0310   Assessing genetic diversity in Canadian beef cattle populations using Illumina BovineSNP50 chip.
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The main objective of this study was to utilize genomic profiles to assess genetic diversity within and between Canadian beef cattle populations to gain insights on population admixture and dynamics. Individuals ($n = 2831$) were genotyped for Illumina BovineSNP50 for 9 populations (Gelbvieh (GVH, $n = 488$), Charolais (CHA, $n = 396$), Angus (AAN, $n = 492$), Simmental (SIM, $n = 404$), Limousin (LIM, $n = 205$), Hereford (HER, $n = 591$), Hays Converter (HC, $n = 208$), Kinsella composites (KC, $n = 15$) and Lacombe Research Centre (LRC, $n = 33$). A total of 2828 individuals with 43,172 SNPs across 29 autosomes passed quality control and were used for further analyses. To study population structure between populations, a principal component analysis (PCA) was performed using SNP1101 software. Genomic inbreeding coefficients for each individual were estimated using 4 methods; VanRaden 2008 (F_v), Leutenegger 2003 (F_l), excess of homozygosity (F_h) and GCTA software (F_g) method implemented in SNP1101 software. The PCA analysis reported clear divergence between GVH, CH, AAN, SIM, LIM, HER and HC populations where 7 clusters were well defined, illustrated in Fig. 1. The KC and LRC populations are distributed between the other clusters confirming their genetic architectures as crossbred. The most genomically divergent breeds were CHA, AAN, GVH and HER. The correlations between inbreeding coefficients F_v with F_l and F_g were strong; 0.98 and 0.93, respectively. The average estimate of genomic inbreeding coefficients (F_v, Fl, and Fg) were highest for the HER ranged from 12.8 ± 0.1 to $18.5 \pm 0.2\%$ followed by AAN ranged from 10 ± 0.1 to $12.7 \pm 0.1\%$. In addition, the genomic inbreeding coefficients for composites/crossbreds ranged from 2.0 ± 1.0 to $4.0 \pm 1.0\%$ and from 1.0 ± 0.7 to $7.0 \pm 1.0\%$ for KC and LRC, respectively, where these inbreeding levels were low across all methods compared with purebred cattle. In conclusion, the genomic assessment of inbreeding using different methods indicated that HER and AAN breeds had the highest inbreeding level and thus inbreeding depression should be assessed for their traits at the genome level. Information on specific regions that are fixed for deleterious alleles allows directed introgres-
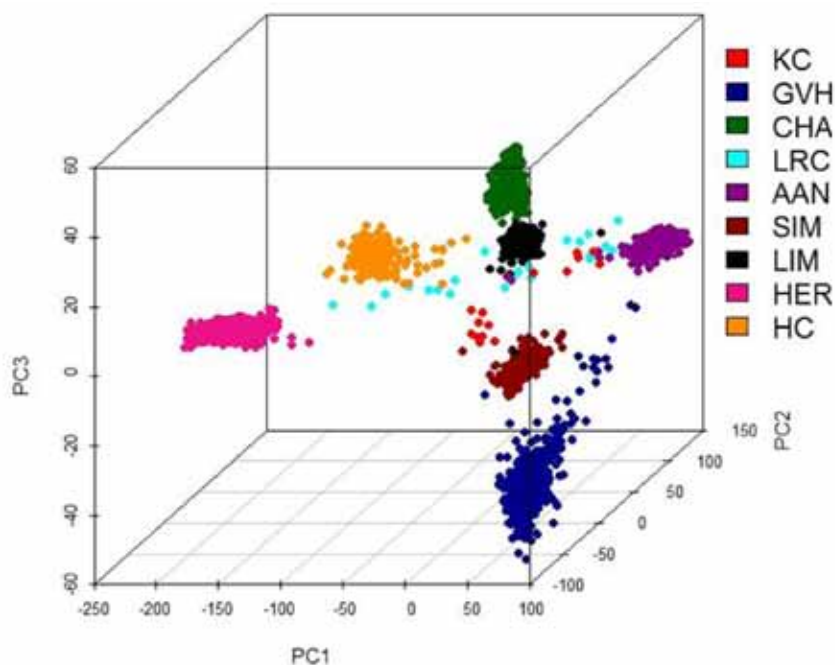
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Figure 1. Population structures identified by principal component analysis. The plot shows the first three principal components (PCs) using Illumina BovineSNP50 (43,172 SNPs) across the 29 autosomes. KC is Kinsella composites, LRC is Lacombe Research Centre, GVH is Gelbvieh, CHA is Charolais, ANG is Angus, SIM is Simmental, LIM is Limousin, HER is Hereford, HC is Hays Converter.

sion between breeds to help address performance.

0311 Joint association analysis of additive and non-additive genomic effects for growth and carcass traits of beef cattle.
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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* (*ICA1*) 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.

Table 0311.

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

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, cm²	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

[1]Purebred 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