Genomic Selection of Purebred Animals for Crossbred Performance in the Presence of Dominant Gene Action

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Jian Zeng, Research Assistant; Ali Toosi, Research Assistant; Rohan Fernando, Professor; Jack Dekkers, Professor; Dorian Garrick, Professor, Department of Animal Science and Center for Integrated Animal Genomics, ISU

Summary and Implications

The primary objective of this study was to assess the performance of different genomic prediction models applied to the selection of purebreds for crossbred performance based on high-density marker data. Our results suggest that in the presence of dominant gene action, selection based on the dominance model is superior to both the a breed-specific allele model and an additive model in terms of maximizing crossbred performance through purebred selection, especially when training is not updated each generation.

Introduction

Recent studies have shown that genomic selection (GS) based on high-density marker genotypes is an appealing method to select purebreds. However, except for dairy cattle, most animals used in livestock production systems are crossbreds, with advantages of heterosis and breed complementarity. For such systems, the breeding goal in purebreds should be to optimize the performance of crossbred descendents.

In the analysis of crossbred records, marker effects could be estimated using an additive model, or a breed-specific allele model (BSAM). In most studies, either additive gene action, perfect knowledge of marker effects, or both have been assumed. It has been argued that dominance is the likely genetic basis of heterosis, therefore explicitly including dominance in the GS model might be beneficial for selection of purebreds for crossbred performance.

Materials and Methods

In this study, a two-way crossbreeding program was simulated for a trait with dominance. The simulated genome consisted of one chromosome of 100 cM with 100 QTL and 1,000 SNPs. With overdominance, the dominance variance and heterosis were first chosen to be large enough to allow clear detection of any advantage of including dominance in the model used for genomic prediction (scenario 1). Parameters were then restricted to a more realistic setting to verify if the advantages would still hold either with (scenario 2) or without overdominance (scenario 3). Finally, the robustness of using the dominance model for genomic prediction was examined under additivity (scenario 4). In each scenario, the performance of the different models was evaluated based on response to 20 generations of GS on purebred candidates for crossbred performance. Training was carried out only once.

Results and Discussion

In scenario 1, where the dominance variance and heterosis were large and overdominance was present, the dominance model gave greater response to selection, accumulating to an advantage of 14.9% over BSAM and of 22.4% over the additive model by generation 20. In scenario 2, where the setting was more realistic but with overdominance, the advantage of the dominance model was reduced to 8.9% over BSAM and 8.6% over the additive model but these advantages were still significant. Extra response was the result of an increase in heterosis but at a cost of reduced purebred performance. In scenario 3, where overdominance was absent, the dominance model was not significantly better than the additive model. In scenario 4, where there was no dominance, response to selection for the dominance model was as high as that for the additive model, indicating the robustness of the dominance model. Model BSAM was inferior to the dominance model in all scenarios and outperformed the additive model only when the dominance variance and heterosis were large and in the presence of overdominance.

Acknowledgments

Table 1. Cumulative response[1] to genomic selection at generation 20 by the BSAM and dominance models compared to the additive model.

Scenario	Dominance Model	BSAM
1 (Large overdominance)	22.4%*	6.5%*
2 (Realistic overdominance)	8.6%*	0.3%
3 (Dominance)	0.2%	-1.7%
4 (Additive)	-0.1%	-5.9%*

[1]Measured as the mean advantage of the additive model based on 1,600 replicates of the simulation
*Significant difference at the 0.01 level