

GENETIC VARIABILITY OF EGG PRODUCTION TRAITS IN PUREBRED AND CROSSBRED LAYING HENS

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SUMMARY

Heritabilities, dominance variation and genetic correlations (r_{pc}) among pure and crossbred performance were estimated for egg production and egg quality traits in 4 generations of two nucleus lines of egg-laying chickens and their cross, all reared in similar environments. Estimates of r_{pc} were high (0.76 to 0.94) and coupled with estimates of dominance variance ($d^2 = 0.04$ to 0.09) and the absence of obvious heterosis, indicate little advantage to be gained from use of crossbred data in genetic improvement, where pure lines and crossbreds are reared in a similar non-stressful environment.

Keywords:

INTRODUCTION

Crossbreeding has become a standard practice in poultry breeding programs. However, the debate continues among geneticists on the most effective way to maximize the genetic response in the crossbred (Bell 1982; Sellier 1982; Wei *et al.* 1991).

In the absence of direct experimental comparison, estimates of genetic parameters related to the crossbred and purebred populations should give some indication as to which method of selection (pure line selection, reciprocal recurrent selection or a combination between them) will be most effective. Bell (1982) and Wei *et al.* (1991) suggested that the genetic correlation between purebred and crossbred performance (r_{pc}) is the most reliable indicator of the relative emphasis to give to purebred vs crossbred information when selecting for crossbred performance. This parameter depends on the degree of dominance and the difference in allele frequencies in the parental populations (Wei *et al.* 1991), which are never known in practical animal breeding situations. Moreover, recent simulations by Uimari and Gibson (*ibid*) indicate that r_{pc} is not a particularly useful predictor of the value of collecting crossbred information, and that amount of dominance variance might be more useful. Dominance variance can be estimated from typical animal breeding data using a variety of recently developed methods (e.g. Hoeschele and VanRaden 1991; Misztal 1997).

The objectives of this study were to estimate 1) the additive and dominance variances in pure lines and 2) the heritabilities of and genetic correlation between crossbred and purebred performance in 2 nucleus populations of egg-laying chickens.

MATERIALS AND METHODS

Data. Data were from 4 generations of purebred and crossbred hens (2 lines and their cross)

raised in individual cages under a well-controlled environment. There were 334, 664 and 334 sires, 1523, 3410 and 1904 dams, and 24611, 47811 and 6288 progeny in lines L1, L2 and the crossbred, respectively.

Egg production and egg quality traits were considered. Traits were the number of eggs laid between 19 and 25 (EN1), 26 and 38 (EN2) and 26 and 54 (EN3) weeks of age and average egg weight (EW) measured between 38 and 54 weeks of age. Egg production traits (EN1, EN2, EN3) showed negatively skewed distributions and were therefore transformed to obtain normal distributions using the Box-Cox approach (Besbes *et al.* 1993).

Methods. *Estimation of additive and dominance effects within line.* The estimation of additive and dominance variances of egg production traits in each line was based on a sire dam model accounting for the fixed effect of hatch (92 levels) and with a regression on level of inbreeding. Estimates of the variance components were obtained using the tilde-hat approximation to REML using the programs of Hoeschele and VanRaden (1991) to compute the inverse of the relationship matrix among dominance effects for sire and dam.

Estimation of genetic correlation between purebred and crossbred performances. The purebred and the crossbred performances were considered as different traits and multivariate analyses were applied to estimate their heritabilities and the genetic correlation between them. In order to avoid the problem associated with heterogeneous variances, we also considered the same trait in the two pure lines as two different traits. Estimation was based on a multivariate sire-dam model using all the records (of purebred and crossbred animals) and the relationships within line, including those between sires and dams. This model is then very close to the reduced animal model. The variances and covariances were estimated by a REML procedure using the VCE algorithm (Groeneveld 1997).

RESULTS AND DISCUSSION

Estimation of additive and dominance effects within line. The estimates of h^2 and d^2 (ratios of additive and dominance variances to phenotypic variance) are presented in Table 1. The h^2 estimates are similar for both lines. They are high for EW (0.7), intermediate for EN1 (0.4) and relatively low for EN2 and EN3 (0.1 to 0.24). The d^2 estimates are also similar for both lines and vary between 0.04 and 0.16. When expressed as a percentage of total genetic variation, the dominance variation (d_g^2) lies between 5 and 56%. Simulation results suggest that the higher ratios obtained for EN2 and EN3 (0.28 to 0.56) are likely due to loci with large partial dominance, complete dominance or overdominance (Uimari and Gibson, personal communication). The present estimates of d^2 are similar to those obtained by Wei and Van der Werf (1993), the only previous report in poultry on simultaneous estimation of h^2 and d^2 using animal model and REML.

The estimated inbreeding depression is quite low for all traits, and less than 1% per 10% increase of inbreeding coefficient. These estimates are lower than the 3 to 4 % reported in the literature (Abplanalp 1990; Flock *et al.* 1991). This may be due to the small number of generations considered here, but also to an efficient mating plan. But, the result is also consistent with the absence of obvious heterosis in this cross (results not shown).

Table 1. Estimation of genetic parameters under the dominance model

Traits	L1				L2			
	b ¹	h ²	d ²	d ² g	b	h ²	d ²	d ² g
EN1	-0.12	0.41	0.04	0.09	-0.36	0.39	0.12	0.23
EN2	-0.07	0.18	0.16	0.47	-0.29	0.24	0.09	0.28
EN3	-0.44	0.12	0.15	0.15	-0.84	0.16	0.14	0.47
EW	-0.01	0.70	0.05	0.06	-0.08	0.69	0.04	0.05

¹Estimate of inbreeding depression, expressed in eggs or g per 100% inbreeding..

Estimation of purebred and crossbred parameters. The purebred heritabilities estimated with the additive model (Table 3) are higher than those estimated with the dominance model (Table 2), because part of the dominance variance appears in the additive variance when dominance is not included in the model. Thus, the difference between the two pure line heritabilities (0.43 and 0.51) for EN1 was due to different levels of dominance variance ($d^2 = 5\%$ for L1 vs 11% for L2). EN1 is a contribution of two traits, early egg production and age at first egg and is dominated by the second trait (Fairfull and Gowe 1990).

In general, crossbred h^2 were higher than purebred h^2 due mainly to a lower residual variance. The relative difference between crossbred and purebred h^2 is usually used as an indirect evidence of non-additive genetic variation. However, there is no clear relationship between these differences and the dominance variance for these traits.

In general, the correlation between purebred and crossbred performance is high (>0.76) but the pattern among the traits varies between the sire and dam lines. These differences between the two lines may be due to the different levels of accuracy of r_{pc} estimation. For the sire line, r_{pc} is fairly well estimated because of the large number of progeny per sire (74 purebred and 20 crossbred daughters, on average). For the dam line, estimation is much less accurate since it is based on crossbred progeny of females that do not have purebred progeny (on average, 2 crossbred daughters per dam).

The estimates of r_{pc} and dominance suggest that the difference in allele frequencies in the two lines must be fairly small, especially for EN2 and EN3. Simulation studies showed that pure line selection tries to fix the favorable alleles in both lines and hence decreases any initial differences in allele frequencies which increases r_{pc} (Wei *et al.* 1991; Swan 1992). This would not be the case for any loci fixed for the recessive allele in one line only, which suggests that predominantly the same loci are segregating in the two lines.

The levels of r_{pc} and d^2 found here are in the range that would indicate little advantage to using crossbred data in a genetic improvement program (see Uimari and Gibson *ibid.*). This conclusion would be appropriate if commercial crossbreds were kept in individual-bird cages and well controlled environment, instead of multiple-bird cages and stressful environments, as it is the case in practice. Under such conditions, the estimates of the crossbred parameters are smaller than those obtained here, e.g., for egg number, Wei and Van der Werf (1995) reported estimates of 0.04 to 0.51 for the crossbred heritability and 0.56 to 0.73 for the genetic

correlation. One explanation of this difference could be GxE interaction when environments differ between pure and crossbred production. Another explanation is Orozco's theory (1986), that in the optimum environment additive genes are acting but not non-additive genes. The later genes control animal vigor or general resistance. In a stressful environment, both groups of genes are active. The absence of heterosis, measured as the difference between the mean of the offspring and the mid-parent, for the traits analyzed here (results not shown) support this theory.

Table 2. Estimation of h^2 and r_{pc} based on a sire-dam model

Genotype	Traits	h^2	r_{pc}	Var(a)	Var(e)
L1	EN1	0.43	0.80	27.0	99.2
	EN2	0.30	0.94	7.4	42.8
	EN3	0.25	0.91	24.4	170.9
	EW	0.69	0.91	11.6	11.0
L2	EN1	0.51	0.93	24.0	69.7
	EN2	0.32	0.76	8.6	44.6
	EN3	0.29	0.78	34.8	205.5
	EW	0.71	0.93	12.2	11.1
L1xL2	EN1	0.51	-	17.1	50.3
	EN2	0.44	-	5.6	30.7
	EN3	0.31	-	26.1	142.0
	EW	0.69	-	11.8	11.3

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