Genetic Correlation and Heritabilities for Purebred and Crossbred Performance in Poultry Egg Production Traits

Ming Wei and Julius H. J. van der Werf

Department of Animal Breeding, Wageningen Agricultural University, 6700 AH Wageningen, The Netherlands

ABSTRACT: Genetic correlations between purebred and crossbred performance and purebred and crossbred heritabilities were estimated for egg production traits of laying chickens using a multivariate sire model accounting for additive relationships between sires. Two sire lines, denoted lines 1 and 2, were crossed to one dam line to produce crossbred progeny. Records for egg weight, egg specific gravity, and egg number were collected on purebred and crossbred hens. In total, 99 sires in line 1 and 292 sires in line 2 were used in the analysis, each sire producing on average 45 purebred and 105 crossbred daughters. Estimates of purebred heritability in lines 1 and 2 were in range of .54 to .74 for egg number traits, .52 to .91 for egg weight traits, and .41 to .83 for egg specific gravity traits. Estimates of crossbred heritability were .04 to .51 for egg numbers, .23 to .45 for egg weight, and .13 to .31 for egg specific gravity. The sire component in crossbreds differed up to 78% from the sire component in purebreds depending on traits. The estimate of genetic correlation (r_{pc}) between purebred and crossbred performance was .56 to .73 for egg number, .69 to .99 for egg weight, and .72 to .82 for egg specific gravity. Although crossbred parameters were strongly affected by environmental factors, the results tend to agree with the theory that traits with a larger dominance variation and a larger difference between sire components in purebreds and crossbreds show a lower r_{pc}. Because the estimates of r_{pc} were significantly lower than 1 for egg number and egg specific gravity, an optimal selection strategy should combine purebred and crossbred information for crossbred progress.

Key Words: Crossbreeding, Egg Production, Genetic Parameters, Multivariate Analysis, Poultry

Introduction

The genetic correlation between crossbred and purebred performance (r_{pc}) and crossbred heritability (h_c^2) are important genetic parameters for optimizing and evaluating crossbreeding systems (Bell, 1982; Wei and van der Steen, 1991). These genetic parameters are especially needed when applying a combined crossbred and purebred selection method to achieve genetic progress in crossbreds (Wei and van der Werf, 1994).

Crossbred heritability is related to the amount of genetic variation among purebreds for crossbred performance. Wei et al. (1991b) showed in a one-locus model that h_c^2 is not a linear function of the heritabilities in parental lines (i.e., purebred heritability, h_p^2) if dominance exists, and it should be estimated separately for different lines and their crosses. Based on a one-locus model (Wei et al., 1991b), purebred heritability (or sire component of variance in purebreds) differs more from crossbred heritability (or sire component in crossbreds) with larger dominance effect and(or) larger gene frequency difference between the parental populations.

Wei et al. (1991a) found based on a two-locus model that r_{pc} is a function of dominance effects and the difference in gene frequency between parental populations and its value decreases with increasing dominance effects and(or) the gene frequency difference. Wei and van der Werf (1993) used an animal model to estimate dominance variance for egg production traits in three purebred lines. These estimates can be compared with crossbreeding parameters (such as r_{pc} and h_c^2) from the same populations to test the locus model theory. The objectives of this study were...
therefore to estimate $r_{pc}$, $h_p^2$, and $h_g^2$, and sire components of variance in purebreds and crossbreds, and to see whether egg production traits with larger dominance variation and bigger difference between sire components of variance in crossbreds and purebreds show a smaller $r_{pc}$, as expected by the locus model theory.

Materials and Methods

Data

Egg production records of purebred and crossbred laying chickens were collected by Euribrid between 1987 and 1989 from a crossing scheme in which sire lines 1 and 2 were crossed to a dam line (i.e., line 3) to produce crossbred progeny. All three lines are White Leghorn with different genetic backgrounds and selection histories. All purebred hens of sire and dam lines were raised in individual cages under a well-controlled environment, and their individual performance was recorded as described in Wei and van der Werf (1993). Each sire was mated to approximately 10 dams from the dam line to produce approximately 90 to 110 female crossbred progeny. Mating sires of both sire lines to the dam line was several weeks earlier than the mating within sire lines. The sires producing purebred progeny were selected based on their crossbred progeny performance (selected fraction was approximately 70%) and mated to approximately five dams to produce approximately 30 to 50 female purebred progeny. In this study, only a part of the purebred data used by Wei and van der Werf (1993) was analyzed (i.e., those generations of data with both purebred and crossbred hens). The numbers of sires and hens for lines 1 and 2 used in analysis are listed in Table 1.

In the crossbred data set, only a cage mean was recorded for three to five hens per cage. Within a cage, most hens were half-sibs and a few of the hens (<10%) were full-sibs. All sires were tested two to three times at different time periods to produce crossbred progeny. All crossbred hens were kept in a commercial environment. The number of sires and records (cage means for crossbred hens) are listed in Table 1.

Animals within lines were bred in groups for management purposes. There were three purebred groups and two crossbred progeny groups for sire line 1. Each purebred group was spread over approximately three to five hatch weeks (i.e., three to five hatches). In data of crossbreds sired by line 1, there were two repeated tests (i.e., sires were tested twice to produce crossbred progeny at different time periods). For sire line 2, four purebred groups and four crossbred progeny groups were involved. The sires of line 2 were tested two to three times to produce crossbred progeny. Hence, sires were tested repeatedly, and sires were nested within groups.

The traits used in this analysis were 1) early egg production defined as egg number produced between 18 and 25 wk of age (EN1); 2) main period egg production between 26 and 65 wk of age (EN2); 3) total egg production between 18 and 65 wk of age (EN3); 4) egg weight measured at 30 to 35 wk of age (EW1); 5) average egg weight measured at 30 to 35 and 40 to 45 wk of age (AEW); 6) egg specific gravity measured between 30 and 35 wk of age (ESG1); and 7) egg specific gravity at 40 to 45 wk of age (ESG2).

Egg number traits EN2 and EN3 showed a negatively skewed distribution and, therefore, were transformed to obtain normal distributions for the purpose of variance component estimation. According to Ibe and Hill (1988), the transformation formula is: $z(t) = (y^t - 1)/(tG^t - 1)$, where $y$ is an original untransformed observation, $z(t)$ is the standardized transformed variate, $G$ is the geometric mean of the original observations, and $t$ is the value obtained by maximizing the log likelihood, $L_{max}(t)$, described as follows. The log likelihood equation applied is as $L_{max}(t) = -(n/2)\log[S_r(t)/n]$, where $n$ is the total number of observations and $S_r(t)$ is the residual sum of squares from analysis of the standardized dependent variable, $z(t)$.

Models

Recognizing purebred and crossbred performance as two different traits with a genetic correlation between them, we applied multivariate sire models in this analyses. For purebred data, the following linear model was used:

**Table 1. Number of sires and their purebred and crossbred progeny used in the analysis**

<table>
<thead>
<tr>
<th>Sire lines</th>
<th>Purebred progeny</th>
<th>Crossbred progeny</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Sires</td>
<td>Daughters</td>
</tr>
<tr>
<td>1</td>
<td>71</td>
<td>3,199</td>
</tr>
<tr>
<td>2</td>
<td>214</td>
<td>6,492</td>
</tr>
</tbody>
</table>

*aRecord refers to the number of cages, each record being a mean performance record of three to five crossbred daughters.
\[ y_{ijkl} = \mu_1 + \text{GROUP}_{li} + \text{HW}_{ij} + s_{lik} + e_{ijkl}, \quad [1] \]

where \( y_{ijkl} \) is the observation of the \( ijkl^{th} \) individual purebred chicken, \( \mu_1 \) is the general mean, \( \text{GROUP}_{li} \) is the \( i^{th} \) group effect (fixed), \( \text{HW}_{ij} \) is the \( ij^{th} \) hatch week effect within groups (fixed), \( s_{lik} \) is the random effect of the \( ik^{th} \) sire within group but across hatch weeks, and \( e_{ijkl} \) is the residual random effect.

For crossbred data, the model was as follows:

\[ y_{2ijkl} = \mu_2 + \text{GROUP}_{2i} + \text{RP}_{ij} + s_{2ik} + e_{2ijkl}, \quad [2] \]

where \( y_{2ijkl} \) is the mean performance of \( n_{ijkl} \) crossbred hens in the \( ijkl^{th} \) cage, \( \mu_2 \) is the general mean, \( \text{GROUP}_{2i} \) is the \( i^{th} \) group effect (fixed), \( \text{RP}_{ij} \) is the \( ij^{th} \) trial effect (fixed) within groups (i.e., sires were repeatedly tested to produce crossbred progeny at different time periods), \( s_{2ik} \) is the random effect of the \( ik^{th} \) sire within group but across trial effects, and \( e_{2ijkl} \) is the residual random effect. The observed residual variance in Equation [2], \( \sigma^2_{e2} \), is equal to the residual variance for individual records \( (\sigma^2_{e2}) \) divided by the number of hens per cage.

In matrix notation, the multivariate model containing purebred and crossbred performance is as follows:

\[
\begin{bmatrix}
  y_1 \\
  y_2
\end{bmatrix} =
\begin{bmatrix}
  X_1 & 0 \\
  0 & X_2
\end{bmatrix}
\begin{bmatrix}
  b_i \\
  b_2
\end{bmatrix} +
\begin{bmatrix}
  Z_1 & 0 \\
  0 & Z_2
\end{bmatrix}
\begin{bmatrix}
  u_i \\
  u_2
\end{bmatrix} +
\begin{bmatrix}
  e_1 \\
  e_2
\end{bmatrix},
\]

where \( y_i \) is a vector of observations with \( i = 1 \) and 2 for purebred and crossbred data, respectively; \( b_i, u_i, e_i \), and \( e_2 \) are unknown vectors of fixed effects, additive sire effects, and residuals in purebreds and crossbreds, respectively; \( X_i \) and \( Z_i \) are the known incidence matrices relating observations to fixed effects and sire effects. The variance of additive sire effects is expressed as

\[
\text{var} \begin{bmatrix}
  u_i \\
  u_2
\end{bmatrix} = G_0 \otimes A,
\]

where \( A \) is a matrix with numerator relationships among sires. The symbol \( \otimes \) is the direct product operator (Searle, 1966). In a bivariate model \( G_0 \) is a 2 \( \times \) 2 sire covariance matrix with the purebred sire variance and the crossbred sire variance on the diagonals, and the sire covariance between purebred and crossbred performance as the off-diagonals. The inverse of \( G_0 \) is expressed as

\[
G_0^{-1} = \begin{bmatrix}
  g_{11} & g_{12} \\
  g_{12} & g_{22}
\end{bmatrix}^{-1} = \begin{bmatrix}
  g_{11}^{-1} & 0 \\
  0 & g_{22}^{-1}
\end{bmatrix},
\]

where \( g_{ij} \) is the variance of sire effects \((i = j)\), or the covariance between sire effects expressed in purebred \((i = 1)\) and crossbred progeny \((j = 2)\).

The variance of residual effects is expressed as

\[
\text{var} \begin{bmatrix}
  e_1 \\
  e_2
\end{bmatrix} = \begin{bmatrix}
  I_{e_1} & 0 \\
  0 & D_{e_2}
\end{bmatrix} = \begin{bmatrix}
  r_{11} & 0 \\
  0 & r_{22}
\end{bmatrix},
\]

where \( I \) is an identity matrix; \( \sigma_{e1}^2 \) and \( \sigma_{e2}^2 \) are the residual variances for individual records for purebreds and crossbreds, respectively. The matrix \( D \) is a diagonal matrix with diagonals equal to \( 1/n_{ijkl} \), where \( n_{ijkl} \) refers to the number of hens per cage. It is assumed there is no within-cage residual covariance between observations on purebred and crossbred progeny, assuming that most of the animals within cages are half-sibs. The small number of full-sibs within cages treated as half-sibs in the analysis was considered to cause negligible bias in estimation of variance components.

The mixed-model equations for the multivariate sire model with sire relationships are in Equation [4],

\[
\begin{bmatrix}
  X()r^{11}X_1 & 0 & X()r^{11}Z_1 & 0 \\
  0 & X()r^{22}X_2 & 0 & X()r^{22}Z_2 \\
  Z()r^{11}X_1 & 0 & Z()r^{11}Z_1 + g^{-1}A^{-1} & g^{12}A^{-1} \\
  0 & Z()r^{22}X_2 & g^{21}A^{-1} & Z()r^{22}Z_2 + g^{22}A^{-1}
\end{bmatrix}
\begin{bmatrix}
  b_1 \\
  b_2 \\
  u_1 \\
  u_2
\end{bmatrix} = \begin{bmatrix}
  X()r^{11}y_1 \\
  X()r^{22}y_2 \\
  Z()r^{11}y_1 \\
  Z()r^{22}y_2
\end{bmatrix},
\]

where \( r^{11} \) and \( r^{22} \) are the elements in the inverse of the residual variance/covariance matrix.

The variances and covariances were determined from the mixed-model Equation [4] by a REML procedure using an expectation-maximization algorithm (Meyer, 1986). The \( r_{pc} \) were calculated as \( g_{12}/(g_{11}g_{22})^{1/2} \). The purebred and crossbred heritabilities were, respectively, calculated by \( h^2_p = 4g_{11}/(g_{11} + \sigma_{e1}^2) \) and \( h^2_c = 4g_{22}/(g_{22} + \sigma_{e2}^2) \). Asymptotic standard errors of \( r_{pc} \), \( h^2_p \), and \( h^2_c \) estimates were approximated using a Taylor’s series. This multivariate model is supposed to account for preliminary selection of purebred sires based on their crossbred progeny performance before their producing purebred progeny and give unbiased estimation of sire components of variance and covariance (Thompson, 1973).

Regression analyses were performed using the SAS Reg procedure (SAS, 1989) to study the relationship among \( r_{pc} \), dominance variance, and the difference between sire components of variance in purebreds and crossbreds.

**RESULTS AND DISCUSSION**

**Sire Components in Purebreds and Crossbreds**

The estimates of sire components of variance in purebreds and crossbreds, purebred and crossbred
heritabilities, and genetic correlations between purebred and crossbred performance for egg production traits are listed in Tables 2 and 3 for sire lines 1 and 2, respectively.

Crossbred heritabilities were generally lower than purebred heritabilities for all traits, and for egg number traits (i.e., EN2 and EN3) they are much lower. Literature values for purebred and crossbred heritabilities vary (Hale and Clayton, 1965; Taran, et al., 1971; Pirchner and Krosigk, 1973; Orozco and Campo, 1975; Pirchner and Mergl, 1977), and slightly more examples of higher \( h_C^2 \) than of \( h_P^2 \) were observed (Wei, 1992). The reason for the very low \( h_C^2 \) found here is discouraging. A better-controlled environment for crossbreds could possibly increase \( h_C^2 \). Therefore, in practical breeding, controlling the testing environment for crossbreds would make such data more valuable.

The theoretical findings from the locus model (Wei et al., 1991a,b) concerning the relationship between crossbred parameters (i.e., \( r_{PC} \), \( h_C^2 - h_P^2 \)) and dominance may be tested by comparing these estimates. Based on the one-locus model theory (Wei et al., 1991b), the difference between sire components of variance in purebreds and crossbreds is determined by the dominance gene effects and the different gene frequency between parental populations. In general, the greater difference of sire components or heritabilities in purebreds and crossbreds is associated with larger dominance gene effects and larger gene frequency difference in parental populations.

### Table 2. Estimates of genetic parameters in sire line 1

<table>
<thead>
<tr>
<th>Trait</th>
<th>( h_P^2 )</th>
<th>( h_C^2 )</th>
<th>( r_{PC} )</th>
<th>( \sigma_{PC}^2 )</th>
<th>( \sigma_{pc}^2 )</th>
<th>( \sigma_{PC}^2 )</th>
</tr>
</thead>
<tbody>
<tr>
<td>EN1</td>
<td>0.74 (.08)</td>
<td>0.51 (.06)</td>
<td>0.70 (.08)</td>
<td>9.75</td>
<td>43.18</td>
<td>7.28</td>
</tr>
<tr>
<td>EN2</td>
<td>0.70 (.09)</td>
<td>0.04 (.01)</td>
<td>0.62 (.21)</td>
<td>21.05</td>
<td>99.74</td>
<td>10.99</td>
</tr>
<tr>
<td>EN3</td>
<td>0.69 (.08)</td>
<td>0.09 (.02)</td>
<td>0.65 (.20)</td>
<td>29.34</td>
<td>140.07</td>
<td>13.02</td>
</tr>
<tr>
<td>EW1</td>
<td>0.63 (.08)</td>
<td>0.27 (.04)</td>
<td>0.69 (.07)</td>
<td>1.26</td>
<td>6.69</td>
<td>2.82</td>
</tr>
<tr>
<td>AEW</td>
<td>0.91 (.10)</td>
<td>0.23 (.03)</td>
<td>0.85 (.09)</td>
<td>1.50</td>
<td>5.06</td>
<td>2.56</td>
</tr>
<tr>
<td>ESG1</td>
<td>0.69 (.08)</td>
<td>0.09 (.02)</td>
<td>0.63 (.20)</td>
<td>26.25</td>
<td>1,013.5</td>
<td>35.76</td>
</tr>
<tr>
<td>ESG2</td>
<td>0.75 (.09)</td>
<td>0.29 (.04)</td>
<td>0.81 (.12)</td>
<td>215.93</td>
<td>929.2</td>
<td>33.64</td>
</tr>
</tbody>
</table>

\( a \) \( h_P^2 \) and \( h_C^2 \) refer to heritabilities in purebreds and crossbreds, \( r_{PC} \) is the genetic correlation between purebred and crossbred performance, \( g_{12} \) and \( g_{22} \) are the genetic variances in purebreds and crossbreds, \( \sigma_{PC}^2 \) and \( \sigma_{pc}^2 \) are estimates of residual variances of single records in purebreds and crossbreds.

For an explanation of symbols and abbreviations see footnotes of Table 2.

### Table 3. Estimates of genetic parameters in sire line 2

<table>
<thead>
<tr>
<th>Trait</th>
<th>( h_P^2 )</th>
<th>( h_C^2 )</th>
<th>( r_{PC} )</th>
<th>( \sigma_{PC}^2 )</th>
<th>( \sigma_{pc}^2 )</th>
<th>( \sigma_{PC}^2 )</th>
</tr>
</thead>
<tbody>
<tr>
<td>EN1</td>
<td>0.73 (.07)</td>
<td>0.40 (.03)</td>
<td>0.73 (.04)</td>
<td>10.95</td>
<td>49.90</td>
<td>7.74</td>
</tr>
<tr>
<td>EN2</td>
<td>0.54 (.05)</td>
<td>0.06 (.01)</td>
<td>0.56 (.08)</td>
<td>15.89</td>
<td>101.52</td>
<td>10.84</td>
</tr>
<tr>
<td>EN3</td>
<td>0.65 (.06)</td>
<td>0.08 (.01)</td>
<td>0.61 (.07)</td>
<td>28.84</td>
<td>147.40</td>
<td>13.28</td>
</tr>
<tr>
<td>EW1</td>
<td>0.52 (.09)</td>
<td>0.44 (.07)</td>
<td>0.96 (.05)</td>
<td>1.19</td>
<td>7.95</td>
<td>3.02</td>
</tr>
<tr>
<td>AEW</td>
<td>0.81 (.12)</td>
<td>0.45 (.06)</td>
<td>0.99 (.04)</td>
<td>1.61</td>
<td>6.33</td>
<td>2.82</td>
</tr>
<tr>
<td>ESG1</td>
<td>0.54 (.09)</td>
<td>0.25 (.05)</td>
<td>0.72 (.09)</td>
<td>231.02</td>
<td>1,487.91</td>
<td>41.46</td>
</tr>
<tr>
<td>ESG2</td>
<td>0.41 (.07)</td>
<td>0.31 (.05)</td>
<td>0.82 (.10)</td>
<td>191.78</td>
<td>1,670.14</td>
<td>43.15</td>
</tr>
</tbody>
</table>

\( a \) For an explanation of symbols and abbreviations see footnotes of Table 2.

\( b \) Values in parentheses are SE.
populations (Wei et al., 1991b). In this study, genetic correlations between lines are not directly known, and dominance variation, which reflects dominance gene effects, can be used for the comparison. Due to the large difference between residual variances in crossbreds and purebreds, the difference between $h_\text{c}^2$ and $h_\text{p}^2$ is not very relevant in the comparison to the dominance variance estimates. Instead, the sire components in purebreds and crossbreds can be compared. Table 4 shows estimates of dominance variance and relative sire component differences between purebreds and crossbreds (expressed as $[g_{11} - g_{22}]/g_{11}$) for the three traits in the two sire lines. Dominance variances were previously estimated from the same lines (Wei and van der Werf, 1993). The dominance variation is positively related to the difference between sire components in purebreds and crossbreds (i.e., traits with a higher dominance variance tend to have a larger difference between sire components in purebreds and crossbreds; see Table 4 and Figure 1).

**Genetic Correlation Between Purebred and Crossbred Performance**

The estimates for genetic correlation between purebred and crossbred performance ($r_{pc}$) are reasonably consistent for all traits in the two sire lines (Tables 2 and 3). The $r_{pc}$ was the lowest for egg number traits, approximately .50 to .70. The $r_{pc}$ for egg weights (EW1 and AEW) were very high (i.e., .69 and .83 for line A, and .96 and .99 for line B). The $r_{pc}$ estimate for specific gravity, which has not been reported before, was found to be approximately .70 to .80. The $r_{pc}$ estimates on egg weight and egg number were in the range of previous estimates (Hale and Clayton, 1965; Biswas and Craig, 1969; Taran et al., 1971; Singh and Dev, 1974; Pirchner and Mergl, 1977; Rabsztyn, 1979).

According to the two-loci model of Wei et al. (1991a), the $r_{pc}$ value would be negatively correlated with dominance variation. Table 4 shows estimates of $r_{pc}$ and dominance variance for all traits in two sire lines. It is demonstrated in Figure 1 that the values of $r_{pc}$ and dominance variance tend to be inversely related (i.e., traits with a higher dominance variance have generally a lower $r_{pc}$). The $r_{pc}$ for egg weight in sire line 1 is lower than expected when considering the low dominance variance, which seems to be an exception to the general pattern.

Due to the fact that both $r_{pc}$ and $(g_{11} - g_{22})/g_{11}$ are determined by gene frequency difference in parenteral lines and dominance gene effects, the negative correlation between them would be expected by the locus model theory (Wei et al., 1991a,b). Larger dominance effects and greater difference in gene frequencies in two populations decreases $r_{pc}$ and increases $(g_{11} - g_{22})/g_{11}$. It is shown in Figure 1 and Table 4 that there is a strong negative correlation between $r_{pc}$ and $(g_{11} - g_{22})/g_{11}$, and this supports the theoretical expectation. Trait EW1 in line 2 with a high $r_{pc}$ (= .96) seems to be an exception (Figure 1). Significant regressions ($P < .05$) of $r_{pc}$ are found on $d^2$ and $(g_{11} - g_{22})/g_{11}$ (i.e., $r_{pc} = .822 - .931[d^2]$ and $r_{pc} = .868 - .354[(g_{11} - g_{22})/g_{11}]$, respectively). Correlation coefficients ($P < .05$) were -.62 and -.71 between $r_{pc}$ and $d^2$ and between $r_{pc}$ and $(g_{11} - g_{22})/g_{11}$, respectively.

The results for $r_{pc}$ as well as sire component differences between purebreds and crossbreds described previously can be used to make inference about the gene frequency difference among lines to some extent according to the locus model theory (Wei et al., 1991a,b). First, both sire lines must have a considerable difference in gene frequency from the dam line concerning all traits so that $r_{pc}$ is lower than 1 and sire components are different in purebreds and crossbreds. Second, both sire lines show $r_{pc}$ of approximately the same size for egg number and egg specific gravity traits, indicating that two sire lines may be genetically similar to each other concerning the two traits. Third, that the values of $(g_{11} - g_{22})/g_{11}$ generally deviate from zero indicates also that sire

<table>
<thead>
<tr>
<th>Item</th>
<th>EN1</th>
<th>EN2</th>
<th>EN3</th>
<th>EW1</th>
<th>ESG1</th>
<th>ESG2</th>
</tr>
</thead>
<tbody>
<tr>
<td>$r_{pc}$</td>
<td>.70</td>
<td>.62</td>
<td>.63</td>
<td>.69</td>
<td>.72</td>
<td>.81</td>
</tr>
<tr>
<td>$d^2$</td>
<td>.11</td>
<td>.15</td>
<td>.15</td>
<td>.01</td>
<td>.08</td>
<td>.01</td>
</tr>
<tr>
<td>$[g_{11} - g_{22}]/g_{11}$</td>
<td>.41</td>
<td>.78</td>
<td>.53</td>
<td>.44</td>
<td>.57</td>
<td>.19</td>
</tr>
<tr>
<td>$r_{pc}$</td>
<td>.73</td>
<td>.76</td>
<td>.61</td>
<td>.96</td>
<td>.72</td>
<td>.82</td>
</tr>
<tr>
<td>$d^2$</td>
<td>.10</td>
<td>.20</td>
<td>.18</td>
<td>.02</td>
<td>.11</td>
<td>.05</td>
</tr>
<tr>
<td>$[g_{11} - g_{22}]/g_{11}$</td>
<td>.43</td>
<td>.40</td>
<td>.39</td>
<td>-.20</td>
<td>.29</td>
<td>-.02</td>
</tr>
</tbody>
</table>

---

`a$r_{pc}$ is the genetic correlation between purebred and crossbred performance. $g_{11}$ and $g_{22}$ are the sire components estimated on basis of purebred and crossbred progeny. $d^2$ is the dominance variance expressed as proportion to total variance as estimated by Wei and van der Werf (1993).

`bFor an explanation of trait abbreviations, see the footnotes of Table 2.
Figure 1. Dominance variance expressed as a proportion of total variance (d², denoted by □) and relative difference between sire components of variance for purebreds and crossbreds ([g₁₁ - g₂₂]/g₁₁, denoted by △) plotted against the genetic correlation between purebred and crossbred performance (r_p). g₁₁ and g₂₂ are the sire components of variance in purebreds and crossbreds. Fitted regression lines (P < .05) are shown also.

lines have different gene frequencies from dam line for all traits. Also, for egg weight, (g₁₁ - g₂₂)/g₁₁ has an opposite sign for sire lines 1 and 2, indicating that sire lines 1 and 2 probably have different gene frequencies on this trait.

Due to the fact that purebred and crossbred hens were kept in different environments (i.e., purebred hens were caged singly in a well-controlled environment, whereas crossbred hens were kept in group cages under a commercial condition), estimates of r_p will be confounded with a possible genotype × environment interaction (G × E). Thus, a G × E can be a factor other than dominance variation affecting r_p. It is not possible to distinguish between G × E interaction and changes in covariance structure due to dominance in this data set. This confounding weakens the hypothesis test concerning the relationship between dominance variance and relative genetic parameters. A specific design can help estimate both r_p and G × E interaction (Wei, 1992).

In animal breeding practice, environments in which purebreds and crossbreds are kept are generally different (i.e., a purebred nucleus is often kept in a well-controlled environment and crossbreds under less-controlled commercial conditions). Selection of purebreds to improve crossbred performance in a commercial environment involves not only the true r_p caused by non-additive genetic effects but also a possible G × E interaction if it is significant. In fact, considering crossbred and purebred performance as two traits with a genetic correlation between them, a combined crossbred and purebred selection method (CCPS) proposed by Wei and van der Werf (1994) would not need to distinguish these effects as long as crossbred performance is measured in the same environment for which the breeding goal has been defined.

Wei and van der Werf (1994) have compared the advantage of a combined crossbred and purebred selection with strictly purebred and strictly crossbred selection methods. They found that a combined crossbred and purebred selection is always better than a pure line selection method to achieve crossbred response under current animal crossbreeding schemes. Even with a fixed testing capacity (i.e., number of animals tested are fixed), the combined method is more valuable compared with pure line selection if the r_p is approximately lower than .8. Conversely, the
value of using crossbred information decreases with a low crossbred heritability. For \( r_{pc} \) found in this study for egg number (.56 to .70), the additional genetic gain of CCPS would be at least 10% higher if purebred and crossbred heritabilities would be equal. With the low crossbred heritability found in this study, including crossbred information would give less additional profit. However, because crossbred information is purely additional and does not have to replace purebred information, the CCPS method would always give more genetic response even for a high \( r_{pc} \) value and low \( h_c^2 \) values.

**Implications**

The results tend to agree with theoretical expectation that the traits with larger dominance variance and larger difference between sire components in purebreds and crossbreds show a lower genetic correlation between purebred and crossbred performance. A low crossbred heritability compared with purebred heritability decreases the value of crossbred data for genetic evaluation, but because it was mostly due to a high residual variance, it may be improved by controlling the environment of crossbreds. Given the results, the use of crossbred information jointly with purebred information in selection can bring more genetic progress in crossbreds.

**Literature Cited**


