BREEDING AND GENETICS

Heterosis and DNA Fingerprinting in Chickens

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ABSTRACT

Enhancement of performance in traits of economic importance by use of heterosis (hybrid vigor) is routine in poultry breeding. There is, however, no reliable method to predict the level of heterosis that will occur from the mating of individuals from two populations. DNA fingerprints (DFP) were used as a measure of genetic distance between mating pairs of chickens where each individual of a pair was from a different population; the association between that genetic distance and levels of heterosis in the offspring of those pairs was assessed for juvenile BW and for age at production of first egg. There was an inverse relationship between DFP bandsharing level of parents and heterosis in their offspring, suggesting that DFP may be useful in predicting heterosis.

(Key words: chicken, DNA, heterosis, molecular markers)

MATERIALS AND METHODS

Animals

The parental generations of chickens used in this experiment were from three types of populations: 1) two closed lines of White Plymouth Rocks selected for 32 generations for high (HW) or low (LW) body weight at 8
Table 1. Means ± SEM for BW4, BW8, and AlE for parental lines (in parentheses) and for offspring of F1 sires and HW, LW, F1, or HA dams and regression coefficients ± SE of BW4, BW8, and AlE of offspring on bandsharing between parents

<table>
<thead>
<tr>
<th>Dam type</th>
<th>BW4</th>
<th>BW8</th>
<th>AlE</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>(g)</td>
<td>(d)</td>
<td></td>
</tr>
<tr>
<td>HW</td>
<td>347 ± 13</td>
<td>978 ± 22</td>
<td>163 ± 4</td>
</tr>
<tr>
<td>LW</td>
<td>134 ± 4</td>
<td>351 ± 11</td>
<td>193 ± 4</td>
</tr>
<tr>
<td>F1</td>
<td>231 ± 8</td>
<td>633 ± 20</td>
<td>177 ± 2</td>
</tr>
<tr>
<td>HA</td>
<td>237 ± 7</td>
<td>640 ± 21</td>
<td>168 ± 6</td>
</tr>
</tbody>
</table>

Regression coefficients:
-54 ± 23* for BW4
-151 ± 67* for BW8
35 ± 8** for AlE

1BW4 = BW at 4 wk of age; BW8 = BW at 8 wk of age; AlE = age at production of first egg.
2HW = high body weight line; LW = low body weight line; F1 = LW × HW cross; HA = White Leghorn.
3NM = not measured.
*P £ 0.05.
**P £ 0.01.

wk of age (Liu et al., 1994); 2) the F1 progeny of the cross of those two lines (LW roosters crossed with HW hens); and 3) a line of White Leghorns selected for 15 generations for high antibody (HA) response to sheep erythrocytes (Martin et al., 1990) that served as a tester population to produce an outcross. Of the F1 progeny produced from Lines HW and LW, two males were used to establish two sire families. Each F1 male was mated via artificial insemination to five females of each population (HW, LW, F1, and HA). Chicks were produced in four different hatches at 2-wk intervals. All parents were individually fingerprinted. Individual body weights were obtained at 4 (BW4) and 8 (BW8) wk of age for all progeny (n = 712) and age at production of first egg (AlE) was obtained for pullets (n = 307). This experimental design was used to ensure a range of differences in DNA fingerprinting between dams and sires. It was necessary to produce F1 and backcross progeny in order to enlarge the heterozygosity of DFP bands so they could be correlated with performance data. The HA birds were used as an outcross to a different type of population (layers rather than broilers).

DNA and DFP Preparation

A 1-mL sample of blood was obtained from each parent. Individual blood samples were combined with anticoagulant (Sequester-sol) and immediately cooled on ice. All samples were stored at −80°C until DNA was extracted from individual samples and DFP prepared using probes 33.6 and R18.1 as described by Dunnington et al. (1990).

Data Analysis

Band sharing was calculated as: BS = (2NaDb)/(Na + Nb), where NaDb = number of scored DFP bands common to individuals a and b; Na = total number of DFP bands scored for individual a, and Nb = total number of DFP bands scored for individual b (Jeffreys and Morton, 1987). Calculations and analyses were conducted using the JMP® statistical package (SAS Institute, 1995). When data for both parents were available (BW4 and BW8), heterosis was calculated as the percentage deviation of the full-sib average from the midparent average: [(offspring − midparent)/midparent] × 100. For AlE, only dam performance was available, so the percentage deviation of daughter average from dam value was calculated: [(daughters − dam)/dam] × 100. This deviation included the effects of sire and heterosis combined. However, because there were two sire families as replicates, the percentage deviation represented, in this case, heterotic effects and can be regarded as percentage heterosis. Two types of analyses for association were: 1) regressions of BW4, BW8, and AlE for offspring on BS of those offspring, and 2) regressions of percentage heterosis (for BW) and percentage deviation (for AlE) for offspring on BS between parents of those offspring.

RESULTS AND DISCUSSION

No significant differences due to hatch were found for BW4, BW8, or AlE, therefore, data for the four hatches were pooled. The BS values (± SEM) between dams and sires were 0.50 ± 0.10, 0.59 ± 0.08, 0.55 ± 0.05, and 0.31 ± 0.05 for dam types HW, LW, F1, and HA, respectively. As expected, the average BS between the tester population (HA birds) and the F1 males was lower than the average BS for the parental and F1 populations.

Means of BW4, BW8, and AlE of offspring reflected their varied maternal backgrounds (Table 1). Regressions of offspring BW4 and BW8 on BS of their parents were negative indicating that, as relationships between parents increased, juvenile BW decreased. Regression of offspring AlE on parental bandsharing was positive, again suggesting that closer relationships between parents were associated with poorer performance of their offspring (i.e., delayed age at first egg).

Percentage heterosis (BW4, BW8) and percentage deviation (AlE) were positive (Table 2) and, consistent with the literature (Fairfull, 1990), heterosis was greater for AlE than for body weights. Regression coefficients of the percentage heterosis or percentage deviation on BS
between dams and sires showed that in all cases, performance of the offspring was inversely associated with BS levels between the parents. Body weights, both at 4 and 8 wk of age, were lower for offspring of parents with high BS levels, and A1E of offspring of such parents was higher (i.e., delayed, indicating lower productivity). The same trend occurred when calculating the regressions of percentage heterosis or percentage deviation on BS of parents. These findings illustrate a nonadditive mode of action, as was expected if BS represented genomic similarity.

The results of this experiment showed that on average, juvenile body weights and age at sexual maturity (traits of moderate to high heritability) were superior (in a production sense) when progeny were from parents of relatively distant relationships (lower bandsharing). Age at sexual maturity is a trait that typically shows considerable heterosis, whereas heterosis for juvenile body weight is generally modest at best. Thus, the consistency of results for such different traits suggests that consideration of genomic similarity between individuals based on molecular marker information may have a role in some breeding programs such as recurrent selection, for prescreening of candidates. It should be mentioned that the presented study was done using genetically different populations to produce the crosses. Whether the same is true for individuals from within a pure line or even individuals from closely related lines, remains to be tested.

### REFERENCES


