Application of Genomic Selection Using an Evenly Spaced Low-density Marker Panel in Broiler Chickens

A.S. Leaflet R2807

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Summary and Implications

In this study, a commercial broiler chicken line was used to verify the feasibility and accuracy of genomic selection using an evenly spaced low-density marker panel. Body weight and hen house production (the cumulative egg production over the laying period, up to 22 weeks or until culled) were used as example traits. The training population included 2,302 birds, of which 1,259 were genotyped using a high-density marker panel with 36,455 markers across the genome, and the other 1,043 birds were genotyped with a low-density marker panel with 384 markers. The validation population included 3,720 birds genotyped with the low-density marker panel. A rule-based method combined with a Gibbs sampler was used to impute missing genotypes for the birds genotyped at low-density. Several methods were employed to predict genomic estimated breeding values for validation birds. Results showed that accuracy of genomic prediction was 7-8% higher compared to estimated breeding values from pedigree for body weight, and 4% higher for hen house production. We conclude that genomic selection can be implemented with low-density marker panels combined with imputation.

Introduction

The use of evenly spaced low-density (ELD) marker panels with imputation to implement genomic selection (GS) can result in large reductions in genotyping costs. The effectiveness of this strategy has been studied using simulation but must be verified in practice. Moreover, whether ELD-genotyped individuals can be used in training data must also be evaluated.

Materials and Methods

A high-density (HD) marker panel including 36,455 SNP markers across the genome was used to genotype 1,259 birds in a commercial broiler chicken line by Aviagen Ltd. A total of 20,630 SNPs were kept for analyses after edits for marker quality. Based on the HD genotypes, an ELD-marker panel was created with 384 SNPs and used to genotype an additional 1,043 birds and 3,760 progeny. A rule-based method was used to infer haplotypes of HD-genotyped individuals. A Gibbs sampler was employed to estimate allele segregation probabilities of ELD-SNPs for the ELD-genotyped birds. Then the missing HD genotypes in ELD-genotyped birds were imputed. The 1,259 HD-genotyped and 1,043 ELD-genotyped birds were used as training data and the 3,760 ELD-genotyped birds as validation data. Methods Bayes-A, -Cπ, -B (using the estimated π from Bayes-Cπ) and GBLUP were used to estimate marker effects using Gensel 4.23R software that was developed at Iowa State University. The estimates of marker effects were used to compute genomic estimated breeding values (GEBV) of the validation individuals. The accuracy of GEBV prediction was calculated based on the correlation of GEBVs with adjusted phenotypes of the validation individuals.

Results and Discussion

For body weight, the accuracy from GEBV by GS prediction methods was 0.07-0.08 higher than the accuracy of EBV from pedigree BLUP (PBLUP); for hen house production, the accuracy of GEBV was 0.04 higher than the accuracy of PBLUP (Table 1). For body weight, the correlation of GEBVs among GS prediction methods was greater than 0.96; the correlation of EBV from PBLUP with GEBV was about 0.62 for all GS prediction methods. For hen house production, the correlation of GEBVs among GS prediction methods was greater than 0.98; the correlation of EBV from PBLUP with GEBV was about 0.73 for all GS prediction methods.

Acknowledgments

We gratefully acknowledge the funding support from Aviagen Ltd. and SABRE Demonstration Funds of EU Framework 7.

Table 1. Accuracy of estimated breeding values in the validation population.

	Method				
Trait	Bayes-A	Bayes-Cπ[1]	Bayes-B	GBLUP	PBLUP
Body weight	0.33	0.33	0.32	0.32	0.25
Hen house production	0.21	0.21	0.21	0.21	0.17

[1]π was estimated to be 0.92 for body weight and 0.96 for hen house production