growth traits in the American Angus male population as only a small proportion of genetic variation was explained by nonadditive effects. A genomic model including the dominance effect did not improve the model fit. Consequently, including nonadditive effects in the genomic evaluation model is not beneficial for growth traits in the American Angus male population.

**Key words:** Angus beef cattle, dominance genetic variance, genomic selection, growth traits

## Introduction

Traditionally, nonadditive effects are ignored in genetic evaluation models due to several reasons such as the lack of informative pedigrees and the need of demanding computation (Varona et al., 2018). Although additive variance includes part of the biological dominant effects of the genes (Hill, 2010), the dominance deviation variance should not be neglected. Knowing its magnitude in real data and exploring the predictive ability of a model that accounts for dominance effects is of relevance.

Availability of large genomic data sets has renewed the interest of including nonadditive genetic effects in genomic evaluation models. Toro and Varona (2010), Su et al. (2012), and Vitezica et al. (2013) proposed different approaches to consider dominance effects in genomic models. Including dominance effects in the model and, consequently, having accurate estimates for those effects can be advantageous (e.g., Varona et al., 2018). If the amount of dominance genetic variance is substantial, including dominance effects in the model can lead to improvements in accuracy of breeding values and in selection response (Toro and Varona, 2010; Aliloo et al., 2016; Duenk et al., 2017), can help in mate allocation procedures (Mäki-Tanila, 2007; Toro and Varona, 2010; Aliloo et al., 2017) and to define convenient breeding schemes (Mäki-Tanila, 2007; Zeng et al., 2013). The inclusion of dominance in genomic models has been studied by several authors in different species (e.g., Ertl et al., 2014; Heidaritabar et al., 2016; Xiang et al., 2016; Moghaddar and van der Werf, 2017) with no gain in accuracy of estimated breeding values and with variable results in terms of the magnitude of the dominance deviation variance estimated for different traits.

In beef cattle systems, growth traits as birth weight (BW), weaning weight (WW), and postweaning gain (PWG) are the most important traits under selection. These traits have moderate narrow-sense heritabilities that range from 0.20 to 0.45, and dominance deviation variance can be important and should be determined. Recently, other studies reported values of dominance variance (expressed as a proportion of phenotypic variance) equal to 0.11 for live weight measured post-weaning (Bolormaa et al., 2015) and around 0.12 for yearling weight (Raidan et al., 2018). The first one was a multibreed study (with animals from 3 different breed types: *Bos taurus*, *Bos indicus*, and composite breeds) and the latter was in Brahman and Tropical Composite beef cattle.

The aims of this study were to estimate additive and dominance variance components on growth traits in American Angus males and to evaluate the predictive ability of the model when dominance effects are included.

## Materials and Methods

### Animals and Genotypes

Data for this study were provided by the American Angus Association. Animal Care and Use Committee approval was not obtained for this study because the data were obtained from an existing database.

Three growth traits were analyzed in this study: BW, WW, and PWG. A total of 19,357 genotyped males with at least 1 record for one of the traits were considered in the analysis. Animals were genotyped or imputed using a panel of 54,609 SNP from BovineSNP50k v2 BeadChip (Illumina Inc., San Diego, CA). Only SNP located in autosomes were used. After quality control using default checks by preGSf90 (Aguilar et al., 2014)—Hardy–Weinberg equilibrium (HWE), minor allele frequency (<0.05),

SNP call rate, and animal call rate (<0.90)—a total of 39,245 autosomal SNP remained and were used to build additive and dominant genomic relationship matrices.

Quality control of phenotypes ensured records fulfilled quality requirements of the American Angus Association national genetic evaluation. Animals from contemporary groups with less than 10 individuals were excluded. As only males with phenotype and genotype data were used in the analysis, this arbitrary size avoided unreliable estimates of contemporary group effects from few records. Table 1 presents a summary of the data. As described in Lourenco et al. (2015), the American Angus Association applied no genotyping strategy; therefore, the members could choose which animals were genotyped (in most of the cases, the chosen ones were young). As there was no genotyping strategy, usually not all the animals within a contemporary group were genotyped. Moreover, the genotyped animals used in this study represented 65 % for BW and WW and 77% for PWG of the total number of males in the “original” contemporary groups (defined by sex) used in the genetic evaluation (e.g., Lourenco et al., 2015). All 19,357 genotyped animals were born between 2001 and 2014, but most of them (18,593) were born after 2010 and they did not have genotyped male progeny in the data set, 38% of the oldest ones (764 males born before 2010) had at least 1 offspring genotyped and with phenotypic records.

### Statistical Models

Phenotypes were analyzed using a univariate GBLUP model. Two linear models were considered: the first included only additive genetic effects (MG) and the second included both additive and dominance genetic effects (MGD). The MG and MGD models were equal to

$$MG : \mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{fb} + \mathbf{Zu} + \mathbf{e}$$

and

$$MGD : \mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{fb} + \mathbf{Zu} + \mathbf{Zv} + \mathbf{e},$$

where  $\mathbf{y}$  is a vector of observed phenotypic values of males for each trait;  $\mathbf{X}$  is a design matrix relating the phenotype to the fixed effect,  $\boldsymbol{\beta}$  is a vector of fixed effects (contemporary groups),  $\mathbf{f}$  is the vector of genomic inbreeding coefficients calculated as the proportion of homozygous loci for each animal (Silió et al., 2013; Xiang et al., 2016),  $b$  is the inbreeding depression parameter,  $\mathbf{Z}$  is an incidence matrix relating the phenotype with the breeding value and dominance deviations (in MGD),  $\mathbf{u}$  is a vector of breeding values distributed as  $\mathbf{u} \sim N(0, \mathbf{G}\sigma_A^2)$ ,  $\mathbf{v}$  is a vector of dominance deviations distributed as  $\mathbf{v} \sim N(0, \mathbf{D}\sigma_D^2)$ , and  $\mathbf{e}$  is a vector of residuals distributed as  $\mathbf{e} \sim N(0, \mathbf{I}\sigma_e^2)$ . Matrix  $\mathbf{G}$  is the additive genomic relationship matrix and  $\mathbf{D}$  is the dominance genomic relationship matrix. Parameters  $\sigma_A^2$ ,  $\sigma_D^2$ , and  $\sigma_e^2$  refer to additive genetic, dominance deviations, and residual variances, respectively. The MGD model assumes

**Table 1.** General statistics for growth traits

Trait <sup>1</sup>	Number of records	Average, kg	SD, kg	Number of contemporary groups
BW	19,357	36.29	3.63	718
WW	19,345	312.07	40.37	730
PWG	14,767	233.60	48.08	532

<sup>1</sup>BW, birth weight; WW, weaning weight; PWG, postweaning gain.

$\text{Cov}(\mathbf{u}, \mathbf{v}) = 0$  under orthogonality (Vitezica et al., 2013). Xiang et al. (2016) proved analytically that, in the presence of directional dominance, inclusion of genomic inbreeding as a covariate in the model is necessary to obtain correct estimates of dominance variance. This has long been known for pedigree analysis (e.g., De Boer and Hoeschele, 1993; Miller and Goddard, 1998).

An exploratory analysis of the data set showed that among all dams, 15,579 (80% of dams) had only 1 offspring, leading to an average of 1.10 offspring per cow. Consequently, maternal effects were completely confounded and were not included in BW and WW analysis.

The additive genomic relationship matrix  $\mathbf{G}$  was calculated according to VanRaden (2008) as follows:

$$\mathbf{G} = \frac{\mathbf{M}\mathbf{M}'}{2 \sum_{k=1}^m p_k q_k},$$

where  $\mathbf{M}$  is a matrix with dimensions of number of animals ( $n$ ) by the number of SNPs ( $m$ ), with elements equal to  $(2 - 2p_k)$ ,  $(1 - 2p_k)$ , and  $(-2p_k)$ , for genotypes AA, Aa, and aa, respectively;  $p_k$  is the frequency for allele A of SNP  $k$  and  $q_k = 1 - p_k$ .

The dominance deviation genomic relationship matrix  $\mathbf{D}$  was built as in Vitezica et al. (2013):

$$\mathbf{D} = \frac{\mathbf{W}\mathbf{W}'}{\sum_{k=1}^m (2p_k q_k)^2},$$

where  $\mathbf{W}$  has the same dimension as in  $\mathbf{M}$ , with elements equal to  $(-2q_k^2)$ ,  $(2p_k q_k)$ , and  $(-2p_k^2)$  for AA, Aa, and aa, respectively;  $p_k$  is frequency for allele A of SNP  $k$  and  $q_k = 1 - p_k$ . Matrices  $\mathbf{M}$  and  $\mathbf{W}$ , their cross-products, and the inverses of  $\mathbf{G}$  and  $\mathbf{D}$  were built using own programs. Parallel programming in Fortran using OpenMP and BLAS-MKL libraries was used. Matrices  $\mathbf{G}$  and  $\mathbf{D}$  were blended in order to make them full rank as  $\mathbf{G}^* = 0.95\mathbf{G} + 0.05\mathbf{I}$ , and  $\mathbf{D}^* = 0.95\mathbf{D} + 0.05\mathbf{I}$ , and then inverted.

### Variance Component Estimation and Model Comparison

Estimation of variance components was performed by Bayesian methods using Gibbs sampling and also by REML using the software GIBBS2F90 and REMLF90 (available at <http://nce.ads.uga.edu/wiki/>), respectively (Miszta et al., 2014). A total of 200,000 iterations were run for each trait under the Bayesian approach, with burn-in of 10,000 initial iterations and sample interval of 10. Posterior means and posterior SD were calculated based on a final chain of 19,000 samples. Convergence to the final distribution was checked by visual inspection of the chains and its variability. Initial

parameters for REML were obtained from the Gibbs sampling estimates.

The maximum likelihood ratio test was performed from REML results to assess goodness of fit and to compare MG and MGD models. The Akaike information criterion (AIC) was also considered for those purposes. The superiority of an alternative model MGD over model MG was evaluated using a likelihood ratio test. The  $\chi^2$  was calculated as  $\chi^2 = -2 \log L_{MG} + 2 \log L_{MGD}$ , the first term involved the MG likelihood and the second one took into account the MGD likelihood. P-values of the chi-square tests were obtained from a mixture of chi-square distributions with 1 and 0 degrees of freedom (Visscher, 2006).

GBLUP, using the software BLUPF90 (Miszta et al., 2014), was used to obtain estimated genetic values ( $\mathbf{u}, \mathbf{v}$ ) by fixing the variance components that were estimated. Conventional cross-validation was conducted to compare the 2 models. Two data sets were used for this purpose: 1) the “complete” data set as described above (Table 1) and 2) the “reduced” data set in which young animals had no own or progeny information. Those animals born in 2014 were considered the “young” males for BW and WW, but as they did not have records for PWG, a different “young” group of animals born in 2013 was considered for this trait. The predictive ability of phenotypes of “young” males for the 2 models was assessed as the  $\text{cor}(y^*, \hat{y})$  (Legarra et al., 2008) where  $y^*$  is the corrected phenotype from the “complete” data set, calculated as  $y^* = y - X\hat{\beta} - f\hat{b}$  and  $\hat{y}$  is the predicted corrected phenotype from the “reduced” data set, equal to the estimated additive genetic effects ( $\mathbf{u}$ ) for MG model, or the sum of estimated additive and dominant genetic effects ( $\mathbf{u} + \mathbf{v}$ ) for MGD model.

## Results

Table 2 shows the variance component estimates for each trait using both MG and MGD models. For all traits, additive variance estimates were not affected by the inclusion of dominance effect in the model. Additive genetic variance did not differ between MG and MGD models, which empirically shows the orthogonality in the partition of the genetic variance. The model used in the analysis in terms of breeding values and dominance deviations (Vitezica et al., 2013) enables an orthogonal partition of the genetic variance in HWE and linkage equilibrium. HWE holds in this dataset, however linkage disequilibrium (LD) exists. Note that a tight linkage is needed to yield substantial LD in outbred populations (Hill and Mäki-Tanila, 2015). Likewise, no changes in  $h_A^2$  were observed when including dominance in the model (going from MG to MGD).

Means of the diagonal and off-diagonal elements of matrices  $\mathbf{G}$  and  $\mathbf{D}$  were calculated. The average of the diagonal elements

**Table 2.** Estimates of additive, dominance deviation, and residual variance components ( $\sigma_A^2$ ,  $\sigma_D^2$ ,  $\sigma_e^2$ ) and heritability for growth traits using MG and MGD models

Trait <sup>1</sup>	Model <sup>2</sup>	$\sigma_A^2$	$\sigma_D^2$	$h_A^2$	$h_D^2$	$(\sigma_D^2/\sigma_A^2)$	$\sigma_e^2$
BW	MG	6.27 (0.33)	—	0.25	—	—	18.82 (0.24)
	MGD	6.28 (0.33)	0.18 (0.15)	0.25	0.01	0.03	18.65 (0.28)
WW	MG	222.75 (14.61)	—	0.16	—	—	1186.28 (14.26)
	MGD	223.55 (14.82)	10.02 (4.98)	0.16	0.01	0.04	1176.88 (14.86)
PWG	MG	270.76 (20.42)	—	0.16	—	—	1388.81 (19.87)
	MGD	270.30 (21.94)	21.68 (10.95)	0.16	0.01	0.08	1369.01 (26.00)

<sup>1</sup>BW, birth weight; WW, weaning weight; PWG, postweaning gain.

<sup>2</sup>MG, model including only additive effects; MGD, model including both additive and dominant effects.

The results are given as estimate (in parenthesis SE);  $h_A^2 = \sigma_A^2/\sigma_P^2$  and  $h_D^2 = \sigma_D^2/\sigma_P^2$ , where  $\sigma_P^2$  is the phenotypic variance.

was close to 1 in both cases (1.02 for G matrix and 1.01 for D matrix) and the off-diagonal average was almost 0 in both cases ( $-5.24 \times 10^{-5}$  for G and 0.02 for D), as expected in a base population with HWE. The SD of the off-diagonal elements of both matrices (0.06 for G and 0.05 for D) was similar, so both matrices were similar in terms of informativity. The relationship between diagonals and off-diagonal elements of G and D was explored. The correlation was 0.96 and 0.05 for the diagonal and off-diagonal elements, respectively. These values agreed with those reported by [Raidan et al. \(2018\)](#), in supplementary figure 1) and confirmed that the studied population was in HWE.

Dominance deviation variance was small for all the analyzed traits ([Table 2](#)). For all growth traits, the proportion of dominance to additive variance was less than 10% (from 3% to 8%) and  $h_D^2$  ( $\sigma_D^2/\sigma_P^2$ ) was 0.01 in all cases, showing that there is little evidence of nonadditive genetic variation in BW, WW and PWG in this Angus male population. Pedigree-based estimates of  $h_D^2$  range from 0 to 0.39 for BW and from 0 to 0.56 for WW ([Rodríguez-Almeida et al., 1995](#); [Gengler et al., 1997](#)). In Limousin cattle,  $h_D^2$  for PWG ranges from 0.10 to 0.18 ([Gengler et al., 1997](#); [Misztal et al., 1998](#)).

Posteriori correlations between variance component estimates were computed for each trait. High correlation between additive and dominant variance components would show difficulty to disentangle both in the MGD model. However, this correlation was close to 0 (ranging from  $-0.04$  to  $0.03$ ) and confirmed that MGD model allowed correct partitioning of the genetic variance. Additive variation was not confounded with dominance variation.

Genomic inbreeding coefficient was calculated as the proportion of homozygous SNPs per genotyped individual, following [Silió et al. \(2013\)](#). The mean of genomic inbreeding coefficient, across animals, was 0.634 with a SD of 0.013. The mean, across animals, of genomic inbreeding coefficient in this population is comparable to those values reported by [Reverter et al. \(2017\)](#) for Bahman (0.597, SD = 0.014) and Tropical Composite (0.602, SD = 0.027) beef cattle using a 70K SNP panel.

Estimated inbreeding depression for each trait using both models is shown in [Table 3](#). Inbreeding depression estimates are expressed as the change in phenotypic mean per 10% increase in inbreeding. For WW, a decrease of 10.20 kg (approximately) is expected per 10% increase in inbreeding and a loss of 10.70 kg is expected for PWG every 10% increase in inbreeding. Inbreeding depression estimates were in the same order of magnitude to those reported in literature for growth traits in beef cattle. The reported values were going from  $-4.40$  kg to  $-8.96$  kg per 10% increase in inbreeding ([Burrow, 1993, 1998](#); [Falcão et al.,](#)

[2001](#); [Santana et al., 2010](#)) for WW. For BW, the estimates in literature are more variable, some authors report no inbreeding depression for this trait ([Burrow, 1998](#); [Davis and Simmen, 2010](#)), whereas others obtained values going from  $-0.60$  kg to  $-3.80$  kg per 10% increase in inbreeding ([Swiger et al., 1961](#); [Burrow, 1993](#)). Values obtained in this study for BW were in this range ( $-0.48$  kg per 10% increase in inbreeding). Recently, [Sumreddee et al. \(2018\)](#) estimated inbreeding depression for BW and WW in a Hereford cattle population using SNP information. Across different measures, BW and WW decreased by 0 to 0.12 kg and 2.12 to 5.29 kg, respectively, for each 10% increase in genomic inbreeding. Both values (BW and WW) were lower than our estimates. However, estimates of inbreeding depression are population specific ([Howard et al., 2017](#)), and differences may be due to differences in allele frequencies and in the magnitude of directional selection.

Goodness of fit of the models was assessed by performing a likelihood ratio test ([Table 4](#)). For all traits, model MG fitted the data as well as MGD, consequently including dominance in the model did not improve model fit. Similar results were obtained with AIC ([Table 4](#)). For all traits, the model with less (or equal) AIC value was MG. In addition to these statistics, a conventional cross-validation was carried out. The predictive ability of phenotypes, measured as the correlation between the phenotypes of selection candidates based on “complete” and “reduced” data set, was around 0.43, 0.21, and 0.30 in BW, WW, and PWG for both models. No differences in the predictive ability of phenotypes for young animals were observed between MG and MGD models.

## Discussion

Additive and dominance deviation variance components were estimated for 3 traits of interest in the American Angus male population. Heritabilities for all 3 growth traits were consistent but lower than values provided for the whole population (males and females) by the American Angus Association. These values were 0.41 for BW and 0.20 for WW and PWG ([Lourenco et al., 2015](#)). The lower values obtained in this study could be explained by 2 reasons. First, only genotyped males were used in this analysis (GBLUP approach), which are a small sample of the whole American Angus population. Second, even if the American Angus Association applied no genotyping strategy and the members choose which animals are genotyped (as described by [Lourenco et al., 2015](#)), by chance the data set used in this study might not be a representative sample of the national herd.

Dominance variance expressed as the proportion to additive variance was less than 10% (going from 3% to 8%) for all traits. Pedigree-based estimates of dominance variance were highly variable and low accurate ([Rodríguez-Almeida et al., 1995](#); [Gengler et al., 1997](#); [Misztal et al., 1998](#)). The lack of accuracy of pedigree-based models to estimate dominance deviations and its variance can explain that dominance was ignored in genetic evaluation models. Dominance is much easier with genomic information. Instead of dealing with probabilities of identical genotypes, heterozygote states are observed. However, to date, few studies have estimated dominance deviation variance in growth traits. Estimates for postweaning and yearling weight were reported in a multibreed population (with animals from 3 different breed types: *Bos taurus*, *Bos indicus*, and composite breeds; [Bolormaa et al., 2015](#)) and in Brahman and Tropical Composite breeds ([Raidan et al., 2018](#)). Compared with these studies, little evidence of dominance genetic variation was

**Table 3.** Estimated inbreeding depression (*b*) for the 3 growth traits using 2 models

Trait <sup>2</sup>	<i>b</i> <sup>1</sup>	
	MG <sup>3</sup>	MGD <sup>3</sup>
BW	-0.480 (0.195)	-0.476 (0.207)
WW	-10.225 (1.510)	-9.998 (1.588)
PWG	-10.695 (1.900)	-10.230 (2.036)

<sup>1</sup>Inbreeding depression estimates are expressed as the change in phenotypic mean (kg) per 10% increase in inbreeding (SE are in parenthesis).

<sup>2</sup>BW, birth weight; WW, weaning weight; PWG, postweaning gain.

<sup>3</sup>MG, model including only additive effects; MGD, model including both additive and dominant effects.



**Table 4.** Goodness of fit, likelihood ratio test and AIC values of models MG and MGD for growth traits

Trait <sup>1</sup>	-2 log likelihood		Likelihood ratio test		AIC	
	MG <sup>2</sup>	MGD <sup>2</sup>	$\chi^2$	P-value	MG <sup>2</sup>	MGD <sup>2</sup>
BW	127,529.78	127,527.76	2.02	0.08	127,533.78	127,533.75
WW	203,515.41	203,515.89	0.00	1.00	203,519.41	203,521.89
PWG	163,439.91	163,441.62	0.00	1.00	163,443.91	163,447.62

<sup>1</sup>BW, birth weight; WW, weaning weight; PWG, postweaning gain.

<sup>2</sup>MG, model including only additive effects; MGD, model including both additive and dominant effects.

observed for growth traits BW, WW, and PWG in American Angus male population.

Even though the data set employed in the analysis was extensive, the results may indicate a lack of power to detect dominance variation. In this respect, 2 issues have to be taken into account. First, even though the number of animals with phenotypic and genomic data was over 19,000, no maternal effects could be taken into account given that they were completely confounded in the model due to the small number of offspring per dam. On the other hand, the proportion of full-sibs was small (7.64%) and, hence, little dominance-specific information was available for the estimation (Ertl et al., 2014). Including in the analysis individuals with phenotypic data but without genomic data could be an alternative to increase the amount of dominance-specific information. However, a Single-step approach with dominance is not a feasible solution yet.

Additive genetic variance estimates did not vary when dominance effect was included in the model (MGD), compared with those obtained with MG. Under orthogonality there is no covariance between the additive and dominant genetic effects (assumption of the model used; Vitezica et al., 2013), and the substitution effect contributes to the additive variance and the dominance deviation contributes to the dominance variance. If the model used in the estimation of variance components is not orthogonal (e.g., Su et al., 2012), biased and reduced estimates of additive genetic variance may be found when the model is expanded from additive to include dominance effects. Linkage disequilibrium may introduce genetic covariances between different genetic effects and complicate the partition of the genetic variance (Hill and Mäki-Tanila, 2015). A relationship between genetic effects (e.g., Wellmann and Bennewitz, 2011, 2012; Bennewitz et al., 2017) can be modeled. However, a model assuming uncorrelated effects and fitting orthogonal breeding values and dominant deviations performed similarly for prediction (Xiang et al., 2018).

No improvement in terms of goodness of fit for any of the analyzed traits, nor in the predictive ability of phenotypes for young animals was observed with the inclusion of dominance in the model. Values of AIC were similar across models and models including dominance did not seem to fit the data better than the simplest model. Similar results were reported by Aliloo et al. (2017), no differences in terms of goodness of fit were found between an additive genomic model including heterozygosity and a model considering additive and dominance effects with heterozygosity. Though speculative, increasing the amount of dominance-specific information might have a positive impact in the goodness of fit of the MGD, specially for BW. Predictive ability was not improved when dominance effects were included in the model. This is in agreement with most of the previous studies (Ertl et al., 2014; Esfandyari et al., 2016; Xiang et al., 2016; Moghaddar and van der Werf, 2017; Vitezica et al., 2018).

Varona et al. (2018) refer to some issues that have to be dealt with before models like the MGD become standard in genomic evaluation. Among those, these authors refer to a major obstacle given by the lack of serious testing as it requires extensive data sets with genotypes and phenotypes. The results, even with these limitations (only males, reduced number of full-sibs), reported here can contribute in this sense as the data set employed was extensive coming from a beef cattle population in which the proportion of genetic variation explained by nonadditive effects in traits of interest such as growth remains unknown.

According to Falconer and Mackay (1996), biological genotypic effects ( $a, d$ ) and allele frequencies ( $p, q$ ) contribute to the additive variance ( $2pq(a + (q - p)d)^2$ ), the dominance variance ( $(2pqd)^2$ ), and the inbreeding depression of a trait ( $2pqdF$ ). Inbreeding  $F$  may thus change (reduce in the case of inbreeding depression) the mean of the trait by an amount  $2pqdF$ . De Boer and Hoeschele (1993) showed that for models considering dominance, this change in the mean due to inbreeding should be fit in the model including the inbreeding coefficient as a covariate in the model together with the dominance deviations. Otherwise, dominance deviations are not centered around 0 and the estimate of the variance of dominance deviations (which refers to the base, noninbred, population) is inflated. Even if dominance deviations are not included in the model, inbreeding depression is an effect in the model that, if deemed considerable, should be included in the model per se as otherwise the model is incomplete and biased. In this study, both models MG and MGD included the effect of inbreeding as a covariate to consider inbreeding depression and also to obtain accurate variance component estimations.

When considering the joint action of several loci with dominance effect, a possibility is to have inbreeding effect with little variance of dominance deviations. This can be explained as follows. Considering several loci, dominance deviation variance,  $\sigma_D^2 = \sum_i (2p_i q_i d_i)^2$  is 0 only if  $d$  is 0 for all loci. In this case, there is no inbreeding depression either as  $\sum_i 2p_i q_i d_i F$  sums to 0. However, if there are several loci implied, some of them with a positive effect  $d$  in the heterozygote and some of them a negative effect  $d$  in the heterozygote; some of them will have a large effect and some a small one. Thus, it is possible to have high inbreeding depression and low dominance deviation variance, and the opposite, depending on the relationship between  $d$  and  $d^2$  across loci. If all loci have  $d > 0$  but with very small values, then  $\sum_i 2p_i q_i d_i F$  is high and these genes will generate large inbreeding depression, but  $\sigma_D^2 = \sum_i (2p_i q_i d_i)^2$  is small and so there will be little variance of dominance deviations. Conversely, if  $d$  effects are equally positive and negative and of large magnitude,  $\sum_i 2p_i q_i d_i F$  will be 0 but  $\sigma_D^2 = \sum_i (2p_i q_i d_i)^2$  will be large.

Little evidence of dominance genetic variation in growth traits like BW, WW, and PWG was found in American Angus

male population. Because of the small variance explained, a genomic model that includes the dominance effect may not be of superior fit compared with only the additive effect. Dominance in the model did not improve predictive ability in the cross-validation study.

## Acknowledgments

This study was partially funded by the projects UBACyT 5015/2016, INRA-SELGEN EpiNet, and the Saint-Exupéry program 2016 to 2017 (MinCyT Argentina—French Embassy). We thank the American Angus Association for the genomic and phenotypic data, the genotoul bioinformatics platform Toulouse Midi-Pyrenees (Bioinfo Genotoul) and anonymous referees for their comments.

## Literature Cited

- Aguilar, I., S. Tsuruta, A. Legarra, and H. Wang. 2014. PREGSF90-POSTGSF90: Computational Tools for the Implementation of Single-step Genomic Selection and Genome-wide Association with Ungenotyped Individuals in BLUPF90 Programs. In: Proceedings, 10th World Congress of Genetics Applied to Livestock Production (Vancouver, Canada). doi:10.13140/2.1.4801.5045
- Aliloo, H., J. E. Pryce, O. González-Recio, B. G. Cocks, M. E. Goddard, and B. J. Hayes. 2017. Including nonadditive genetic effects in mating programs to maximize dairy farm profitability. *J. Dairy Sci.* **100**:1203–1222. doi:10.3168/jds.2016-11261
- Aliloo, H., J. E. Pryce, O. González-Recio, B. G. Cocks, and B. J. Hayes. 2016. Accounting for dominance to improve genomic evaluations of dairy cows for fertility and milk production traits. *Genet. Sel. Evol.* **48**:8. doi:10.1186/s12711-016-0186-0
- Bennewitz, J., C. Edel, R. Fries, T. H. Meuwissen, and R. Wellmann. 2017. Application of a Bayesian dominance model improves power in quantitative trait genome-wide association analysis. *Genet. Sel. Evol.* **49**:7. doi:10.1186/s12711-017-0284-7
- Bolormaa, S., J. E. Pryce, Y. Zhang, A. Reverter, W. Barendse, B. J. Hayes, and M. E. Goddard. 2015. Non-additive genetic variation in growth, carcass and fertility traits of beef cattle. *Genet. Sel. Evol.* **47**:26. doi:10.1186/s12711-015-0114-8
- Burrow, H. M. 1993. The effects of inbreeding in beef cattle. *Anim. Breed. Abstr.* **61**:737–751.
- Burrow, H. M. 1998. The effects of inbreeding on productive and adaptive traits and temperament of tropical beef cattle. *Livest. Prod. Sci.* **55**:227–243.
- Davis, M. E., and R. C. Simmen. 2010. Estimates of inbreeding depression for serum insulin-like growth factor I concentrations, body weights, and body weight gains in Angus beef cattle divergently selected for serum insulin-like growth factor I concentration. *J. Anim. Sci.* **88**:552–561. doi:10.2527/jas.2009-2232
- De Boer, I. J. M., and I. Hoeschele. 1993. Genetic evaluation methods for populations with dominance and inbreeding. *Theor. Appl. Genet.* **86**:245–258. doi:10.1007/BF00222086
- Duenk, P., M. P. L. Calus, Y. C. J. Wientjes, and P. Bijma. 2017. Benefits of dominance over additive models for the estimation of average effects in the presence of dominance. *G3 (Bethesda)* **7**:3405–3414. doi:10.1534/g3.117.300113
- Ertl, J., A. Legarra, Z. G. Vitezica, L. Varona, C. Edel, R. Emmerling, and K. U. Götz. 2014. Genomic analysis of dominance effects on milk production and conformation traits in Fleckvieh cattle. *Genet. Sel. Evol.* **46**:40. doi:10.1186/1297-9686-46-40
- Esfandyari, H., P. Bijma, M. Henryon, O. F. Christensen, and A. C. Sørensen. 2016. Genomic prediction of crossbred performance based on purebred Landrace and Yorkshire data using a dominance model. *Genet. Sel. Evol.* **48**:40. doi:10.1186/s12711-016-0220-2
- Falcão, A. J. da S., R. Martins Filho, C. de U. Magnabosco, R. Bozzi, and F. de A. M. Lima. 2001. Effects of inbreeding on reproductive and growth traits, and breeding values in a closed Brown Swiss herd. *Rev. Bras. Zootec.* **30**:83–92.
- Falconer, D. S., and T. F. C. Mackay. 1996. *Introduction to quantitative genetics*. Longman, New York.
- Gengler, N., L. D. Van Vleck, M. D. MacNeil, I. Misztal, and F. A. Pariaacote. 1997. Influence of dominance relationships on the estimation of dominance variance with sire-dam subclass effects. *J. Anim. Sci.* **75**:2885–2891. doi:10.2527/1997.75112885x
- Heidaritabar, M., A. Wolc, J. Arango, J. Zeng, P. Settar, J. E. Fulton, N. P. O'Sullivan, J. W. Bastiaansen, R. L. Fernando, D. J. Garrick, et al. 2016. Impact of fitting dominance and additive effects on accuracy of genomic prediction of breeding values in layers. *J. Anim. Breed. Genet.* **133**:334–346. doi:10.1111/jbg.12225
- Hill, W. G. 2010. Understanding and using quantitative genetic variation. *Philos. Trans. R. Soc. Lond. B Biol. Sci.* **365**:73–85. doi:10.1098/rstb.2009.0203
- Hill, W. G., and A. Mäki-Tanila. 2015. Expected influence of linkage disequilibrium on genetic variance caused by dominance and epistasis on quantitative traits. *J. Anim. Breed. Genet.* **132**:176–186. doi:10.1111/jbg.12140
- Howard, J. T., J. E. Pryce, C. Baes, and C. Maltecca. 2017. Invited review: Inbreeding in the genomics era: inbreeding, inbreeding depression, and management of genomic variability. *J. Dairy Sci.* **100**:6009–6024. doi:10.3168/jds.2017-12787
- Legarra, A., C. Robert-Granié, E. Manfredi, and J. M. Elsen. 2008. Performance of genomic selection in mice. *Genetics* **180**:611–618. doi:10.1534/genetics.108.088575
- Lourenco, D. A., S. Tsuruta, B. O. Fragomeni, Y. Masuda, I. Aguilar, A. Legarra, J. K. Bertrand, T. S. Amen, L. Wang, D. W. Moser, et al. 2015. Genetic evaluation using single-step genomic best linear unbiased predictor in American Angus. *J. Anim. Sci.* **93**:2653–2662. doi:10.2527/jas.2014-8836
- Mäki-Tanila, A. 2007. An overview on quantitative and genomic tools for utilising dominance genetic variation in improving animal production. *Agric. Food Sci.* **16**:188–198. doi:10.2137/145960607782219337
- Miller, S. P., and M. E. Goddard. 1998. The super-breed approach to modelling additive and non-additive genetic effects between and within breeds in a multi-breed evaluation. *Proc. Sixth World Congr. Genet. Appl. Livest. Prod.* **23**:97–100.
- Misztal, I., S. Tsuruta, D. Lourenco, I. Aguilar, A. Legarra, and Z. Vitezica. 2014. *Manual for BLUPF90 family of programs*. University of Georgia, Athens, GA.
- Misztal, I., L. Varona, M. Culbertson, J. K. Bertrand, J. Mabry, T. J. Lawlor, C. P. Van Tassel, and N. Gengler. 1998. Studies on the value of incorporating the effect of dominance in genetic evaluations of dairy cattle, beef cattle and swine. *Biotechnol. Agron. Soc. Environ.* **2**:227–233.
- Moghaddar, N., and J. H. J. van der Werf. 2017. Genomic estimation of additive and dominance effects and impact of accounting for dominance on accuracy of genomic evaluation in sheep populations. *J. Anim. Breed. Genet.* **134**:453–462. doi:10.1111/jbg.12287
- Raidan, F. S. S., L. R. Porto-Neto, Y. Li, S. A. Lehnert, Z. G. Vitezica, and A. Reverter. 2018. Evaluation of nonadditive effects in yearling weight of tropical beef cattle. *J. Anim. Sci.* **96**:4028–4034. doi:10.1093/jas/sky275
- Reverter, A., L. R. Porto-Neto, M. R. S. Fortes, P. Kasarapu, M. A. R. de Cara, H. M. Burrow, and S. A. Lehnert. 2017. Genomic inbreeding depression for climatic adaptation of tropical beef cattle. *J. Anim. Sci.* **95**:3809–3821. doi:10.2527/jas2017.1643
- Rodríguez-Almeida, F. A., L. D. Van Vleck, R. L. Willham, and S. L. Northcutt. 1995. Estimation of non-additive genetic variances in three synthetic lines of beef cattle using an animal model. *J. Anim. Sci.* **73**:1002–1011. doi:10.2527/1995.7341002x

- Santana, M. L., Jr., P. S. Oliveira, V. B. Pedrosa, J. P. Eler, E. Groeneveld, and J. B. S. Ferraz. 2010. Effect of inbreeding on growth and reproductive traits of Nellore cattle in Brazil. *Livest. Sci.* **131**:212–217. doi:10.1016/j.livsci.2010.04.003
- Silió, L., M. C. Rodríguez, A. Fernández, C. Barragán, R. Benítez, C. Óvilo, and A. I. Fernández. 2013. Measuring inbreeding and inbreeding depression on pig growth from pedigree or SNP-derived metrics. *J. Anim. Breed. Genet.* **130**:349–360. doi:10.1111/jbg.12031
- Su, G., O. F. Christensen, T. Ostersen, M. Henryon, and M. S. Lund. 2012. Estimating additive and non-additive genetic variances and predicting genetic merits using genome-wide dense single nucleotide polymorphism markers. *PLoS One* **7**:e45293. doi:10.1371/journal.pone.0045293
- Sumreddee, P., S. Toghiani, E. H. Hay, A. Roberts, S. E. Aggrey, and R. Rekaya. 2018. Inbreeding depression in line 1 Hereford cattle population using pedigree and genomic information. *J. Anim. Sci.* **97**:1–18. doi:10.1093/jas/sky385
- Swiger, L. A., K. E. Gregory, R. M. Koch, and V. A. Arthaud. 1961. Effect of inbreeding on performance traits of beef cattle. *J. Anim. Sci.* **20**:626–630.
- Toro, M. A., and L. Varona. 2010. A note on mate allocation for dominance handling in genomic selection. *Genet. Sel. Evol.* **42**:33. doi:10.1186/1297-9686-42-33.
- VanRaden, P. M. 2008. Efficient methods to compute genomic predictions. *J. Dairy Sci.* **91**:4414–4423. doi:10.3168/jds.2007-0980
- Varona, L., A. Legarra, M. A. Toro, and Z. G. Vitezica. 2018. Non-additive effects in genomic selection. *Front. Genet.* **9**:78. doi:10.3389/fgene.2018.00078
- Visscher, P. M. 2006. A note on the asymptotic distribution of likelihood ratio tests to test variance components. *Twin Res. Hum. Genet.* **9**:490–495. doi:10.1375/183242706778024928
- Vitezica, Z. G., A. Reverter, W. Herring, and A. Legarra. 2018. Dominance and epistatic genetic variances for litter size in pigs using genomic models. *Genet. Sel. Evol.* **50**:71. doi:10.1186/s12711-018-0437-3
- Vitezica, Z. G., L. Varona, and A. Legarra. 2013. On the additive and dominant variance and covariance of individuals within the genomic selection scope. *Genetics* **195**:1223–1230. doi:10.1534/genetics.113.155176
- Wellmann, R., and J. Bennewitz. 2011. The contribution of dominance to the understanding of quantitative genetic variation. *Genet. Res. (Camb.)* **93**:139–154. doi:10.1017/S0016672310000649
- Wellmann, R., and J. Bennewitz. 2012. Bayesian models with dominance effects for genomic evaluation of quantitative traits. *Genet. Res. (Camb.)* **94**:21–37. doi:10.1017/S0016672312000018
- Xiang, T., O. F. Christensen, Z. G. Vitezica, and A. Legarra. 2016. Genomic evaluation by including dominance effects and inbreeding depression for purebred and crossbred performance with an application in pigs. *Genet. Sel. Evol.* **48**:92. doi:10.1186/s12711-016-0271-4
- Xiang, T., O. F. Christensen, Z. G. Vitezica, and A. Legarra. 2018. Genomic model with correlation between additive and dominance effects. *Genetics* **209**:711–723. doi:10.1534/genetics.118.301015
- Zeng, J., A. Toosi, R. L. Fernando, J. C. Dekkers, and D. J. Garrick. 2013. Genomic selection of purebred animals for crossbred performance in the presence of dominant gene action. *Genet. Sel. Evol.* **45**:11. doi:10.1186/1297-9686-45-11