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## **Accuracy of genomic evaluation in pure line layers**

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### **Summary**

Avian breeders are actually putting in place genomic selection in their selection schemes. One key parameter to optimize selection schemes is to correctly predict the accuracy of genomic evaluation. This paper presents results obtained by comparing accuracy of genetic and genomic evaluations on multiple traits, using several reference populations with different amount of phenotypic informations. Genetic parameters (heritability and genetic correlations) were observed, and found very stable. EBVs and GEBVs accuracies showed that genomic evaluation was each time more accurate than genetic evaluation, especially when phenotypic information was restrained. It was also found that the use of sexual chromosome genotype had a negative impact on traits evaluation for dams (no effect found on sires). In any case, genomic evaluation of breeding birds at birth seems to be a promising strategy for layers.

*Keywords: laying hens, genomic evaluation, accuracy, single step*

### **Introduction**

For the last few years, avian breeders are starting to put in place genomic selection in their selection schemes. This methodology seems highly promising for the avian sector (Wolc et al., 2016, Wolc et al., 2015, Liu et al., 2014), and studies are currently being conducted to optimize avian selection schemes. One key parameter for this optimization is to correctly predict the accuracy of genomic evaluation.

Studies in mammals show that this accuracy strongly depend on the structure of the linkage disequilibrium (Wientjes et al., 2013, Meuwissen et al., 2001). However, avian genomes are characterized by a very heterogenic structure of linkage disequilibrium, with micro-chromosomes in where a lot of recombination events appends (Burt, 2002, Hillier et al., 2004). It has also been shown that the accuracy of the evaluation is impacted by the number of training generations used (Weng et al., 2016), or the relation between reference and candidate population (Elsen, 2016, Clark et al., 2012, Habier et al., 2007). In the present study, multiple traits evaluations have been done on egg quality traits, with BLUP or ssGBLUP methodology. Accuracy of the estimated genetic breeding values have been compared, depending on the amount of phenotypic informations available: evaluations on ancestry, or on ancestry and relatives compared to evaluation on ancestry, relatives and offspring.

### **Material and Methods**

## **Phenotyped females**

Data used in this study came from a pure line of Rhode Island layers, created and selected by Novogen breeding company. Seven traits, on egg shell and internal quality have been studied: egg weight (PO), shell colour (LAB), fracture strength (FF), shell deformation (De), egg diameter (Di), albumen height (HA), and shape index (SI).

Data relates to more than 19,000 birds, from 2008 to 2015, divided in 4 generations (G0 to G3), each generation separated in 3 batches. Depending the type of cage used in the buildings, data are organised in two different group:

- Multiple Cages (CM): Birds 18 to 60 weeks old, with 5 birds by cage. Each cage contained only full sisters, and each performance were associated to the cage. A total of 19,220 birds (in 12 batches), with 27,970 performances, are concerned.

- Individual Cages (CI): Birds older than 60 weeks, selected from birds in multiple cage. Each measured egg is directly associated to a bird. A total of 7,983 birds (in 15 batches), with 75,121 performances, are concerned.

## **Genotypes**

2,374 birds were genotyped using the 600K Affymetrix R Axiom R HD genotyping array. Blood samples were collected from brachial veins of individuals and DNA was extracted. DNA was hybridized on the 600K Affymetrix R Axiom R HD genotyping array (Kranis et al., 2013) by the high-throughput genotyping platform by Ark-Genomics (Edinburg, UK).

In total, 1,214 males and 1,148 females were genotyped for 580,953 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, 302,102 SNP were kept for the study and 12 individuals were excluded.

Using the complete genotype, another genotype was obtained, without the SNPs of sexual chromosomes. This genotype concerned 291,978 SNPs.

## **Evaluations**

Seven traits were evaluated with BLUP and single-step GBLUP methodology, using BLUPF90 family of programs (Misztal et al., 2002). The candidat population was the parents of G2 birds, namely the birds selected from G1. This group contain 200 sires and 747 dams. The pedigree file contained the candidates, all their known ancestors back to the funding of the line, and all their offspring.

To estimate the genetic evaluation accuracy, depending on the amount of information, several reference populations were generated from the base data, for each type of cage:

- Full: all data were used. This population allow an evaluation on ancestry, relatives and offspring. Results obtained have been considered as the birds true EBV/GEBV, and used as a reference for accuracy estimation.

- ssG3: without the last generation, grand-daughters of the candidate population.
- ssG2G3: without the 2 last generation, grand-daughters and daughters of the candidate population.
- ssG1G3: only G0 is used. Evaluations using this population will be only on ancestry.

The different traits were assumed to follow a classical animal model:

$$y = 1\mu + X(\beta + \lambda + \alpha) + Zu + e$$
$$\text{with } Var\left(\begin{matrix} u \\ e \end{matrix}\right) = \left( \begin{pmatrix} A\sigma_u^2 & 0 \\ 0 & I\sigma_e^2 \end{pmatrix} \right)$$

where  $y$  is a vector containing performance records,  $\mu$  is the general mean of the model,  $\beta$ ,  $\lambda$ ,  $\alpha$ ,  $u$  and  $e$  are vectors, of batch fixed effects, of battery fixed effects, of position fixed effects, of random polygenic effects and of random residuals respectively.  $A$  is the pedigree kinship matrix;  $I$  is the identity matrix;  $X$  and  $Z$  are incidence matrices for fixed and random polygenic effects.  $\sigma_u^2$  is the genetic variance,  $\sigma_e^2$  is the residual variance.

### Accuracy comparison

For each dataset (CM or CI), and type of evaluation (genetic or genomic), a Pearson correlation have been computed between EBV/GEBV for the evaluation using the "Full" population, and EBV/GEBV for ssG3, ssG2G3 and ssG1G3. It was done for both sires and dams. Correlations between different evaluations using the complete populations were also calculated.

## Results and Discussion

### Genetic parameters

#### *Heritability*

Heritability was very stable between each evaluation, and in accordance to the litterature data (BEAUMONT et al., 2010), as the egg weight (PO), which is estimated around 0.65, or the fracture strength (FF), around 0.35. Heritabilities in CI were estimated a little bit higher than in CM, with around 5% of difference between the evaluations. That was expected, because of the data structure (egg performances were linked to the cage), heritabilities were slightly underestimated in CM.

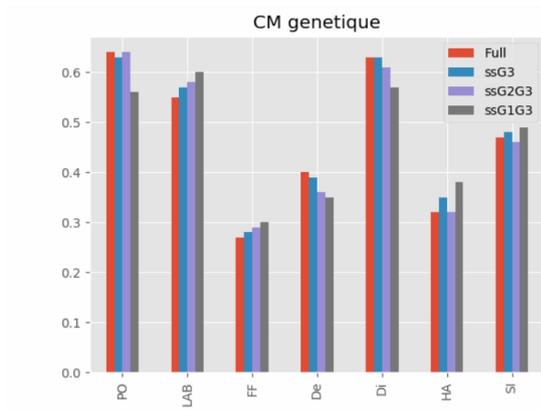


Figure 1: Heritabilities for the different genetic evaluations in CM

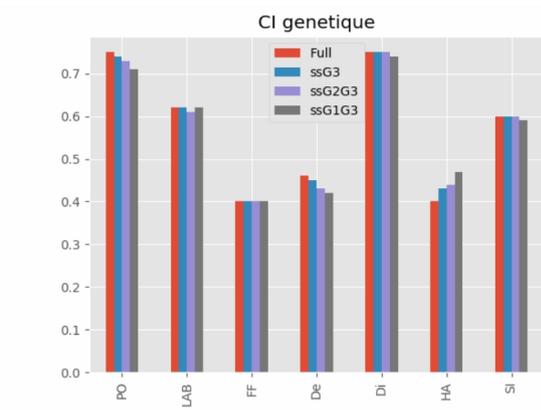


Figure 2: Heritabilities for the different genetic evaluations in CI

### Genetic correlations

Genetic correlations were very stable between each evaluation, both in CI and CM. A strong link between egg weight (PO) and diameter (Di); and between shell deformation (De) and fracture force (FF) was brought to light each time, both in CM and CI. Shape index (Si) and fracture force (FF); and diameter (Di) and shape index (SI) were also slightly correlated.

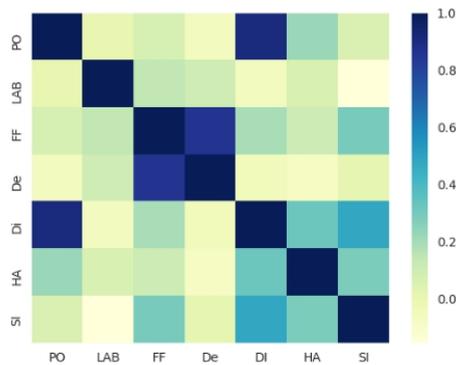


Figure 3: Genetic correlation for CI in genetic evaluation with complete dataset

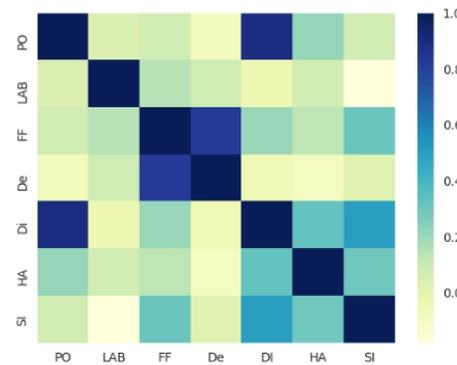


Figure 5: Genomic correlation for CI in genomic evaluation only on ancestors

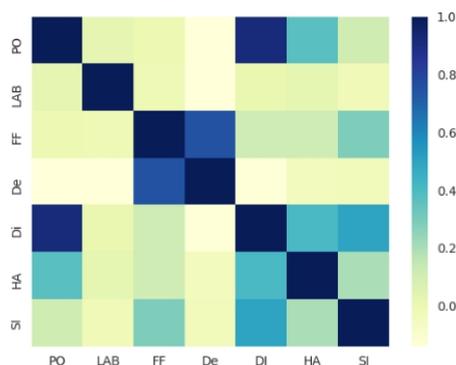


Figure 4: Genetic correlation for CM in genetic evaluation with complete dataset

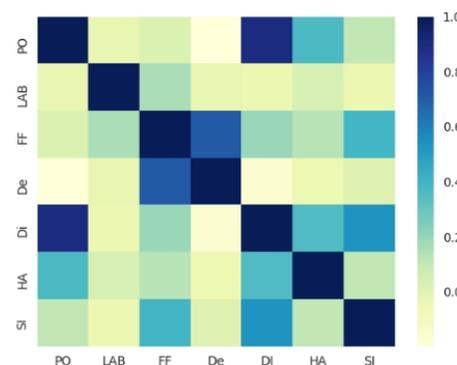


Figure 6: Genomic correlation for CM in genomic evaluation only on ancestors

### EBVs and GEBVs accuracies

Accuracies were not homogeneous between traits: some were significantly more precisely evaluated than other, depending the reference population and the use of genotype.

In evaluations using ssG3, EBV/GEBV for each traits were very accurate, around 98%, showing that the grand-daughter bring few informations to the evaluation. There was very few differences between genetic and genomic evaluation.

For the evaluations using ssG2G3, both EBV/GEBV values were between 48% (PO, Di) and 62% (LAB, De). However, some differences appeared between genetic and genomic evaluation, with traits being more precisely estimated: FF went from 52% to 60%, and SI from 48% to 52%.

The evaluations using ssG1G3 were those with the largest differences between genetic and genomic evaluation. EBV were ranged between 15% (PO, Di) and 25% (De, Si), but GEBV were ranged between 20% (PO, Di) and 38% (FF, HA). Traits accuracy improvement was not homogenous, with trait like PO obtaining a 5% gain, and other like FF going from 20% to 38%.

It could be explained by the fact that some traits, as the egg weight (PO), are controlled by few SNPs, with a strong effect, which negatively impact the accuracy of the

genomic evaluation (Romé et al., 2015).

In any case, genomic evaluation is always more precise than genetic evaluation, for every trait. And the accuracy gains were the strongest when phenotypic information is restricted (evaluation on ancestry).

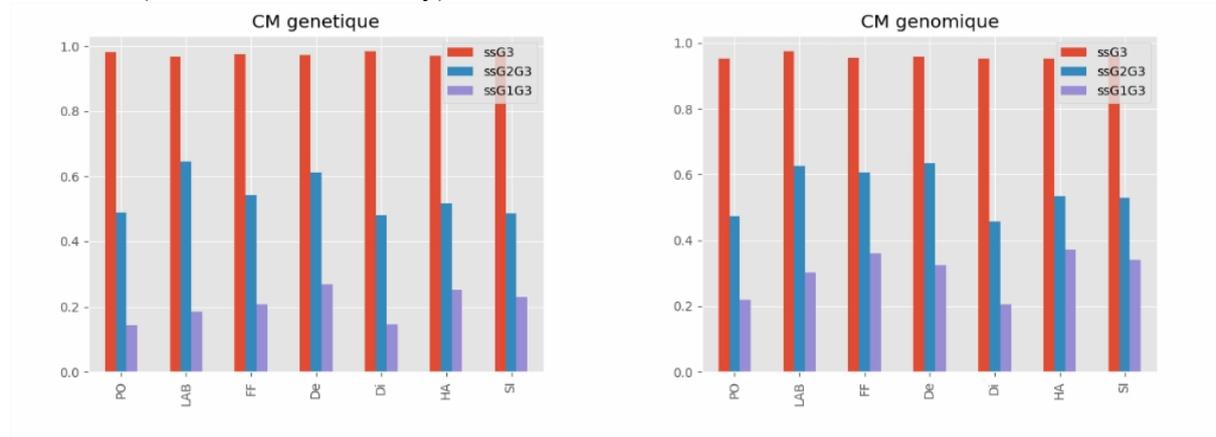


Figure 7: Correlations between results for Full and ssG3, ssG2G3 and ssG1G3 for sires in CM, in genetic evaluation

Figure 8: Correlations between results for Full and ssG3, ssG2G3 and ssG1G3 for sires in CM, in genomic evaluation

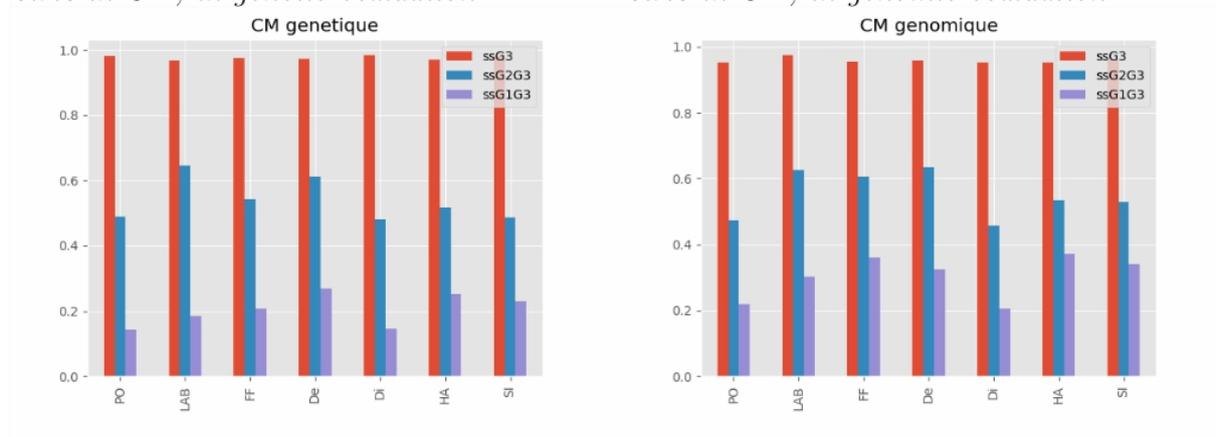


Figure 7: Correlations between results for Full and ssG3, ssG2G3 and ssG1G3 for sires in CM, in genetic evaluation

Figure 8: Correlations between results for Full and ssG3, ssG2G3 and ssG1G3 for sires in CM, in genomic evaluation

In addition, it could be seen that the use of a genotype without sexual chromosomes SNPs have a positive impact on the evaluation accuracy for the females (no effect was found for the sires). This impact seems stronger for the evaluation using ssG2G3, traits being evaluated on average 11% more precisely. The accuracy is also improved for the evaluation with G1G3, but only for some traits, in particular PO and Di which were the ones the most improve in the evaluation on ancestry and relatives.

Table 1: Accuracy of genomic evaluation for CM G2 dams, using complete genotype

Pop. Ref	PO	LAB	FF	De	Di	HA	SI
ssG2G3	0.47	0.62	0.60	0.63	0.45	0.53	0.52
ssG1G3	0.22	0.30	0.36	0.32	0.20	0.37	0.34

Table 2: Accuracy of genomic evaluation for CM G2 dams, using genotype without Z&W

Pop. Ref	PO	LAB	FF	De	Di	HA	SI
ssG2G3	0.63	0.70	0.72	0.72	0.58	0.67	0.61
ssG1G3	0.37	0.30	0.34	0.34	0.30	0.40	0.32

## Conclusion

Results of this study show that the accuracy of prediction for the different traits involved in egg quality strongly vary depending on the estimated trait. There is also an influence of sexual chromosomes for the females evaluation.

In any case, genomic evaluation of breeding birds at birth seems to be a promising strategy in this population.

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