Use of data from crossbred animals for genomic evaluation

In poultry selection programmes, pyramidal schemes are traditionally used to produce crossbred animals issued from several pure lines. Each pure line is selected independently of the others and its genetic evaluation is carried out using purebred performances. One major drawback is that the performances of purebred individuals (PB) may prove to be an imperfect predictor of the performances of crossbred individuals (CB).

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Indeed, because of the presence of non-additive genetic effects, for example dominance and epistasis, and genotype by environment interactions, the genetic correlation between PB and CB for a given trait can be significantly different from 1.

To overcome this limitation, Wei (1992) proposed the joint use of both PB and CB information. Recent studies confirmed the interest of this strategy in optimising genomic selection in crossbreeding schemes. However, in practice, this approach has its limitations since only purebred selection candidates are genotyped.

To overcome this problem, Christensen et al. (2014) extended the Wei and van der Werf (1994) model in order to implement the single step method which allows for a joint evaluation of animals, whether genotyped or not.

Furthermore, a strategy commonly applied by layers breeding companies consists of checking the overall ability for combination of purebred males, by using the performances of different crossbred progeny.

In this case, genotyping is available only for these purebred males, that represent only one of the various purebred lines used in the crossbreeding scheme. The performances are recorded on their crossbred daughters, which are half-sisters with unknown dam pedigree.

In Picard Druet et al. (2019), the relevance of genomic evaluation of egg quality traits using the ssGBLUP was analysed in a purebred line, i.e. using purebred performances. The present study focuses on the use of performances from crossbred individuals issued from the same purebred line.

Material and methods

● **Animals and genotypes:**
PB individuals come from a pure line of Rhode Island layers selected by Novogen. Hens were hatched in 12 batches, born between 2008 and 2015, which corresponds to four generations (PB1 to PB4).

Egg quality traits were measured once a week, from 60 weeks of age to 80 weeks of age (7,982 hens issued from 514 sires and 1,759 dams). Purebred birds were genotyped using the 600K Affymetrix Axiom HD genotyping array for 580,961 SNP markers.

After quality control was completed, 302,102 SNPs genotypes of 1,214 males and 1,148 females were kept for the study. In addition, the performances of CB individuals, which were crossbred offspring issued from PB1 to PB3 males (37,232 hens issued from 1,384 sires), were available.

Each purebred male had 45 crossbred daughters in expectation, with unknown dams of different genetic type. Crossbred hens were hatched in collective cages of 12 half-sisters from the same sire. Egg quality traits were measured once they reached 70 weeks of age.

Trait	Heritability PB	Heritability CB	Genetic correlation
EW	0.43	0.76	0.82
ESC	0.37	0.48	0.78
ESS	0.21	0.28	0.73

Table 1. Genetic parameters.

● **Traits:**
Three egg quality traits were studied: egg weight (EW), eggshell colour (ESC), and eggshell strength (ESS). The first step consisted of measuring EW (in g). Then, eggshell colour was measured with a Minolta chromometer and three measurements were recorded: redness of eggshell a*, yellowness of eggshell b* and lightness of eggshell L*. Eggshell colour was then calculated as: ESC = 100 - (L* - a* - b*).

Finally, shell strength was measured using a compression machine, to evaluate the static stiffness of the shell.

The egg was compressed between two flat plates moving at constant speed. ESS is the maximum force recorded before eggshell fracture (in N, multiplied by 100).

● **Genetic and genomic evaluations:**
Performances were centred and standardised prior to evaluations. Each trait was first evaluated using PB performances only, applying an uni-trait animal model. Then, three bi-variate animal models (EW(PB) and EW(CB), ESC(PB) and ESC(CB), ESS(PB) and ESS(CB)) were applied.

For all the traits, the statistical model took into account environmental effects: batch, cage position in the poultry house, waiting time between sample and egg measurement covariable (in days), and age of the hen (in weeks) covariable.

For PB performances, several measurements were available for each hen, and a random common environmental effect of the hen was taken into account in the model.

The evaluations were performed using the BLUP methodology (to obtain Estimated Breeding Values (EBV)) and the single-step GBLUP methodology (to obtain Genomic Estimated Breeding Values (GEBV)), implemented in the BLUPF90 family of programs.

Variance-covariance matrices were estimated using REMLF90. Standard errors of genetic parameters estimates were then obtained with AIREMLF90.

● **Reliability of prediction:**
To assess the relevance of the evaluations, the estimated breeding

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Table 2. Relative accuracy of (G)EBVs.

Trait	Evaluation	At birth		At 80 weeks	
		EBV	GEBV	EBV	GEBV
EW(PB)	Unitrait PB	0.35	0.54	0.49	0.63
	Bitrait PB&CB	0.41	0.54	0.65	0.78
EW(CB)	Bitrait PB&CB	0.29	0.42	0.59	0.72
ESC(PB)	Unitrait PB	0.30	0.42	0.35	0.54
	Bitrait PB&CB	0.43	0.57	0.58	0.76
ESC(CB)	Bitrait PB&CB	0.37	0.51	0.56	0.76
ESS(PB)	Unitrait PB	0.49	0.52	0.57	0.71
	Bitrait PB&CB	0.46	0.53	0.70	0.82
ESS(CB)	Bitrait PB&CB	0.23	0.44	0.49	0.70

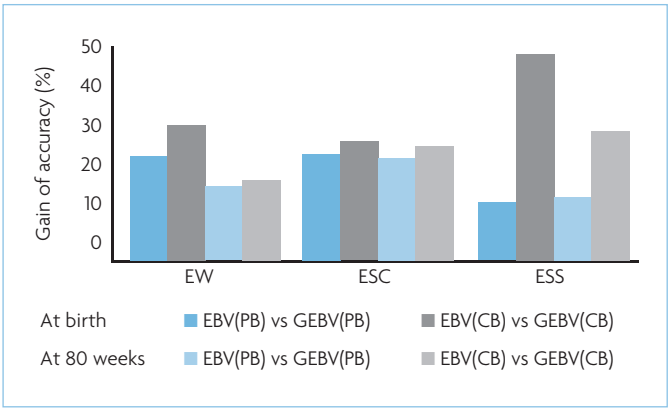

Fig. 1. Accuracy gain between EBVs and GEBVs resulting from bi-trait evaluations.

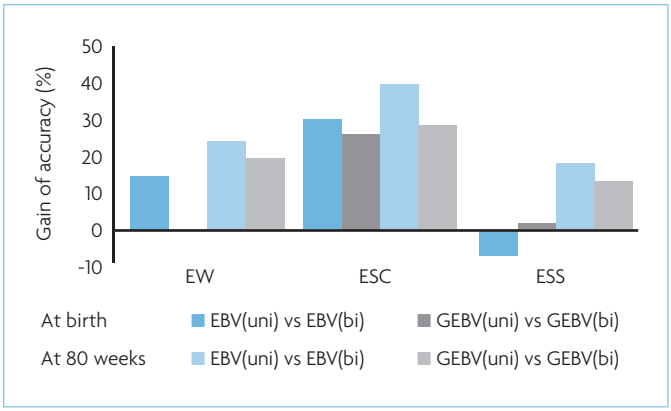

Fig. 2 Accuracy gain between uni-trait PB evaluation and bi-trait PB & CB evaluation.

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values, i.e. EBVs and GEBVs of selection candidates, were compared to their true breeding values (TBVs).

For the purpose of this study, a male candidate population comprised of 93 PB3 males, with PB4 daughters and CB3 daughters, was used.

However, their TBVs were unknown and the LR method (Legarra and Reverter, 2018) was therefore used.

This method is based on a comparison between evaluations realised with complete and partial data sets, as the deviation between GEBVs resulting from consecutive evaluations is a function of GEBVs respective accuracy.

Two different cases of partial data sets were studied, based on the amount of phenotypic information available when the evaluation was carried out: at the birth of candidates and at 80 weeks of age.

In the first case, the phenotyped population was limited to the ancestors of the candidates. In the second case, the phenotyped population included the ancestors as well as the contemporary relatives of the candidates.

This case corresponds to the classical scheme in layers selection. The available phenotypes made up the complete data set, which included the performances of candidates' daughters (PB and CB).

The correlation between (G)EBVs resulting from complete and partial evaluations was an estimate of their relative accuracy.

In order to compare evaluations, in a given case, the ratio between their relative accuracy was used. The statistics allow us to quantify the expected increase in accuracy from one evaluation to the other.

Results and discussion

● Genetic parameters:

Genetic parameters were very steady between REMLs carried out with BLUP and REMLs carried out with GBLUP, regardless of the trait studied. The same variance-covariance matrix, i.e. the one obtained with genomic evaluation using the complete data set, was then used to perform subsequent BLUP and GBLUP evaluations.

Estimates of heritability in PB were in accordance with the literature (Table 1). As expected, they were higher in CB, which is probably due to the presence of non-additive effects, in particular as what regards EW.

Moreover, for all traits, a strong link was observed between PB and CB traits, with genetic correlations estimated between 0.73 and 0.82 (Table 1).

However, these values were significantly different from 1. This shows the potential interest of bi-variate models in obtaining accurate estimates of (G)EBVs, for both PB traits and CB traits.

● (G)EBVs relative accuracy

For all traits and all evaluations, relative accuracy of (G)EBVs dramatically increased between the evaluation carried out at birth and the one carried out at 80 weeks of age (Table 2).

When using bi-trait models, the accuracy gain between genetic evaluation and genomic evaluation was always significant, although it varied depending on the trait and the period of evaluation (Fig. 1).

The deviation between PB traits and CB traits was moderate for what regards EW and ESC.

It was greater for ESS, ranging from 13% (ESS in PB at birth) to 48% (ESS in CB at birth). As a consequence, genomic evaluation of ESS(CB) sounds very promising. The role played by CB performances in the accuracy of (G)EBVs for PB traits is presented in Fig. 2. The gain for EBVs and for GEBVs was quite similar, with slightly higher values for EBVs.

CB performances proved useful in the case of ESC, with a gain ranging from 26% to 40%.

Accuracy gain was lower in the case of EW (from 15% to 20%), and null in the case of GEBVs carried out at birth. In the case of ESS, the gain only shows at 80 weeks of age for both EBVs and GEBVs.

Conclusion

Whichever egg quality trait, the genetic correlation observed between PB performances and CB performances shows that these traits should be considered and evaluated as two different traits.

In every case, genomic evaluation proved more accurate than genetic evaluation. Great heterogeneity in accuracy gain was observed from one trait to the other.

This heterogeneity could be due to the differences in the genetic architecture of the traits.

Notably, the potential accuracy gain resulting from the inclusion of CB performances in the evaluation of PB traits, varied depending on the trait and on the period of evaluation. ■

References are available from the authors on request