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Genomic Evaluation for Egg Weight in Crossbred Layers Receiving Various Diets

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ABSTRACT: This paper presents the preliminary results obtained during the implementation of a genomic evaluation for egg weight in laying hens. One originality of the project is to have used a population of crossbred hens to estimate GEBV of purebred sires. Moreover, hens were divided in 2 groups fed with 2 diets of Low Energy and High Energy. The genomic evaluation from performance of crossbred daughters is more accurate than traditional genetic evaluation in purebred. The interaction genotype x diet seems to be low.

Keywords: laying hens; genomic selection; egg weight

Introduction

One of the main limitations of layers breeding programs is that selection is carried out in purebred lines housed in high health environments while the ultimate goal of selection is to improve crossbred performances under commercial conditions. Due to genetic differences between purebred and crossbred animals, and environmental differences between nucleus and field conditions, performance of purebred can be a poor predictor of performance of their crossbred progeny, particularly for traits subject to non additive effects.

Recently, the development of a high density chip for chicken by Affymetrix, i.e. the 600K Affymetrix® Axiom® HD genotyping array (Kranis et al. (2013)), allows envisaging the use of high density genotype data for genomic selection in laying hens. Furthermore, the disconnection between phenotyping and genotyping in the genomic evaluation process gives hope taking better account of crossbreeding and genotype by environment interaction (Dekkers (2007)). Thus, find routes to select more robust animals, that is to say, adapting better to the changing conditions of a less controlled environment, is also an issue for genomic selection in layers.

In the present study, an experimental approach was implemented to compare pedigree breeding values (EBV) estimated from pure line information and genomic breeding values (GEBV) estimated from performances of crossbred animals fed with various diets. The aim is to know which ones are best suited for selection of purebred sires to produce crossbred layers housed in various environments.

Material and Methods

Males genotyped. A population of males of the pure line A, created and selected by the NOVOGEN breeding company (Quintin, France), was genotyped using the 600K Affymetrix® Axiom® HD genotyping array. Blood samples were collected from brachial veins of individuals and DNA was extracted. DNA was hybridized on the 600K Affymetrix® Axiom® HD genotyping

array (Kranis et al. (2013)) by Ark-Genomics (Edinburg, UK). In total 1004 males were genotyped for 580,961 markers. These markers covered chromosomes from 1 to 28, two linkage groups (LGE22C19W28_E50C23 and LGE64), two sex chromosomes and a group of markers with unknown locations. Genotypes were filtered according to 5 successive steps: SNP with a call rate less than 5% were discarded; animals with a call rate less than 95% were excluded; SNP with a MAF less than 0.05 were excluded; SNP with a call rate less than 95% were discarded; SNP significantly ($P < 5\%$) deviated from Hardy-Weinberg Equilibrium were excluded. Thus, 284,643 SNP were kept for the study and no individual was excluded.

The males were hatched in 6 successive batches separated by 6 months from 2010-1 to 2012-2. Only the performances of progenies of the sires of the 3 first hatches, i.e. 2010-1 to 2011.1, were used in the genetic or genomic evaluations. The sires of the 3 last hatches, i.e. 2011-2 to 2012-2, were candidates to selection with no progeny information.

Females phenotyped. Results presented here concerned only the egg weight. This trait was measured at 65 weeks of age in the pure line A for which the hens were housed in individual cages and fed ad libitum with a diet with 2,700kcal.

The males were also evaluated on the basis of the performances of 31,381 of F1 crossbred daughters AxD issued from the sires of the 3 first hatches. These “experimental” hens were hatched in 3 batches in November 2010, May 2011 and November 2011. At 18 weeks of age, they were housed in a production farm in collective cages of 12 half-sibs of sire. The egg weight was measured at 70 weeks of age. Half of hens were fed ad libitum with a “high energy diet (HE)” with 2,881kcal of metabolizable energy (ME) (1,342 cages) and the others with a “low energy diet (LE)” with 2,455kcal of ME (1,346 cages).

Purebred evaluation. Using purebred hens performances, hereafter referred as EW, genetic evaluation was realized through a BLUP animal model methodology (Henderson (1975)) on the basis of all information available since the line creation in 2008. Two EBVs were calculated for each of the candidates, one “at birth”, without his sisters performances (EBV_1), and one “at 70 weeks”, taking into account his sisters performances (EBV_2). In both cases, egg weight was assumed to follow a classical animal model:

$$y = 1\mu + X\beta + Zu + e$$

$$\text{with Var} \begin{pmatrix} \mathbf{u} \\ \mathbf{e} \end{pmatrix} = \begin{pmatrix} \mathbf{A}\sigma_u^2 & \mathbf{0} \\ \mathbf{0} & \mathbf{I}\sigma_e^2 \end{pmatrix}$$

where \mathbf{y} is a vector containing performance records, μ is the general mean of the model, β , \mathbf{u} and \mathbf{e} are vectors, of batch fixed effects, of random polygenic effects and of random residuals respectively. \mathbf{A} is the pedigree kinship matrix; \mathbf{I} is the identity matrix; \mathbf{X} and \mathbf{Z} are incidence matrices for fixed and random polygenic effects. σ_u^2 is the genetic variance, σ_e^2 is the residual variance. The pedigree was known from 2008, whence the total number of animals in the pedigree file was 16,126 among which 3,127 and 4,544 hen phenotypes were used to derive EBV_1 and EBV_2 respectively. VCE6 (Groeneveld et al. (2010)) was used to estimate genetic parameters and derive EBVs.

Crossbred evaluation. Using crossbred performances, bivariate genetic and genomic evaluations were carried out on the egg weights of hens fed with Low Energy (EW_{LE}) or High Energy (EW_{HE}) diet. Animal BLUP model was used according to the single-step methodology proposed by Aguilar et al. (2010). Two EBVs, i.e. EBV_{HE} and EBV_{LE} , and 2 GEBVs, i.e. GEBV_{HE} and GEBV_{LE} , were derived for each candidate. Egg weights were considered as a repeated measure of the sire:

$$\mathbf{y} = \begin{pmatrix} \mathbf{y}_{\text{LE}} \\ \mathbf{y}_{\text{HE}} \end{pmatrix} = \mathbf{1}\mu + \mathbf{X}\mathbf{c} + \mathbf{Z}\mathbf{s} + \mathbf{e}$$

with $\text{Var} \begin{pmatrix} \mathbf{c} \\ \mathbf{s} \\ \mathbf{e} \end{pmatrix} = \begin{pmatrix} \mathbf{I}\mathbf{C} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{H}\mathbf{S} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{I}\mathbf{E} \end{pmatrix}$ were \mathbf{C} , \mathbf{S} and \mathbf{E} are the the 2x2 (co)variance matrix of cage effects, sire effects and residuals.

\mathbf{H} is either the pedigree kinship matrix in the pedigree model (used to derive EBV_{HE} and EBV_{LE}) or the combined pedigree-genomic kinship matrix in the genomic evaluation (used to derive GEBV_{HE} and GEBV_{LE}); \mathbf{X} and \mathbf{Z} are incidence matrices for cage, environment and sire effects. To compute heritabilities, variance ratios should be multiplied by 4, as performances were actually measured on the candidate daughters.

The pedigree file contained the candidates from batches 2011-2, 2012-1 and 2012-2 and all their known ancestors back to the founding of the line. The pedigree concerned 2,151 animals among which 438 sires with performances.

The above model was fitted using BLUPF90 family of programs (Misztal et al. (2002)). The variance components were estimated with the gibbs2f90 program. Final sets of 4,000 independent observations were obtained from chains of 125,000 iterations launched with a thin rate of 25, after discarding the 25,000 first iterations as a burn-in period. 90% confidence intervals of genetic parameters were calculated from a posteriori distributions. As a byproduct the Gibbs Sampling estimation provides an estimation of the sampling error of the EBVs, ie. $\text{Var}(\mathbf{u} - \hat{\mathbf{u}})$. After some derivation it is easy to obtain the CD of EBVs.

Population of validation. After the evaluation, 60 males among the candidates produced crossbred progeny. Each of them had 80 daughters of the preceding AxD cross and 80 daughters of another genetic type (AxB). All these hens were housed in one farm. For each cross, half of hens were fed with the HE diet and half with the LE diet. Presently, egg weights of these females were available at 21, 25 and 30 weeks of age.

The correlations between EBVs and GEBVs of the 60 sires and the average performance of their progeny were calculated. Because of the deviation between heritabilities, these correlations were divided by the square root 0.4 for EBVs and of 0.6 for GEBVs to be compared.

Results and Discussion

Genetic parameters. Heritability of egg weight at 65 weeks of age was estimated to 0.38 ($\text{se}=0.007$) at birth and 0.40 ($\text{se}=0.017$) at 70 weeks using purebred data. Table 1 shows estimates of genetic parameters obtained on crossbred data, bracketed by the 90% confidence interval limits. The 4 estimates of heritability are between 0.60 and 0.64 which is consistent with the data from the literature. The genetic correlation between EW_{HE} and EW_{LE} is close to 0.9 with the pedigree model and close to 1 with the genomic model. Thus, it does not seem to be a large interaction between genotype and diet for egg weight at 70 weeks in crossbred hens.

Table 1. Estimates of genetic parameters^a on crossbred data.

	EW_{HE}	EW_{LE}
	Pedigree model	
EW_{HE}	0.52<0.60<0.68	0.86<0.89<0.93
EW_{LE}		0.56<0.64<0.72
	Genomic model	
EW_{HE}	0.56<0.64<0.72	0.95<0.99<1.00
EW_{LE}		0.52<0.60<0.68

^aHeritabilities on the diagonals and genetic correlations above the diagonals.

EW_{HE} : egg weight at 70 weeks of "HE" crossbred hens.

EW_{LE} : egg weight at 70 weeks of "LE" crossbred hens.

Correlation between EBVs and GEBVs. Table 2 shows correlations between EBVs and GEBVs of the 565 candidates. In purebred, the correlation between EBVs at birth and at 70 weeks of age is close to 0.8 which is large but also shows the potential gain of accuracy provided by the inclusion of males' sisters performances. The correlation between the GEBVs obtained with "HE" or "LE" crossbred hens is close to 1. That result is consistent with the genetic correlation seen previously. Finally, the correlation between EBVs and GEBVs increases from 0.26 to 0.33 between EBV "at birth" and "at 70 weeks".

Table 2. Rank correlations between EBVs and GEBVs of candidates.

	EBV_1	EBV_2	GEBV_{HE}
EBV_2	0.795		
GEBV_{HE}	0.250	0.323	
GEBV_{LE}	0.263	0.337	0.996

EBV_1 : pedigree BV estimate in purebred without sisters data

EBV_2 : pedigree BV estimate in purebred with sisters data

GEBV_{HE} : genomic BV estimate in "HE" crossbred

GEBV_{LE} : genomic BV estimate in "LE" crossbred

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Evaluation validation. Table 3 gives the correlations between the EBVs or GEBVs and the average performances of progeny of the 60 sires constituting the population of validation. The accuracy of prediction is clearly greater with GEBVs than with EBVs, especially for performances in the young age. The correlations increase with the age of progeny which is consistent. There are few differences in function of the diet. Strangely, the predictions are systematically more accurate for the genetic type AxB.

Table 3. Correlations[&] between EBVs or GEBVs of candidates and average performance of their crossbred progeny (n=60 sires).

	Hens AxD		Hens AxB	
	EW _{HE}	EW _{LE}	EW _{HE}	EW _{LE}
	At 21 weeks			
EBV ₁	0.00	-0.08	0.08	0.14
EBV ₂	0.06	-0.02	0.35	0.33
GEBV _{HE}	0.17	0.22	0.36	0.52
GEBV _{LE}	0.18	0.23	0.37	0.50
	At 25 weeks			
EBV ₁	0.11	0.09	0.25	0.22
EBV ₂	0.27	0.20	0.36	0.41
GEBV _{HE}	0.39	0.28	0.54	0.62
GEBV _{LE}	0.37	0.28	0.54	0.61
	At 30 weeks			
EBV ₁	0.28	0.19	0.43	0.25
EBV ₂	0.46	0.39	0.51	0.47
GEBV _{HE}	0.40	0.49	0.61	0.61
GEBV _{LE}	0.40	0.48	0.59	0.58

[&]Correlations were divided by the square root of the heritability.

The figure 1 gives an example of regression between GEBVs and average performances. The bias seems to be little and the slope is close to 1.

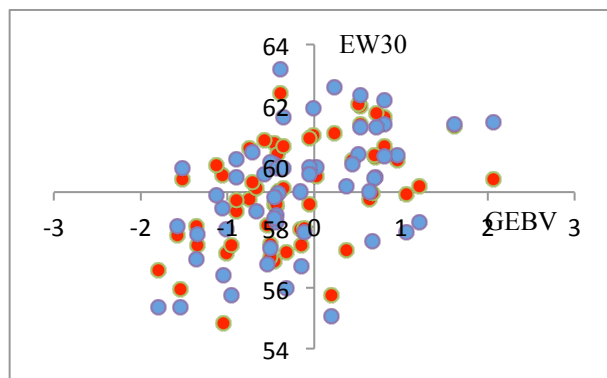


Figure 1. Regression of EW[&] on GEBV (n=60 sires).

[&]In red EW_{HE} diet and in blue EW_{LE} at 30 weeks of age of AxB hens

Conclusion

The results of this project are still preliminary but they reveal a potential large gain of accuracy for prediction of egg weight using genomic evaluation on the basis of crossbred performances. Otherwise, the interaction between genotype and diet seems to be not large for egg weight at 70 weeks in crossbred hens.