

sion between breeds to help address performance.

Key Words: genetic diversity, inbreeding, single nucleotide polymorphism, Canadian beef cattle
doi: 10.2527/jam2016-0310

0311 Joint association analysis of additive and non-additive genomic effects for growth and carcass traits of beef cattle.

E. C. Akanno^{*1}, M. K. Abo-Ismaïl^{1,2}, L. Chen¹, C. Li^{1,3}, J. Basarab^{1,4}, and G. Plastow¹, ¹*Livestock Gentec, Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Canada*, ²*Animal and Poultry Production, Damanshour University, Egypt*, ³*Lacombe Research and Development Centre, Agriculture and Agri-Food Canada, Edmonton, AB, Canada*, ⁴*Lacombe Research Centre, Alberta Agriculture and Forestry, Lacombe, Canada*.

The biological dominance effects of genes have been suggested as one of the genetic mechanism explaining heterosis. We performed a joint association analysis using genotypes from Illumina BovineSNP50 (50K) BeadChip to evaluate the contributions of additive and dominance genomic effects to the variance of growth and carcass traits in beef cattle and to identify genomic regions that potentially harbor genes or quantitative trait loci underlying the variation. A total of 6794 multi-breed and crossbred beef cattle with phenotype and 50K genotypes were used. Traits studied included birth weight (BWT), weaning weight (WWT), pre-weaning daily gain (PDG), average daily gain (ADG), yearling weight (YWT), hot carcass weight (HCW), back fat thickness (BFT), rib-eye area (REA), marbling score (MS), lean meat yield (LMY) and yield grade (YG). Additive and dominance genomic relationships were created based on 42,610 single nucleotide polymorphism (SNP) markers that passed the quality control. The

model used accounted for fixed contemporary group effects (herd, year, data source, and sex), covariates of genomic breed composition, age of dam, weaning age, age at start of feedlot test, and slaughter age, and random maternal and maternal permanent effect depending on the trait analyzed. A single SNP analysis that partitions the SNP effects into additive and dominance components was used for genome-wide association. The proportions of total phenotypic variance explained by additive and dominance effects for the studied traits are presented in Table 1. After applying a false discovery rate at a 5% significance level, a total of 66, 20, 2, 36, 66, 22, 9, 15, 10, and 3 SNPs were significantly associated with BWT, WWT, PDG, ADG, YWT, HCW, BFT, REA, LMY, and YG, respectively, for the additive component. For the dominance component, three SNPs (rs110564527, rs110361335, and rs41663796) and one SNP (rs43624164) were significantly associated with MS and WWT, respectively. The SNP rs110361335 located on chromosome 4 was found to be within *islet cell autoantigen 1 (ICAI)* gene which is involved in insulin regulation. In addition, SNP rs43624164 on chromosome 10 found to be near the gene *ribosomal protein L10-like (RPL10L)* had significant additive and dominance effects on WWT. Although, the proportions of phenotypic variance explained by dominance were moderate for growth traits with known heterosis effects, the results of this study suggest that dominance effects are polygenic.

Key Words: beef cattle, dominance genetic effect, genomic prediction
doi: 10.2527/jam2016-0311

Table 0311.

Table 1. Proportions of phenotypic variance explained by additive and dominance effects in purebreds, crossbreds and overall populations¹

Traits	Purebreds (n = 2060)		Crossbreds (n = 4734)		Overall (n = 6794)	
	Additive	Dominance	Additive	Dominance	Additive	Dominance
Birth weight, kg	0.54±0.053	0.21±0.066	0.56±0.034	0.10±0.043	0.51±0.026	0.08±0.028
Weaning weight, kg	0.21±0.052	0.25±0.081	0.34±0.031	0.03±0.039	0.30±0.024	0.06±0.027
Pre-weaning daily gain, kg/d	0.31±0.055	0.21±0.069	0.35±0.035	0.04±0.049	0.27±0.026	0.07±0.031
Average daily gain, kg/d	0.27±0.048	0.01±0.078	0.33±0.029	0.01±0.038	0.30±0.023	0.02±0.026
Yearling weight, kg	0.47±0.050	0.12±0.073	0.56±0.029	0.10±0.038	0.47±0.023	0.08±0.026
Hot carcass weight, kg	0.29±0.066	0.05±0.125	0.44±0.042	0.00±0.000	0.43±0.035	0.00±0.000
Back fat thickness, mm	0.48±0.070	0.00±0.000	0.23±0.039	0.01±0.070	0.31±0.036	0.01±0.054
Rib eye area, cm ²	0.40±0.069	0.11±0.133	0.40±0.041	0.00±0.000	0.41±0.036	0.00±0.000
Marbling score	0.32±0.066	0.00±0.000	0.35±0.041	0.13±0.067	0.32±0.035	0.00±0.000
Lean meat yield, %	0.45±0.070	0.03±0.125	0.30±0.040	0.03±0.067	0.37±0.036	0.05±0.053
Yield grade	0.43±0.071	0.10±0.129	0.32±0.041	0.05±0.068	0.39±0.036	0.03±0.053

¹Purebred individuals have > 90% of their representative breeds (Angus, Hereford and Charolais); Crossbred individuals included beef-dairy hybrids, Beefbooster composite (www.beefbooster.com), and two and three way crossbreds involving Angus, Hereford, Charolais, Gelbvieh, Simmental, Limousine, and Piedmontese