Accuracy of Genomic Predictions for Birth, Weaning and Yearling Weights in US Simmental Beef Cattle

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Summary and Implications

Direct genomic breeding values (DGV) based on actual or imputed GeneSeek Genomic Profiler HD (GGPHD) genotypes were obtained for birth, weaning and yearling weights using Bayesian regression on about 20,000 US Simmental pure- or cross-bred beef cattle. Accuracies of DGV were quantified using 4-fold cross validation. Accuracies expressed as genetic correlations between DGV and trait ranged from 0.61 to 0.65, and the regressions of phenotype on DGV ranged from 0.61 to 0.66. These results indicate good predictive ability of genomic prediction with GGPHD chips but DGV need to be adjusted for bias.

Introduction

The American Simmental Association has been providing genomic predictions for high percentage Simmental animals as part of their cattle evaluation. The DGV were based on genotypes from the Illumina BovineSNP50 BeadChip and reported genetic correlations were 0.65 for birth weight, 0.52 for weaning weight and 0.45 for yearling weight (Saatchi et al., 2012, GSE). Since that time, various density arrays have been used on additional animals. The objective of this study was to re-estimate genetic correlations using real or imputed GGPHD genotypes and a much larger dataset of admixed breeds.

Materials and Methods

A total of 1,770 Angus (AAN), 1,788 Gelbvieh (GVH), 2,251 Red Angus (RAN), 585 Maine-Anjou (RDP), and 15,397 Simmental (SIM) cattle were genotyped with the Illumina BovineSNP50 BeadChip (50k), BovineHD BeadChip (770k), GeneSeek Genomic Profiler LD (GGPLD, v1: 9k, v3: 26k), GGPHD (77k) or Affymetrix Axiom Bovine chip (650k). All genotypes were imputed to GGPHD with FImpute software (Sargolzaei et al., 2014, BMC Genomics). The SIM registered individuals were grouped into 6 subsets according to their pedigree-based SIM breed percentages: high percentage Simmental animals were SIM1 and the lowest percentage were SIM6. Within each breed or group (SIM1, SIM2-6, AAN, RAN, GVH, RDP), principal component analysis of genotypes was performed, in order to separate animals into 4 equal-sized groups by applying an equal-K-means clustering algorithm using the two largest principal components. These groups formed within-breed were then pooled across breeds to produce 4 admixed groups for training and validation.

Marker effect estimation (training) was undertaken after further pooling 3 of the 4 admixed groups to predict the performance (validation) of animals in the group that was not included in training. Training was based on weighted Bayesian regression of deregressed estimated breeding values (DEBV, Garrick et al., 2009, GSE) but after adding the parent average (PA) back to the genotyped individuals' deregressed data. The PA DEBV includes breed effects. BayesC with pi=0.99 implemented in GenSel software v4.84r (Fernando et al., 2013, Iowa State University) was used in all training analyses.

Validation was undertaken by fitting bivariate models separately for each of birth, weaning and yearling weights with the four validation groups and breed percentage as fixed effects in ASReml (Gilmour et al, 2009, VSN Int Ltd). One "trait" was the DGV obtained from training using only the other 3 groups, while the other trait consisted of individual animal phenotypes adjusted for fixed effects. The phenotypes were those measured on the genotyped animals, their ancestors, their mates and their immediate descendants. The accuracies of DGVs were expressed as the genetic correlations between phenotype and DGV.

Results and Discussion

The estimated heritabilities, phenotype-DGV genetic correlations and regressions of phenotype on DGV are in Table 1. Heritabilities of DGV were as expected close to 1.00, and heritabilities of phenotype close to published values. The estimates of genetic correlations with DGV were 0.61 or higher for all three traits, but linear regressions of phenotype on DGV were significantly lower than 1.0. These genetic correlations indicate good across-breed predictive ability, but demonstrate that predictions must be adjusted for bias before blending or combining with other traits, which involves multiplying DGV by the regression.

Table 1. Estimates of heritabilities, genetic correlations and regressions of phenotype on DGV.

Weight	h^2_{Phe}	h^2_{DGV}	r_g	$b_{Phe/DGV}$
Birth	0.42	0.95	0.64	0.61
Weaning	0.28	0.96	0.61	0.61
Yearling	0.41	0.96	0.65	0.66

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