Genetic Evaluation For Pure-Line And Cross-Line Performance In Layers

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Introduction

Crossbreeding is a standard practice in poultry breeding programmes as a way of exploiting heterosis. However, there is no consensus on the most effective way of maximising the genetic response in cross-bred animals (Besbes and Ducrocq (2003)). Furthermore, the goal of commercial breeding is not to maximise heterosis, but to maximise overall profitability in the commercial cross, the parents and the pure lines (Flock *et al.* (1991)). Environmental differences exist between breeding farms (single cages) and commercial farms. Thus, both environments should be taken into account in the breeding program, in order to minimise possible genotype-environment-iterations that can reduce the response to selection on the commercial level. However, considering cross-bred and pure-bred performance as two traits and their correlations, does not require distinction between these environmental effect. The cross-bred performance is captured in the environment in which the breeding goal is defined (Wei and van der Werf (1995)). In order to optimise a breeding programme, ranking based on pure-bred performance has to be compared with ranking based on cross-bred performance from commercial farms. If there are significant differences, cross-bred information has to be included in the selection process.

The aim of this study is to estimate the genetic correlations between pure-bred and cross-bred performances, in order to optimise the breeding program.

Material and methods

Data from three generations of a White Leghorn (WL) and a Rhode Island Red (RIR) pure-line recorded in single cages in the breeding farm were analysed. Cross-bred daughters of the same sires were housed in group cages (4 hens per cage) in four commercial farms each generation, two farms for each cross. These cross-bred hens only had sire pedigree. On average, 70 sires in the WL line and 69 sires in the line RIR from each generation were used for the analysis with each sire producing an average of 50 and 69 pure-bred, respectively. Both producing 30 cross-bred daughters per generation.

The traits used for this study were cumulative early egg production between 20 and 27 weeks of age (P1), peak production between 28 and 47 weeks of age (P2) and late egg production between 48 and 68 weeks of age (P3). The average egg weight measured at 29, 34 and 45 weeks of age (EW). Furthermore, the average shell breaking strength (SS) measured at 40, 43 and 46 weeks of age. Shell colour (SC) was measured at the age of 30 weeks and for RIR, at another time with 45 weeks (a mean of the two values was calculated). Mortality was

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taken into account for egg production in group cages, dividing production per cage by the number of hens alive. Additionally to the laying performance and the three egg weight measurements, one day clutch per cage was used for measuring egg quality traits: EW, SS and SC on individual eggs and a cage mean was calculated. Only cages with 4 hens were included in this study, in order to avoid the heterogeneity of residual variances of cage data due to different group sizes.

A total of 10,002 and 13,367 records for the pure-bred and 1,426 and 1,394 cage average for the cross-bred for WL and RIR, were analysed respectively. Table 1 shows an overview of the general statistics for the different traits.

Table 1: General Statistics

Trait	**White Leghorn**				**Rhode Island Red**			
	Pure-line		**Cross-line**		**Pure-line**		**Cross-line**	
	Mean	**s**	**Mean**	**s**	**Mean**	**s**	**Mean**	**s**
P1 (%)	66.1	16.1	82.8	7.4	69.8	18.8	77.6	11.4
P2 (%)	96.0	4.3	94.4	5.5	94.5	5.2	91.4	8.0
P3 (%)	92.5	7.3	90.0	7.6	87.4	9.0	85.6	10.2
EW (g)	60.1	3.4	62.6	2.3	61.9	4.2	64.9	2.6
SS (N)	47.6	5.8	48.6	6.3	46.7	6.4	50.8	6.9
SC	85.5	3.7	88.6	2.2	12.0	8.4	14.3	5.9

The program VCE 4 (Neumaier and Groeneveld (1998)) based on the REML method and a multiple traits animal model was used to estimate (co)variance components, with the model:

$$y_{ijk} = \mu + GHHT_i + a_j + e_{ijk}$$

where y_{ijk} is the vector of observations for the different traits; μ is the population mean; $GHHT_i$ is the fixed effect of the multicode: generation, house, hatch and tier; a_i is the random additive genetic effect of animal i; and e_{ijk} is the random residual effect. In the case of the cross-line data for laying rate, only a cage average could be measured and only the sire was known. Therefore, in the model the cage mean was used in the model as vector of observations and the cage as “animal effect”.

Results and discussion

A better performance in the cross-bred than in the pure-breed due to heterosis should be expected, however, it should be borne in mind that the pure-line was kept under optimal biosecurity and management conditions, whereas the cross-bred were kept under commercial environment.

Egg production during the first two periods yielded the highest heritability, which is strongly influenced by variation at an age of sexual maturity. The heritability decreased during peak production and increased towards the end of lay (table 2), similar to values from the literature (e.g. Anang *et al.* (2000)). No or slightly negative correlation was found between the production at sexual maturity and at the end of lay. As expected, the genetic correlation was high between peak production and persistency.

Table 2: Genetic Parameters for egg production traits in pure-line and cross-line (cross-line data as cage average, WL in the first row and RIR in the second)

Pure-line (breeding farm - single cages)			**Cross-line** (commercial farm – group cages)		
P1	**P2**	**P3**	**P1**	**P2**	**P3**
0.40	0.31	0.07	0.63	0.44	0.14
0.37	0.15	0.02	0.83	-0.29	-0.32
	0.13	0.75	-0.10	0.50	0.33
	0.24	0.83	0.34	0.10	0.05
		0.17	-0.20	0.30	0.27
		0.30	0.26	0.26	0.33
			0.69	0.40	-0.06
			0.42	0.11	-0.10
				0.11	0.55
				0.15	0.63
					0.19
					0.24

The heritabilities for production for both, pure-line and cross-line, were on similar levels. The genetic correlations between pure-bred and cross-bred performances were moderate to high at sexual maturity (r_g= 0.63 and 0.83), whereas the correlations decreased to moderate to low levels in the other two stages of production (r_g between 0.1 and 0.5). The heritabilities obtained in this study were approximately at the same level as Nurgiartiningsih *et al.* (2004).

Theoretically, it is expected that the residual variance estimated based on pooled observations is n times which are estimated based on individual observations (Biscarini *et al.* (2008)). According to this author, the heritability for pooled data should be recalculated as: $h^2= \sigma_a^2 / (\sigma_a^2 + n\ \sigma_e^2)$; where 'n' is the number of hens/cage. This is in line with Simianer and Gjerde (1991) who explained that estimation based on group means contains less information on the group variation, which essentially contributes to the estimation of residual variance components. This would mean a reduction of the heritabilities calculated for mean cage, while the genetic correlation remains constant.

Table 3: Genetic Parameters for egg quality traits in pure-line and cross-line, with cross-bred data as cage average and as individual records

			Cage average		**Individual records**	
		h^2 pure-line	**h^2 cross-line**	**rg**	**h^2 cross-line**	**rg**
EW	WL	0.67	0.99	0.93	0.66	0.90
	RIR	0.64	0.99	0.84	0.59	0.73
SS	WL	0.38	0.57	0.85	0.32	0.84
	RIR	0.43	0.46	0.83	0.29	0.73
SC	WL	0.70	0.98	0.83	0.53	0.82
	RIR	0.49	0.98	0.89	0.61	0.88

Additionally, for egg quality traits in the cross-bred, individual egg measurements of one day clutch per cage was done and randomly assigned to one of the hens in the cage. With the heritability parameters shown in table 3, it becomes clear that the reducing effect of rest variance which is the consequence of using a cage average. The values for the heritabilities are then according to literature, and at a lower level than in the pure-bred, which would be expected under "sub-optimal" conditions. This is also due to the fact that the hens in group cages only contributed with one egg, while in single cage several measurements of eggs from the same hen are captured (Nurgiartiningsih *et al.* (2004)).

Wei et al. (1995) argued that a combined cross-bred and pure-bred selection is better than a pure line selection method to achieve cross-bred response. This strategy is more valuable where the values of the genetic correlation are lower than 0.8, which is the case laying rate.

It is of major importance to capture information from well-designed crossbreeding tests to augment the valuable information for the selection process. If the residual variance is too high, the heritability will be low and the gain of using this information decrease.

Conclusions

Based on the results of this study, it could be summarised that the genetic correlations of production traits between pure-line and cross-line was moderate, whereas the genetic correlation for egg quality traits were high. It could be therefore argued, that it is necessary to measure the production data of the cross-line under commercial environment, while it would be enough to capture the egg quality data in the pure-line. The results of this study show the loss of statistical information produced by working with cage mean, but on the other hand shows that group cage data is essential to avoid genotype-environment-interaction and to take heterosis into account. It could be concluded that with this study, the fact is confirmed that a combination of pure-line and cross-line selection is the better way to breed.

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