Estimating variance components for growth, feed efficiency and carcass merit traits in Angus steers using additive and dominance genomic relationship matrices

L. Chen[*], G. Plastow[*], C. Li[*,†]

[*]University of Alberta, [†]Agriculture and Agri-Food Canada, Lacombe Research Centre, Lacombe, Alberta, Canada.

ABSTRACT: Variance components were estimated in a purebred Angus population of 742 steers using additive and dominance genomic relationship matrices constructed from genotypes of the Illumina BovineSNP50 Beadchip. Traits studied were birth weight (BWT), weaning weight (WWT), feedlot dry matter intake (DMI), average daily gain (ADG), residual feed intake (RFI), hot carcass weight (HCW), lean meat yield (LMY), carcass marbling score (CMAR), rib eye area (REA), and backfat thickness (AFAT). Estimated narrow sense heritability ranged from 0.25 ± 0.08 for ADG to 0.56 ± 0.08 for DMI. Maternal heritability estimates were 0.15 ± 0.05 and 0.17 ± 0.05 for BWT and WWT, respectively. Proportions of phenotypic variances explained by dominance were zero for DMI, RFI, and CMAR, very small for HCW (3%) and REA (5%), low for WWT (10%), LMY (14%) and AFAT (11%), and relatively larger for BWT (24%) and ADG (25%).
Keywords: additive; dominance; genomic relationship matrix

Introduction

In beef cattle and other livestock populations, genetic evaluations currently focus on additive genetic effects. Dominance effects have been ignored mainly due to inadequate pedigree relationships (large data size with a high proportion of full-sibs is needed for accurate estimation of dominance variance components), and computational limitations (Misztal et al. (1998)). With the advent of genomics technology, interests in dominance effects have been renewed (Toro and Varona (2010); Su et al. (2012); Wellmann and Bennewitz (2012); Vitezica et al. (2013); Zeng et al. (2013)). Including dominance in genetic evaluations would provide more accurate breeding value estimates and allow mate allocations for maximizing total genetic value for the progeny, and therefore, result in greater selection response (Toro and Varona (2010); Zeng et al. (2013)).

Accurate estimates of variance components are prerequisites for genetic/genomic evaluations. Appropriately constructed additive and dominance genomic relationship matrices from high density marker genotypes can provide unbiased estimates of additive and dominance variance components (Yang et al. (2011); Vitezica et al. (2013)). In beef cattle, except for pre-weaning growth traits (Rodriguez-Almeida et al. (1995); Duangjinda et al. (2001)), contributions of dominance to total phenotypic variance have not been quantified for economically important traits. The

goal of this study was to estimate variance components for growth, feed efficiency and carcass merit traits in an Angus steer population using additive and dominance genomic relationship matrices constructed based on marker genotypes from the Illumina BovineSNP50 Beadchip.

Materials and Methods

A total of 742 purebred Angus steers from 55 sires were used in this study. All animals were managed according to the guidelines established by the Canadian Council of Animal Care (1993). Steers were born at the Onefour Research Substation of the Agriculture and Agri-Food Canada Research Centre (AAFC) at Lethbridge from 2004 to 2008 and at the University of Alberta's Kinsella Research Station from 2009 to 2011 with birth weight (BWT) recorded for each animal. All calves were vaccinated for bovine viral diarrhea and clostridial diseases, and were not treated with growth promotants after castration. Around the age of 6 months, the steers were weaned with actual weaning weights measured. Actual weaning weights were then adjusted to weaning weight (WWT) at age of 180 d using a formula as follows, WWT = (Actual weaning weight – BWT) / days from birth to weaning × 180 + BWT. Steers were background fed for about four and half months, followed by a transition diet for a period of approximately three weeks. Steers were then randomly assigned to 4 pens of 6 feed bunks per pen. Feed intake data were collected using the GrowSafe automated feeding system (GrowSafe Systems Ltd., Airdrie, Alberta, Canada). Details of feedlot tests using the GrowSafe system, and serial weight measurements during the feedlot tests were described previously (Mao et al. (2013)). For each animal, ADG was derived as regression coefficient by regressing bi-weekly body weight measurements on days on test. Midpoint body weight (BW) was computed as the initial weight of test plus ADG times half of the days on test, and mid-point metabolic body weight (MWT) was calculated as midpoint $BW^{0.75}$. Daily dry matter intake (DMI) was calculated as animal's average daily feed intake standardized to 12 MJ ME/kg dry matter based on the energy content of the diet. Daily DMI was regressed on ADG and MWT to derive a prediction equation to predict an animal's expected DMI required for maintenance of its body weight and growth. The difference between an animal's actual daily DMI and predicted DMI was defined as RFI. At the end of the feedlot test, steers were slaughtered within a week at a commercial packing plant. Standard carcass data including hot carcass weight (HCW), carcass average backfat thickness (AFAT), LM area (REA),

carcass marbling score (CMAR) were collected by trained personnel. Lean meat yield (LMY) was calculated as described previously (Basarab et al. (2013); Mao et al. (2013)).

All animals were genotyped on the Illumina BovineSNP50 Beadchip with 54,609 single nucleotide polymorphisms (SNP). SNPs with minor allele frequency less than 0.05, missing call rate greater than 0.10, or significantly deviated from Hardy-Weinberg equilibrium ($P < 10^{-6}$) were removed. After editing, 40,495 SNPs were kept for analyses.

A single trait animal model was used for analyses. The model included fixed effects of birth year, fixed covariate of dam age for BWT and WWT, fixed effects of contemporary groups (combinations of 8 test year and 4 pens per year) and fixed covariate of age at start of feedlot test for DMI, ADG, RFI, fixed effects of contemporary groups and fixed covariate of age at slaughter for HCW, LMY, CMAR, REA, and AFAT. Random effects included additive direct, dominance, and residual effects for all traits, and additive maternal genetic effects for BWT and WWT. Additive direct and dominance relationship matrices were constructed from genotypes using methods described by Vitezica et al. (2013). The additive maternal relationship matrix was constructed from a pedigree containing 2,319 animals. Variance components were estimated by average-information REML using ASReml v3.0 software package (VSN International Ltd., Hemel Hempstead, UK; Gilmour et al. (2009)).

Results and Discussion

Estimates of variance components along with direct (h_a^2) and maternal (h_m^2) heritability, and proportion of phenotypic variance explained by dominance ($V_d\%$) are presented in Table 1, 2, and 3. Estimated direct heritability ranged from 0.25 ± 0.08 for ADG to 0.56 ± 0.08 for DMI. Estimates of maternal heritability were 0.15 ± 0.05 and 0.17 ± 0.05 for BWT and WWT, respectively. Proportions of phenotypic variances explained by dominance were zero for DMI, RFI, and CMAR, very small for HCW ($3 \pm 14\%$) and REA ($5 \pm 18\%$), low for WWT ($10 \pm 13\%$), LMY ($14 \pm 16\%$) and AFAT ($11 \pm 15\%$), and relatively higher for BWT ($24 \pm 12\%$) and ADG ($25 \pm 20\%$).

Table 1. Estimates of variance components and heritability for birth weight and weaning weight[1]

Items[2]	BWT	WWT
σ_a^2	67.65 ± 14.43	853.69 ± 240.13
σ_m^2	23.25 ± 7.49	476.44 ± 138.17
σ_d^2	36.73 ± 19.01	259.92 ± 361.47
σ_e^2	25.78 ± 17.28	1145.11 ± 353.56
h_a^2	0.44 ± 0.08	0.31 ± 0.08
h_m^2	0.15 ± 0.05	0.17 ± 0.05
$V_d\%$	24 ± 12	10 ± 13

[1]BWT = Birth weight; WWT = (Actual weaning weight – BWT) / days from birth to weaning × 180 + BWT
[2]σ_a^2= direct additive genetic variance; σ_m^2= maternal genetic variance; σ_d^2= dominance genetic variance; σ_e^2= residual variance; h_a^2= direct heritability; h_m^2= maternal heritability; $V_d\%$= proportion of phenotypic variance explained by dominance

Table 2. Estimates of variance components and heritability for feed efficiency traits[1]

Items[2]	DMI	ADG	RFI
σ_a^2	0.43 ± 0.08	0.0095 ± 0.0033	0.14 ± 0.03
σ_d^2	0	0.0094 ± 0.0077	0
σ_e^2	0.34 ± 0.05	0.0187 ± 0.0076	0.19 ± 0.02
h_a^2	0.56 ± 0.08	0.25 ± 0.08	0.43 ± 0.08
$V_d\%$	0	25 ± 20	0

[1]RFI = residual feed intake; DMI = average daily dry matter feed intake; ADG = average daily gain
[2]σ_a^2= direct additive genetic variance; σ_d^2= dominance genetic variance; σ_e^2= residual variance; h_a^2= direct heritability; $V_d\%$= proportion of phenotypic variance explained by dominance

Table 3. Estimates of variance components and heritability for carcass merit traits[1]

Items[2]	HCW	LMY	CMAR
σ_a^2	764.1 ± 184.3	6.92 ± 1.31	0.05 ± 0.01
σ_d^2	72.1 ± 297.4	1.73 ± 2.00	0
σ_e^2	1229.7 ± 300.8	4.19 ± 1.98	0.13 ± 0.01
h_a^2	0.37 ± 0.08	0.50 ± 0.08	0.26 ± 0.07
$V_d\%$	3 ± 14	14 ± 16	0

Table 3 (continued).

Items[2]	REA	AFAT
σ_a^2	16.15 ± 4.30	8.67 ± 1.71
σ_d^2	2.16 ± 8.38	1.84 ± 2.61
σ_e^2	28.57 ± 8.52	6.56 ± 2.59
h_a^2	0.34 ± 0.08	0.51 ± 0.08
$V_d\%$	5 ± 18	11 ± 15

[1]HCW = hot carcass weight; LMY = lean meat yield; CMAR = marbling score; REA = rib eye area; AFAT = backfat thickness
[2]σ_a^2= direct additive genetic variance; σ_d^2= dominance genetic variance; σ_e^2= residual variance; h_a^2= direct heritability; $V_d\%$= proportion of phenotypic variance explained by dominance

Direct heritability estimates for feed efficiency and carcass merit traits have been reported previously using pedigree information in the same population with a smaller sample size (Mao et al. (2013)), with direct heritability of 0.39 ± 0.10 for DMI, 0.38 ± 0.12 for ADG, 0.47 ± 0.12 for RFI, 0.23 ± 0.08 for HCW, 0.41 ± 0.13 for LMY, 0.37 ± 0.11 for CMAR, 0.49 ± 0.14 for REA, and 0.35 ± 0.12 for AFAT. Heritability estimates of RFI are similar between current and the previous studies (0.43 ± 0.08 vs. 0.47 ± 0.12), whereas for other traits the heritability estimates dif-

fer to some extent, which may be due to the different sample sizes used. However, in this study the additive relationship matrix was constructed from marker genotypes instead of pedigree. Vitezica et al. (2013) suggested that using genomics rather than pedigree information would result in more accurate estimates of variance components, as the genomic relationship matrix constructed with dense DNA markers will likely better capture the Mendelian sampling terms. In addition, including the dominance effect will also likely improve the model fitness and therefore, improve the accuracy of estimates of additive variance components. In this study, we compared different genetic models with and without dominance effects in the model and found that models with dominance had a higher likelihood of fitting the data in general than those without dominance (results not shown).

Estimated proportions of phenotypic variance explained by dominance were relatively larger for BWT and ADG compared to other traits. Rodriguez-Almeida et al. (1995) reported 18% and 28% of phenotypic variance explained by dominance for birth weight and weaning weight in crossbred beef cattle, and Duangjinda et al. (2001) found that dominance explained 18% to 23% phenotypic variance for weaning weight in Hereford, Gelbvieh, and Charolais breeds. In this study, dominance accounted for 24% of phenotypic variance for BWT, which is similar to that reported by Rodriquez-Almeida et al. (1995). But for weaning weight, the dominance variance proportion (10%) was much lower than previously reported. The inconsistent estimates of phenotypic variance proportions explained by dominance for weaning weight in different studies may be due to the different biological types of breeds used in the studies. Although the dominance variance for RFI is 0, dominance variance proportion for its component trait ADG is relatively large (25%). However, relatively large standard errors for dominance variance components were observed in this study, which is likely due to a relatively small sample size used. Further studies with larger sample sizes are required to estimate dominance variance components and to exploit the benefits of including dominance effects for beef cattle genetic evaluation using genomics.

Conclusion

Dominance accounted for zero or small proportions of phenotypic variances for DMI, RFI, CMAR, HCW and REA (0 to 5%), low for WWT (10%), LMY (11%) and AFAT (14%), and relatively larger for BWT (24%) and ADG (25%). Results from this study may provide insights into possible genomic applications of predicting breeding values or total genetic values by incorporating dominance effects into the prediction model. Standard errors for the estimates of variance components in this study are still large, especially for the dominance variance components. To provide accurate genetic parameters for genetic evaluations, further studies with a larger sample size are required.

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