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

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 Recommended Citation  
Available at: http://lib.dr.iastate.edu/ans_air/vol661/iss1/20
Accuracy of Genomic Predictions for Birth, Weaning and Yearling Weights in US Simmental Beef Cattle

A.S. Leaflet R2957

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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 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.

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

<table>
<thead>
<tr>
<th>Weight</th>
<th>$h^2_{Phe}$</th>
<th>$h^2_{DGV}$</th>
<th>$r_g$</th>
<th>$b_{Phe/DGV}$</th>
</tr>
</thead>
<tbody>
<tr>
<td>Birth</td>
<td>0.42</td>
<td>0.95</td>
<td>0.64</td>
<td>0.61</td>
</tr>
<tr>
<td>Weaning</td>
<td>0.28</td>
<td>0.96</td>
<td>0.61</td>
<td>0.61</td>
</tr>
<tr>
<td>Yearling</td>
<td>0.41</td>
<td>0.96</td>
<td>0.65</td>
<td>0.66</td>
</tr>
</tbody>
</table>

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 1.0, 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.

Acknowledgments

We acknowledge the American Simmental Association, Canadian Simmental Association and other US breed
associations that provided data as well as US and Canadian researchers that kindly shared their genotypes.