GENETICS

Heritability and Genetic Correlation Estimates for Performance and Carcass and Body Composition Traits in a Male Broiler Line

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ABSTRACT The current research was conducted to estimate the heritability coefficients and the genetic correlations for performance and carcass and body composition traits in a single sire broiler line. The performance traits analyzed were BW at 38 d, ultrasound records of pectoral muscle depth, feed intake, feed conversion ratio, and BW at 42 d. The carcass traits analyzed were eviscerated BW, breast weight, and leg weight, and the body composition traits analyzed were abdominal fat content, heart weight, gizzard weight, liver weight, and intestine weight. The number of observations varied between 4,120 and 29,040 for each trait. The (co)variance components, heritability, and genetic correlation estimates were obtained by restricted maximum likelihood. The numerator relationship matrix had 42,912 animals. Based on the heritability estimates obtained, the analyzed traits seemed to be able to respond to selection, at variable intensities. The genetic correlation estimates between a great number of performance traits, as well as between a great number of carcass traits, were suggestive of a close genetic relationship between these traits. The genetic correlation estimates between body composition traits were variable. A large genetic association between a great number of performance and carcass traits seemed to exist. The genetic correlation estimates between performance and body composition traits were variable, and important associations between carcass and body composition traits did not seem to exist.

Key words: abdominal fat, animal breeding, broiler, genetic parameter, organ weight

INTRODUCTION

In the last few decades, Brazilian broiler production has made great progress in the industry. This evolution has resulted mostly from the intense selection process realized since the beginning of the use of breed crosses in broilers. However, the intense selection for economic traits induced an increase in fat deposition (Cartwright, 1991; Kessler et al., 2000; Rance et al., 2002) as well as changes in size, shape, and function of various organs (Cartwright, 1991; Rance et al., 2002).

According to Michelan Filho (1986), the abdominal fat pad is one of the main regions of fat deposition in chicken, and it is directly related to total carcass fat (Griffiths et al., 1978; Becker et al., 1981). With the increased demand for lean meat by consumers, it is necessary to direct more attention toward fat content in chicken meat (Kessler et al., 2000). According to Kessler et al. (2000), fat deposition must be discarded, which increases production costs. According to Leenstra and Pit (1988), animal breeding programs should search for ways to reduce carcass lipid content, which may be possible through selection against abdominal fat deposition.

As described by McEntee et al. (2000), the relative value of broiler organ size is decreasing, whereas organ size, especially the heart, may become a limiting factor for broiler development (Lin, 1981). These modifications in organ size suggest the need for these traits to be considered a selection objective in breeding programs. It is important to understand the genetic behavior of these traits and their relationship to other production traits that are used as selection criteria in animal breeding programs. Similarly, it is also necessary to elucidate which of the selection criteria are responsible for the observed decrease in relative organ weights.

Estimation of heritabilities and genetic correlation coefficients for such traits are primordial to the establishment of strategies to be used in animal breeding programs because with the study of these parameters, the evaluation of response to selection for a trait and genetic associations among traits become possible. In agreement with Eler (2001), a constant monitoring of these parameters in a selection program is also required. The objective of the

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present study was to estimate the heritability and the genetic correlation coefficients for performance and carcass and body composition traits in a single male broiler line.

MATERIALS AND METHODS

Data Origin

In the current study, the data of sibs from an elite flock that had undergone selection for development of a sire line were used. The use of carcass information of these sibs comprises a program named sib test, which aids in choosing the best animals during the selection of an elite flock. Pedigree chicks were housed by Agroceres Ross M. G. de Aves S. A. at its installations and were raised as recommended by Agroceres Ross (2000). The control of individual pedigree was made at hatch via banding which contains a number and a corresponding bar code with all necessary information for individual identification.

Data Collecting

Data collected from elite and sib test flocks were BW at 38 d (BW38) and ultrasound records for pectoral muscle depth that were accessed from longitudinal and transversal direction (US1 and US2, respectively). Based on this information, individual birds of the elite flock were submitted to a selection and a feed conversion test; data relative to individual feed intake (FI) and partial feed conversion ratio (FCR) were collected from 5 to 7 wk of age for 14 d.

At 42 d of age, from November 2002 to July 2003, each flock of sibs was transported to the Experimental Processing Plant of the University of São Paulo (Pirassununga, São Paulo, Brazil). The birds were submitted to a minimum of 10 h of feed withdrawal prior to slaughter. After slaughter, the carcasses were stored at 0°C for 24 h postmortem and were deboned. The abdominal fat pad and the viscera were also stored at 0°C and were weighed 24 to 72 h postmortem.

Data collected from the sib test flock were BW at 42 d (BW42), measured at the slaughterhouse, before slaughter; eviscerated BW (EVBW), corresponding to the hot carcass weight, eviscerated, without neck and feet; breast weight (BRST), boneless and without skin; leg weight (LEG), corresponding to thigh plus drumstick with skin and bones; abdominal fat content (AFC), corresponding to abdominal fat pad weight plus gizzard fat weight; heart weight (HRT); gizzard weight (GIZ), full and without the fat adhering; liver weight (LIV); and intestine weight with contents (INT).

The identification of each animal and data collected were automatically recorded using portable terminals and bar code readers. A software program developed by Gaya et al. (2003) was used to collect and weigh the abdominal fat and the viscera.

Statistical Methods

The data were processed at the Animal Breeding Group of the Department of Basic Sciences from the Faculty of Animal Science and Food Engineering, São Paulo University (Pirassununga, São Paulo, Brazil). Extreme values (outliers) were identified through box-plot procedure and were removed from the data set. The descriptive statistics were calculated by PROC MEANS of SAS software (SAS Institute, 1999).

(Co)variance component estimates and genetic parameters were obtained by restricted maximum likelihood using the animal model and MTDFREML software (Boldman et al., 1993). The numerator relationship matrix had 42,912 animals. The mathematical model used in the one-trait analysis was \( y = Xb + Zu + e \), where \( y \) is the dependent variables vector; \( X \) is the fixed effects incidence matrix; \( Z \) is the random effects incidence matrix, associating elements from \( u \) to \( y \); \( b \) is the fixed effects vector; \( Z \) is the random effects incidence matrix, associating elements from \( u \) to \( y \); \( b \) is the fixed effects vector; and \( e \) is the residual effects vector.

The mathematical model used in the 2-trait analysis was

\[
\begin{bmatrix}
  y_1 \\
  y_2
\end{bmatrix} =
\begin{bmatrix}
  X_1 & 0 \\
  0 & X_2
\end{bmatrix} \begin{bmatrix}
  b_1 \\
  b_2
\end{bmatrix} +
\begin{bmatrix}
  Z_1 & 0 \\
  0 & Z_2
\end{bmatrix} \begin{bmatrix}
  a_1 \\
  a_2
\end{bmatrix} +
\begin{bmatrix}
  e_1 \\
  e_2
\end{bmatrix}
\]

where \( y_1 \) and \( y_2 \) represent different traits. The vectors of fixed effects for trait 1 \( (b_1) \) and trait 2 \( (b_2) \) are the same as described in the univariate model. The vectors \( a_1 \) and \( a_2 \) are random additive genetic effects, and \( e_1 \) and \( e_2 \) are residual effects for trait 1 and trait 2, respectively. The incidence matrices \( X_1 \) and \( X_2 \) associate elements of \( b_1 \) and \( b_2 \) with the records in \( y_1 \) and \( y_2 \). The incidence matrices \( Z_1 \) and \( Z_2 \) associate elements of \( a_1 \) and \( a_2 \) with the records in \( y_1 \) and \( y_2 \). The expectation of \( y_1 \) is \( X_1b_1 \), and the expectation of \( y_2 \) is \( X_2b_2 \); the variance-covariance structure of random effects of the bivariate animal model was as follows:

\[
V =
\begin{bmatrix}
  \sigma_{a1}^2 & A\sigma_{a1a2} & 0 & 0 \\
  A\sigma_{a1a2} & \sigma_{a2}^2 & 0 & 0 \\
  0 & 0 & \sigma_{e1}^2 & I\sigma_{e1e2} \\
  0 & 0 & I\sigma_{e1e2} & \sigma_{e2}^2
\end{bmatrix}
\]

where \( \sigma_{a1}^2 \) and \( \sigma_{a2}^2 \) are direct additive genetic variances, \( \sigma_{e1}^2 \) and \( \sigma_{e2}^2 \) are the residual variances for trait 1 and 2, respectively; \( \sigma_{a1a2} \) is the direct genetic covariance between traits 1 and 2, and \( \sigma_{e1e2} \) is their residual covariance. Standard errors for heritabilities were estimated using the delta method and the average information matrix at convergence (Searle et al., 1992).

The fixed effects considered were flock, parents mating group, and sex. The parents mating groups are the flocks from which the parents of each individual originated,
The heritability estimates for traits studied are shown in Table 3. The heritability estimate for BW38 (0.40 ± 0.02) was greater than the heritability estimate for BW42 (0.24 ± 0.03); therefore, detection of genetic variability for BW seems to be more difficult in chicks at 42 d compared with chicks at 38 d of age. Thus, the use of BW38 as a selection criterion seems to be more efficient than the use of BW42. The heritability estimates for BW38 and BW42 were similar to those found by Argentão et al. (2002) and Ledur et al. (1994), respectively, and diverged from those found by Cahaner and Nitsan (1985), Le Bihan-Duval et al. (1998), Mignon-Grasteau et al. (1999), and Rance et al. (2002). The heritability estimates for US1 and US2 were similar to each other (0.29 ± 0.02 and 0.28 ± 0.02, respectively), and the heritability estimate for US1 was similar to that described by Argentão et al. (2002). Therefore, direct selection for US1 or US2 could result in similar intensity of response if these traits were used individually as a selection criterion.

The lowest heritability estimate found was for FCR (0.16 ± 0.03), which was similar to that reported by Leenstra and Pit (1988). Different values for heritability estimates for FCR have been found in other studies (Leenstra and Pit, 1988; Campos and Pereira, 1999; Argentão et al., 2002); however, this trait remains to be an important criterion in selection programs because feed costs represent the greatest expense for broiler production. The heritability estimate for FI (0.20 ± 0.03) was slightly higher than that obtained for FCR, and heritability estimates were not found in the literature for this trait.

The heritability estimates for EVBW and LEG (0.24 ± 0.03 and 0.22 ± 0.03, respectively) were similar to those presented by Argentão et al. (2002), but diverged from those found by Cahaner and Nitsan (1985) and Rance et al. (2002). The heritability estimate for BRST (0.33 ± 0.03) was similar to that described by Singh and Trehan (1994) and was in agreement with the data of Le Bihan-Duval et al. (1998). However, these estimates diverged from those described by Argentão et al. (2002) and Rance et al. (2002). Based on estimated heritability values for BRST, EVBW, and LEG, it appears that direct selection would be effective in improving these traits.

Considerable direct additive genetic effects seemed to exist in the expression of body composition traits based on their heritability estimates. The heritability estimate for AFC was 0.53 ± 0.04, suggesting that this trait would respond to selection. This estimate was similar to those described by Leenstra and Pit (1988) and Rance et al. (2002) and was situated within the range of values observed in the literature for this trait [i.e., from 0.40 ± 0.15 (Leenstra and Pit, 1988) to 0.82 ± 0.28 (Cahaner and Nitsan, 1985)].

The heritability estimate for HRT (0.38 ± 0.04) was similar to that found by Rance et al. (2002). Nevertheless, the heritability estimate for GIZ (0.39 ± 0.04) was different from that described by Cahaner and Nitsan (1985) and Rance et al. (2002). The heritability estimate for INT (0.29 ±

### Table 1. Number of observations (n), observed mean, SD, CV, and minimum (MIN) and maximum (MAX) values of performance and carcass and body composition traits

<table>
<thead>
<tr>
<th>Trait1</th>
<th>n</th>
<th>Mean</th>
<th>SD</th>
<th>CV (%)</th>
<th>MIN</th>
<th>MAX</th>
</tr>
</thead>
<tbody>
<tr>
<td>BW38 (g)</td>
<td>28,755</td>
<td>2,250.75</td>
<td>290.40</td>
<td>12.90</td>
<td>1,450.00</td>
<td>3,030.00</td>
</tr>
<tr>
<td>BW42 (g)</td>
<td>6,155</td>
<td>2,354.44</td>
<td>286.96</td>
<td>12.18</td>
<td>1,540.00</td>
<td>3,186.00</td>
</tr>
<tr>
<td>US1 (mm)</td>
<td>12,284</td>
<td>26.32</td>
<td>2.15</td>
<td>8.18</td>
<td>22.00</td>
<td>31.00</td>
</tr>
<tr>
<td>US2 (mm)</td>
<td>12,048</td>
<td>26.53</td>
<td>2.22</td>
<td>8.37</td>
<td>22.00</td>
<td>31.00</td>
</tr>
<tr>
<td>FI (g)</td>
<td>4,074</td>
<td>2,680.20</td>
<td>455.30</td>
<td>16.98</td>
<td>1,390.00</td>
<td>3,186.00</td>
</tr>
<tr>
<td>FCR</td>
<td>3,189</td>
<td>1.91</td>
<td>0.19</td>
<td>10.28</td>
<td>1.24</td>
<td>2.29</td>
</tr>
<tr>
<td>EVBW (g)</td>
<td>6,156</td>
<td>1,671.56</td>
<td>214.51</td>
<td>12.83</td>
<td>1,078.00</td>
<td>2,294.00</td>
</tr>
<tr>
<td>BRST (g)</td>
<td>6,123</td>
<td>477.74</td>
<td>66.87</td>
<td>13.99</td>
<td>296.00</td>
<td>666.00</td>
</tr>
<tr>
<td>LEG (g)</td>
<td>6,153</td>
<td>553.27</td>
<td>76.45</td>
<td>13.81</td>
<td>352.00</td>
<td>770.00</td>
</tr>
<tr>
<td>AFC (g)</td>
<td>6,089</td>
<td>42.70</td>
<td>10.66</td>
<td>24.98</td>
<td>12.80</td>
<td>72.20</td>
</tr>
<tr>
<td>HRT (g)</td>
<td>6,022</td>
<td>12.15</td>
<td>2.31</td>
<td>19.06</td>
<td>6.40</td>
<td>18.60</td>
</tr>
<tr>
<td>GIZ (g)</td>
<td>5,996</td>
<td>26.50</td>
<td>7.21</td>
<td>27.22</td>
<td>13.00</td>
<td>47.00</td>
</tr>
<tr>
<td>LIV (g)</td>
<td>6,123</td>
<td>477.74</td>
<td>66.87</td>
<td>13.81</td>
<td>352.00</td>
<td>770.00</td>
</tr>
<tr>
<td>INT (g)</td>
<td>6,167</td>
<td>81.16</td>
<td>16.48</td>
<td>20.31</td>
<td>39.40</td>
<td>128.40</td>
</tr>
</tbody>
</table>

1 BW38 = BW at 38 d; BW42 = BW at 42 d; US1 = ultrasound measure of pectoral muscle depth accessed from longitudinal direction; US2 = ultrasound measure of pectoral muscle depth accessed from transversal direction; FI = feed intake; FCR = feed conversion ratio; EVBW = eviscerated BW; BRST = breast weight; LEG = leg weight; AFC = abdominal fat content; HRT = heart weight; GIZ = gizzard weight; LIV = liver weight; INT = intestine weight.
Table 2. Estimates of genetic (in bold on the diagonal, bottom) and environmental (in bold on the diagonal, top) variance components and genetic (below the diagonal) and environmental (above the diagonal) covariance components for performance and carcass and body composition traits obtained by restricted maximum likelihood.

<table>
<thead>
<tr>
<th>Trait</th>
<th>BW38</th>
<th>BW42</th>
<th>US1</th>
<th>US2</th>
<th>FI</th>
<th>FCR</th>
<th>EVBW</th>
<th>BRST</th>
<th>LEG</th>
<th>AFC</th>
<th>HRT</th>
<th>GIZ</th>
<th>LIV</th>
<th>INT</th>
</tr>
</thead>
<tbody>
<tr>
<td>BW38</td>
<td>268.40</td>
<td>3,025.36</td>
<td>12.25</td>
<td>14.59</td>
<td>44.14</td>
<td>0.11</td>
<td>1,934.86</td>
<td>567.51</td>
<td>630.24</td>
<td>63.81</td>
<td>12.10</td>
<td>18.62</td>
<td>45.05</td>
<td>71.52</td>
</tr>
<tr>
<td>BW42</td>
<td>951.01</td>
<td>14,161.39</td>
<td>55.78</td>
<td>70.86</td>
<td>2,455.74</td>
<td>15.07</td>
<td>10,476.16</td>
<td>3,229.00</td>
<td>3,363.66</td>
<td>341.71</td>
<td>67.05</td>
<td>144.20</td>
<td>226.32</td>
<td>440.83</td>
</tr>
<tr>
<td>US1</td>
<td>6.43</td>
<td>18.53</td>
<td>2.11</td>
<td>0.87</td>
<td>1.80</td>
<td>0.48</td>
<td>47.80</td>
<td>18.99</td>
<td>11.92</td>
<td>1.31</td>
<td>0.25</td>
<td>0.74</td>
<td>1.27</td>
<td>1.35</td>
</tr>
<tr>
<td>US2</td>
<td>7.30</td>
<td>18.68</td>
<td>0.91</td>
<td>0.54</td>
<td>1.39</td>
<td>0.01</td>
<td>58.47</td>
<td>23.33</td>
<td>11.92</td>
<td>1.53</td>
<td>0.34</td>
<td>0.86</td>
<td>1.44</td>
<td>1.72</td>
</tr>
<tr>
<td>FI</td>
<td>158.68</td>
<td>1,700.95</td>
<td>-0.73</td>
<td>0.54</td>
<td>895.33</td>
<td>0.17</td>
<td>2,725.74</td>
<td>720.94</td>
<td>648.99</td>
<td>-27.60</td>
<td>30.27</td>
<td>25.60</td>
<td>-0.92</td>
<td>-99.21</td>
</tr>
<tr>
<td>FCR</td>
<td>0.05</td>
<td>1.50</td>
<td>-2.00 × 10^{-3}</td>
<td>-4.00 × 10^{-3}</td>
<td>0.34</td>
<td>4.00 × 10^{-3}</td>
<td>3.73</td>
<td>3.66</td>
<td>3.01</td>
<td>0.70</td>
<td>0.16</td>
<td>0.45</td>
<td>0.40</td>
<td>0.89</td>
</tr>
<tr>
<td>EVBW</td>
<td>1,283.17</td>
<td>3,303.96</td>
<td>19.59</td>
<td>20.63</td>
<td>22.75</td>
<td>1.06</td>
<td>8,420.52</td>
<td>2,589.88</td>
<td>2,615.61</td>
<td>245.65</td>
<td>49.27</td>
<td>105.23</td>
<td>153.17</td>
<td>277.47</td>
</tr>
<tr>
<td>BRST</td>
<td>344.46</td>
<td>678.00</td>
<td>15.16</td>
<td>17.24</td>
<td>736.74</td>
<td>0.15</td>
<td>745.71</td>
<td>533.99</td>
<td>1,087.09</td>
<td>542.37</td>
<td>39.48</td>
<td>20.20</td>
<td>-3.19</td>
<td>11.88</td>
</tr>
<tr>
<td>LEG</td>
<td>442.03</td>
<td>1,315.02</td>
<td>3.67</td>
<td>3.67</td>
<td>380.38</td>
<td>0.15</td>
<td>1,004.24</td>
<td>-96.68</td>
<td>90.38</td>
<td>16.24</td>
<td>35.92</td>
<td>46.39</td>
<td>98.42</td>
<td></td>
</tr>
<tr>
<td>AFC</td>
<td>44.53</td>
<td>115.06</td>
<td>-0.99</td>
<td>-0.87</td>
<td>172.92</td>
<td>0.15</td>
<td>42.03</td>
<td>-17.77</td>
<td>15.64</td>
<td>43.67</td>
<td>16.10</td>
<td>0.19</td>
<td>2.01</td>
<td>2.64</td>
</tr>
<tr>
<td>HRT</td>
<td>9.59</td>
<td>18.71</td>
<td>0.12</td>
<td>0.10</td>
<td>18.95</td>
<td>0.01</td>
<td>8.78</td>
<td>0.92</td>
<td>3.47</td>
<td>0.29</td>
<td>0.98</td>
<td>0.19</td>
<td>2.01</td>
<td>2.64</td>
</tr>
<tr>
<td>GIZ</td>
<td>20.31</td>
<td>56.53</td>
<td>0.57</td>
<td>0.22</td>
<td>1.55</td>
<td>0.03</td>
<td>27.75</td>
<td>7.81</td>
<td>7.79</td>
<td>2.39</td>
<td>-0.08</td>
<td>26.09</td>
<td>16.58</td>
<td>0.75</td>
</tr>
<tr>
<td>LIV</td>
<td>31.62</td>
<td>82.21</td>
<td>-0.03</td>
<td>-0.02</td>
<td>53.24</td>
<td>0.04</td>
<td>46.52</td>
<td>3.11</td>
<td>23.76</td>
<td>1.20</td>
<td>1.33</td>
<td>1.24</td>
<td>23.07</td>
<td>9.33</td>
</tr>
<tr>
<td>INT</td>
<td>55.72</td>
<td>134.31</td>
<td>-1.00</td>
<td>-0.88</td>
<td>177.70</td>
<td>0.09</td>
<td>64.42</td>
<td>-15.76</td>
<td>23.75</td>
<td>12.88</td>
<td>1.42</td>
<td>-3.44</td>
<td>5.81</td>
<td>68.44</td>
</tr>
</tbody>
</table>

1BW38 = BW at 38 d; BW42 = BW at 42 d; US1 = ultrasound measure of pectoral muscle depth accessed from longitudinal direction; US2 = ultrasound measure of pectoral muscle depth accessed from transversal direction; FI = feed intake; FCR = feed conversion ratio; EVBW = eviscerated BW; BRST = breast weight; LEG = leg weight; AFC = abdominal fat content; HRT = heart weight; GIZ = gizzard weight; LIV = liver weight; INT = intestine weight.
Table 3. Estimates of heritabilities (in bold on the diagonal; SE in parenthesis) and genetic correlations (below the diagonal) for performance and carcass and body composition traits obtained by restricted maximum likelihood

<table>
<thead>
<tr>
<th>Trait1</th>
<th>BW38</th>
<th>BW42</th>
<th>US1</th>
<th>US2</th>
<th>FI</th>
<th>FCR</th>
<th>EVBW</th>
<th>BRST</th>
<th>LEG</th>
<th>AFC</th>
<th>HRT</th>
<th>GIZ</th>
<th>LIV</th>
<th>INT</th>
</tr>
</thead>
<tbody>
<tr>
<td>BW38</td>
<td>0.40</td>
<td>0.24</td>
<td>0.50</td>
<td>0.52</td>
<td>0.61</td>
<td>0.07</td>
<td>0.97</td>
<td>0.75</td>
<td>0.93</td>
<td>0.46</td>
<td>0.60</td>
<td>0.35</td>
<td>0.68</td>
<td>0.65</td>
</tr>
<tr>
<td></td>
<td>(0.02)</td>
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1BW38 = BW at 38 d; BW42 = BW at 42 d; US1 = ultrasound measure of pectoral muscle depth accessed from longitudinal direction; US2 = ultrasound measure of pectoral muscle depth accessed from transversal direction; FI = feed intake; FCR = feed conversion ratio; EVBW = eviscerated BW; BRST = breast weight; LEG = leg weight; AFC = abdominal fat content; HRT = heart weight; GIZ = gizzard weight; LIV = liver weight; INT = intestine weight.

0.03) was similar to that found by these same researchers. These traits have not been used as a selection criterion in this sire line; even so, they may be potentially useful if these traits become limiting factors to the physiological integrity of broilers. Thus, direct selection to modify these traits may be efficient, if necessary.

**Genetic Correlation Estimates**

The genetic correlation estimates among and within groups of performance and carcass and body composition traits are presented in Table 3. Traits that represent chicken BW (BW38 and BW42) seemed to be highly genetically associated with carcass traits (EVBW, BRST, and LEG) because the genetic correlation estimates between these traits varied between 0.43 and 0.97, which suggests that the direct selection for BW38 or BW42 could produce indirect genetic gains for EVBW, BRST, and LEG. Similar genetic correlation estimates between these traits were obtained by Cahener and Nitsan (1985), Singh and Trehan (1994), Le Biihan-Duval et al. (1998), Argentão et al. (2002), and Rance et al. (2002).

A genetic association between FCR and EVBW seemed to exist based on the genetic correlation estimates between these traits (0.32; Table 3). The genetic correlation estimates between FCR and BRST (0.10) and between FCR and LEG (0.10) were indications of a low genetic association between these traits; in other words, the direct selection for these carcass traits would have little effect on FCR.

The US1 and US2 measures could be efficient if used as a selection criterion for obtaining heavier BRST, because the genetic correlation estimate between US1 and BRST was 0.64 and that between US2 and BRST was 0.69 (Table 3). Then, there is a possibility of choosing between US1 and US2 as a selection criterion for producing indirect genetic gains for BRST because both traits seem to have a high genetic association with BRST in addition to presenting a similar ability to respond to selection, as discussed previously.

Despite the genetic correlation estimate between BW38 and FCR, which was near zero (0.07), the genetic correlation estimates between BW38 and FI (0.61), between BW42 and FCR (0.35), and between BW42 and FI (0.91; Table 3) were indications of the relationship of direct selection for BW to a higher FCR, at 38 d of age, and to a higher FI, at 38 and 42 d. The difference between genetic correlations for FCR and BW38 or BW42 might have been due to an overestimation of BW38. That trait was measured on the farm, when chickens had a full gastrointestinal tract and were not submitted to the stress of transportation; BW42 was measured at the slaughterhouse after at least 10 h of fasting. These birds were also submitted to stress effects of transportation and lack of water. This difference in weights would certainly affect the FCR. Chickens that had the best FCR and heavier BR38, but had, for example, 150 g of feed in their intestinal tract, would lead to wrong estimations of correlations. At 42 d of age, this problem did not exist.
Heavier individuals, mainly at 38 d of age, also tended to have higher AFC based on the genetic correlation estimates between BW38 and AFC and between BW42 and AFC (0.46 and 0.26, respectively; Table 3). These genetic correlation estimates were similar to those described by Griffiths et al. (1978) and Rance et al. (2002).

Direct selection for BW could directly or indirectly cause higher AFC, supporting the observations of Lin (1981), Leenstra (1986), and Havenstein et al. (1988) that heavier chickens usually have higher FI and FCR and, in turn, deposit a higher amount of fat. Also in agreement with these studies was the genetic correlation estimate between FI and FCR (0.38; Table 3), suggesting that FI seems to be directly related to FCR.

As reported by Leenstra and Pit (1988), AFC seemed to be directly associated with FCR, based on the genetic correlation estimate between AFC and FCR (0.35; Table 3). A high relationship between AFC and FI also seemed to exist, based on the genetic correlation estimate between these traits (0.79). Therefore, a decreasing AFC in broilers could be reached by direct selection for lower FCR. According to Leenstra (1986) and Leenstra and Pit (1987), selection against AFC would generally be related to a better FCR. This unfavorable association of fat and feed efficiency could be related to the deviation of nutrients by the organism to the adipose tissue (Farrel et al., 1982) because according to Lin (1981), fat demands a great amount of energy to be deposited. However, based on the heritability estimates obtained, AFC seemed to have a higher ability to respond to selection than FCR, which suggests that direct selection against AFC would be more efficient in decreasing fat deposition and improving FCR in the line analyzed.

Animals with a higher BW38 tended to present a higher HRT based on the genetic correlation estimate between these traits (0.60; Table 3), which is similar to the results described by Rance et al. (2002). This estimate supports the observation of Rance et al. (2002) that selection with BW as a criterion could increase a broiler’s absolute HRT. A lower genetic association between BW42 and HRT seemed to exist because the genetic correlation estimate between these traits was 0.28.

Direct selection for US1 and US2 as a selection criterion for a lower FCR would do little to affect HRT based on the genetic correlation estimates between US1 and HRT (0.12), US2 and HRT (0.10), and FCR and HRT (0.16; Table 3). The GIZ did not seem to be related to FCR or FI based on the genetic correlation estimates between GIZ and FI (0.03) and between GIZ and FCR (0.12). The LIV seemed to be related directly to FCR and to FI of the individuals studied based on the genetic correlation estimates between LIV and FI (0.73) and between LIV and FCR (0.23).

The genetic correlation estimates between INT and BW38 (0.65) and between INT and BW42 (0.37; Table 3) were suggestive of a genetic association between these traits, similar to the results obtained by Konarzewski et al. (2000) and Rance et al. (2002), and suggested that selection for a higher BW would increase the size and capacity of the gastrointestinal tract of broilers. However, according to Katanbaf et al. (1989), there were no differences between selected and nonselected broiler lines for intestine development. A biochemical approach for those events can be obtained on the studies published by Walker et al. (1981) and Lacy et al. (1987). Genetic association between INT and FI and between INT and FCR also seemed to exist based on the genetic correlation estimates between these traits (0.92 and 0.26, respectively), which indicated that chicks with a higher BW tended to present higher FI and FCR. Then, a higher BW could cause indirectly higher AFC in broilers because INT seemed to be related to FI and FCR, which were genetically associated with AFC, as discussed previously.

The association between INT and AFC also seemed to be direct based on the genetic correlation estimate between these traits (0.36; Table 3). In this manner, chicks with a higher digestive capacity seemed to deposit a higher AFC, which may be caused by a higher capacity for nutrient absorption in these animals (Uni et al., 1995).

The genetic correlation estimate between AFC and HRT was near zero (0.04; Table 3), which indicated that a direct selection against AFC would not cause changes in HRT. The HRT represents a critical point for metabolic disorders that have been observed in broilers (Havenstein et al., 1994).

Direct selection against AFC would not greatly change carcass traits based on the genetic correlation estimates between AFC and EVBW (0.12), AFC and BRST (–0.12), and AFC and LEG (0.13; Table 3). These results differed from the results of Leenstra and Pit (1988), who found that selection for a lower fat deposition would normally be associated with higher carcass yields. Therefore, selection for higher BRST, which represents a great interest for the poultry industry, would have little effect on abdominal fat deposition in broilers, as the magnitude of the genetic correlation was small. The same occurred between the other carcass traits studied (EVWB and LEG) and AFC.

The genetic correlation estimates between HRT and EVBW (0.17), HRT and BRST (0.04), and HRT and LEG (0.15; Table 3) differed from those of Rance et al. (2002) in which an important genetic association was reported. According to Rance et al. (2002), high genetic associations between HRT and the tissues that it supplies would be expected; however, this affirmation was not confirmed by the genetic correlation estimates found between HRT and the carcass traits. Other studies on the evaluation of the importance of HRT in broiler breeding programs are recommended because of the existence of differences between the current research and other reports in the literature regarding the relationship between this organ and carcass traits.

Also, in agreement with McEntee et al. (2000) was the finding that selection for higher protein deposition in broilers could cause a decrease in organ sizes, and according to Lin (1981), any increase in an organ component, in relative terms, would cause a decrease in another. Nevertheless, these affirmations were not confirmed by the genetic correlation estimates between HRT and the carcass traits.

High genetic association between EVBW and BRST and EVBW and LEG seemed to exist based on the genetic corre-
lation estimates between these traits (0.61 and 0.85, respectively). Therefore, direct selection for total carcass weight would increase its parts. A low increase in BRST by direct selection for LEG and vice versa also seems to be possible based on the genetic correlation estimate between BRST and LEG (0.18).

The current study presents several aspects of the impact of selection criteria for performance and carcass traits used in animal breeding programs, especially those that support an increase in protein deposition but caused an unfavorable abdominal fat deposition in the line analyzed. Concerning the relationship between HWT and protein deposition in broilers, there were divergences between literature results and the present study; therefore, further studies are necessary.

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REFERENCES


