Genomic Selection in Crossbreeding Programs

Jack Dekkers
Genomic Selection for Field Performance

Potential benefits

(Dekkers 2007 JAS)

Selection
Genomic EBV
Genotype
SNP effect estimates
Production herds

Genetic correlation (purebred – commercial) = 0.7

Genetic Selection for Field Performance

Accuracy of selection for commercial performance

\[ r_{\text{pb,cb}} = 0.7 \]

\[ \hat{r}_{\text{pb}} = 0.4 \quad - \quad 0.38 \quad 0.27 \]

Accuracy of marker information (\( r_{\text{MG}} \))

\[ r_{\text{MG}} = q_{\text{P}} r_{\hat{Q}_p} \]

\[ r_{\text{MG}} = q_{\text{cb}} r_{\hat{Q}_p} \]

Select
20 / 240 males
60 / 240 females

Inbreeding

\[ r_{\text{pb,cb}} = 0.7 \]
GS training on Crossbred data

1. Genotype parents and train on crossbred progeny performance – requires pedigree
2. Genotype crossbreds and train on own phenotype – does not require pedigree

NUCLEUS herds

SNP effect estimates

Genotype Phenotype

Production herds

Genotype

Genomic EBV

Selection

Genotype

Genomic EBV

Selection

Production herds

Need to estimate breed-specific SNP effects?

Reasons:
- Dominance
- Epistasis
- GxEnvironment
- Marker-QTL LD

Across-line Breed-specific effects

Estimation of marker effects in crosses

Complete LD

Partial LD

Marker effects expected to differ in pure lines vs. crossbreds

MAS/GS for field performance

Complete LD

Partial LD

Across-line

Breed-specific effects

Need to estimate breed-specific SNP effects?
Noelia Ibanez-Escrí;e, Rohan Fernando, Ali Toosi, Jack Dekkers
GSE 2009 Additive QTL model

Impact of Dominance

Across-breed Breed-specific
50 550 infin 50 550 infin 50 550 infin 50 550 infin

0 markers 2000 markers
1000 phenotypic records 4000 phenotypic records

Impact of Dominance

Allele substitution effect in sire breed for varying dam breed frequencies $p_0$ and degrees of dominance

$\alpha_S = a + (q_S - p_S)d$

$p_D = 0.1$
$p_D = 0.9$
$p_D = 0.75$
$p_D = 0.5$
$p_D = 0.25$
$p_D = 0.1$

Crossbred allele substitution effect

$\alpha_{S,c} = (p_D a + q_D d) - (p_D d - q_D a) = a + (q_D - p_D)d$

Purebred allele substitution effects

$\alpha_S = a + (q_S - p_S)d$

$\alpha_D = a + (q_D - p_D)d$

Impact of Dominance

Estimate ‘$a$’ and ‘$d$’ vs allele substitution effects

Effects change over time

Allele substitution effect in one parental breed depends on allele freq.s in other parental breed

Breed-specific allele effects

Impacts of Dominance

Allele substitution effect in one parental breed depends on allele freqs in other parental breed

Breed-specific allele effects

Effects change over time
Genomic selection of purebred animals for crossbred performance in the presence of dominant gene action

Jan Feng1, Ali Toor1, Rohan L. Fernandez², Jack CM Dickerson3 and Dorian J. Garrick¹

Abstract

Genomic selection is an appealing method to select purebred bovines for crossbred performance in the case of economic traits. Single nucleotide polymorphism (SNP) effects can be estimated using additive and dominance models to account for genetic basis of inheritance. Advantages of incorporating dominance in genomic selection were investigated in a new year crossbreeding program for a wide range of different magnitudes of dominance. Testing was carried out on four different levels of dominance.

Results

When dominance variance and dominance variance were large and dominance was present, a dominance model estimated dominance variance and dominance variance in the absence of dominance. A dominance model estimated the effect of an increase in dominance as a cost of reduced dominance performance. When dominance variance and dominance variance were small, the advantage of the dominance model decreased but was not significant. When dominance variance and dominance were large, the dominance model estimated the effect of dominance as a cost of reduced dominance variance in the absence of dominance. When dominance variance and dominance variance were large, the dominance model estimated the effect of dominance as a cost of reduced dominance variance in the absence of dominance. When dominance variance and dominance variance were large, the dominance model estimated the effect of dominance as a cost of reduced dominance variance in the absence of dominance.

Dominance Model

\[ y_i = \mu + \sum_{j=1}^{k} (X_{ij}a_j + W_{ij}d_j) + e_i \]

- \( W_{ij} \in \{0, 1\} \) is the indicator for heterozygous genotype
- \( a_j \) is the additive effect and \( d_j \) the dominance effect
- \( d_j/\mu_d, \sigma_d^2 \sim 0 \) with probability \( \pi_d \)
- \( N(\mu_d, \sigma_d^2) \) with probability \( 1 - \pi_d \)
- \( \mu_d/\sigma_d^2 \sim N(\eta, \sigma_d^2/\phi) \), where \( \eta = \sum_{i=1}^{k} (X_{ij} - \bar{X}_j) \) and \( \phi \) measures the strength of the prior belief in terms of \( \sigma_d^2 \)

Design of Study

<table>
<thead>
<tr>
<th>Scenario</th>
<th>Gene Action</th>
<th>( h_{BS}^2 )</th>
<th>( h_{NS}^2 )</th>
<th>Heterosis</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Overdominance</td>
<td>0.5</td>
<td>0.33</td>
<td>31%</td>
</tr>
<tr>
<td>2</td>
<td>Overdominance</td>
<td>0.5</td>
<td>0.4</td>
<td>9.1%</td>
</tr>
<tr>
<td>3</td>
<td>Incomplete Dominance</td>
<td>0.5</td>
<td>0.35</td>
<td>8.4%</td>
</tr>
<tr>
<td>4</td>
<td>Additive</td>
<td>0.5</td>
<td>0.5</td>
<td>0</td>
</tr>
</tbody>
</table>

- Other parameters, such as LD, allele frequencies, QTL positions, etc., were kept constant across scenarios
- Training was carried out only once
Cumulative response to genomic selection one chromosome, 100 QTL and 1000 SNPs

(a) large V_D with overdominance
(b) Realistic V_D with overdominance
(c) realistic V_D without overdominance
(d) No dominance

Changes in heterozygosity for over-dominant QTL in crossbreds over generations.
Plotted values are changes in heterozygosity for over-dominant QTL in crossbreds over generations of selection, under the dominance model, BSAM and the additive model, with one chromosome and large dominance

Conclusions
Genomic Selection provides great opportunities for genetic improvement of commercial crossbred performance

• Can substantially increase rates of response for commercial crossbred performance
• Reduces rate of inbreeding - Compared to CCPS
• Requires statistical methods for estimation of marker-effects in crossbred populations
  • Breed-specific allele models
  • Dominance models