Breeding Value Prediction For Production Traits In Layers Using Pedigree And Marker Based Methods

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Introduction

The 21st century is the age of rapid development of genomic selection tools. Through the application of genomic selection (Meuwissen et al. 2001), marker information from high-density SNP genotyping might improve accuracy of selection at young ages, shorten generation interval and provide better control of inbreeding, which should lead to higher genetic gain per time unit. Multiple simulation studies have been conducted showing the benefits of the technology depend on heritability, number and effects of QTL, population structure, size of training data set, and other factors (Goddard, 2009). There are however few studies on real data. If genomic selection is to be implemented in practical breeding in chickens, as has already occurred in dairy cattle (Hayes et al., 2009), it must prove its advantage over traditional methods and be used in a way which optimally uses available information. The value of EBV derived from large numbers of markers for within-breed selection is difficult to evaluate analytically and must be validated by correlating predictions to performance in future generations. The objective of this study was to evaluate the accuracy of breeding values estimated using high-density SNP genotypes in predicting the next generation in a commercial layer breeding line, and to compare the accuracy of different methods of breeding value estimation.

Material and methods

Data on eight traits collected during the first 22 weeks of production were collected on 13,049 birds from five consecutive generations of a single layer line: egg production (PD); shell quality (PS); weight of first 3 eggs (E3); color of first 3 eggs (C3); egg weight (EW); albumen height (AH); egg color (CO); and yolk weight (YW). In total 2,708 animals were genotyped for 25,597 segregating SNPs (minor allele frequency > 0.025) using a custom high-density Illumina SNP panel. Of these, 1,563 were females with individual phenotypes and 1,145 were males without phenotypes. The genotyped set included parents of generations 2 to 5 and progeny from generation 6. Breeding values were estimated for two stages of selection. To represent selection at a young age when phenotypes on female sibs

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are not yet available, training was on all phenotypic data, excluding generation 6, and used to predict breeding values for 290 genotyped individuals from generation 6. To represent selection of males at a later age when phenotypes on female sibs are available, phenotypes of 2393 hens (of which 146 were genotyped) from generation 6 were also included in training and the remaining 144 hens were used for validation.

Three single trait models were used to predict breeding values of individuals in generation 6:

1) PBLUP - Reduced animal model using pedigree relationships between genotyped birds.
2) GBLUP - Reduced animal model using marker-based relationships derived by the method of VanRaden (2008) between genotyped birds.
3) Bayes-C-π - A genomic selection analysis method similar to Bayes-B of Meuwissen et al. (2001), except with estimation of the proportion of SNPs with zero effects (π) and assuming a common variance for non-zero SNP effects (Habier et al., 2010). In this analysis, the average genotype (# of 'B' vs. 'A' alleles) of the genotyped parents was to fit SNP genotype effects to the mean performance of their ungenotyped progeny, with weights to account for different residual variances.

All models included the fixed effect of hatch within generation. Analyses were performed using ASREML (Gilmour et al., 2006) and GenSel (Fernando and Garrick, 2009). The correlation between predicted breeding values with hatch-corrected phenotype in the validation data sets and regression of phenotype on predicted breeding values were used as measurements of accuracy and bias, respectively. To evaluate the extent to which improvements in accuracy with use of markers come from more accurate estimates of Mendelian sampling terms versus more accurate EBV of the parents, marker based parental averages (PA) were also calculated for animals in the validation sets.

Results and discussion

Estimates of heritability obtained from a Reduced Animal Model with pedigree-based relationships on the whole data set are in Table 1. Estimates ranged from 0.28 for PS to 0.77 for EW, which classifies the analyzed traits in the moderate to high heritable category.

Table 1: Estimates of heritability[1]

PD	EW	PS	AH	CO	E3	C3	YW
0.39	0.74	0.29	0.55	0.72	0.64	0.66	0.47

[1] Standard errors were 0.02

Marker based breeding values had higher predictive ability than estimates exploiting the pedigree information (Table 2). The difference was less at later selection, when data on sibs of selection candidates were available, which increased accuracy from all methods but in particular from PBLUP. Use of markers increased accuracies up to two-fold for early selection, and by up to 37% for late selection. Accuracies from GBLUP were on average slightly larger than accuracies from Bayes-C-π.

Table 2: Validation of predicted breeding values and parental average (PA) breeding values from three methods (PBLUP, GBLUP, and Bayes-C-π)

Method	PD	EW	PS	AH	CO	E3	C3	YW
EARLY SELECTION								
Accuracy of EBV[1]								
PBLUP	0.18	0.45	0.22	0.34	0.45	0.38	0.45	0.29
GBLUP-PA	0.32	0.47	0.35	0.41	0.44	0.40	0.48	0.31
GBLUP	0.35	0.64	0.34	0.57	0.60	0.58	0.56	0.40
Bayes-C-π -PA	0.33	0.37	0.32	0.38	0.42	0.33	0.48	0.31
Bayes-C-π	0.36	0.57	0.38	0.55	0.58	0.58	0.55	0.39
Slope from regression of phenotype on EBV								
PBLUP	0.63	1.12	0.71	0.87	0.93	0.88	0.85	0.67
GBLUP	0.53	0.87	0.58	0.93	0.70	0.81	0.67	0.58
Bayes-C-π	0.68	0.83	0.80	1.01	0.75	0.85	0.74	0.66
LATE SELECTION								
Accuracy of EBV[1]								
PBLUP	0.42	0.60	0.44	0.57	0.54	0.68	0.67	0.52
GBLUP-PA	0.45	0.59	0.49	0.65	0.54	0.65	0.67	0.51
GBLUP	0.52	0.68	0.54	0.71	0.74	0.78	0.66	0.55
Bayes-C-π-PA	0.42	0.57	0.50	0.62	0.53	0.60	0.68	0.45
Bayes-C-π	0.53	0.69	0.51	0.73	0.71	0.74	0.66	0.49
Slope from regression of phenotype on EBV								
PBLUP	0.82	1.00	0.93	1.30	0.93	1.05	1.05	0.86
GBLUP	0.73	0.84	0.81	1.15	0.96	0.92	0.79	0.70
Bayes-C-π	0.92	0.91	0.89	1.32	0.95	0.93	0.82	0.76

[1] accuracy is measured as the correlation between predicted breeding values and hatch-corrected phenotype in the validation set divided by square root of heritability from Table 1.

At early selection, correlations between predicted breeding values obtained by PBLUP and GBLUP ranged from 0.58 to 0.64; correlations between PBLUP and Bayes-C-π from 0.43 to 0.57; and correlations between GBLUP and Bayes-C-π from 0.81 to 0.93. This indicates that reranking of top individuals is very likely between pedigree and marker based methods, but less so between GBLUP and Bayes-C-π. A similar tendency was observed for rankings at late selection but the correlations between the methods were higher.

In table 2, the difference between the accuracy of marker-based and pedigree-based parental average EBV (e.g. GBLUP-PA vs. PBLUP) reflects the gain of information from more accurate estimation of EBV of parents, while the difference between the accuracy of marker-based parental average EBV and marker-based individual EBV (e.g. GBLUP-PA vs.

GBLUP) arises from markers providing information on Mendelian sampling terms. The improvement of accuracy at an early age could be attributed mostly to better estimates of parental EBV for PS and PD, but mostly to providing information on Mendelian sampling terms for other traits. For late selection, the majority of improvement originated from Mendelian sampling terms, probably because the pedigree parental averages were much more accurate than at early selection.

The slope of regression coefficients of phenotype on breeding value tended to be closer to unity for PBLUP, indicating smaller biases of EBV. Sib information improved the performance of all methods in this aspect.

Conclusions

The marker-based methods exhibited better ability to predict future performance compared to the classical pedigree based approach, with most of the accuracy improvement attributed to estimation of Mendelian sampling terms. The advantage of marker-based methods was greater for selection at a young age, before information on sibs of selection candidates is available.

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