HERITABILITY ESTIMATES FOR MEAT QUALITY TRAITS
IN A MALE BROILER LINE


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INTRODUCTION
Brazilian broiler production is the industry that has had a very large progress in the last few decades. In the last five years, broiler production in Brazil grew more than 41%, reaching close to 9.3 million tons in 2005 (Avisite, 2006). It represents 45.3% of the total amount of meat produced in Brazil and close to 12% of the total broiler produced in the world. This evolution, in Brazil and worldwide, resulted not only from number of producers and their size, but mainly due to the intense selection process realized since the beginning of the use of breed crosses in broilers. However, the selection for economic traits might be induced several changes in broiler meat quality (Dransfield and Sosnicki, 1999). According to Sams (1999) and to Solomon et al. (1998), broiler meat quality is influenced by several factors, however, mainly by genetics. According to Campos and Pereira (1999), animal breeding might search for chicken compatible with market exigencies, so, in this context, the estimation of heritabilities for such traits are primordial to the establishment of strategies to be used in breeding programs. With the study of this parameter, the evaluation of response to selection for a trait becomes possible.

In literature, heritability estimates for meat quality traits in chicken were mostly moderate to high, indicating an important genetic factor in the control of these traits. According to Le Bihan-Duval et al. (2001), heritability estimate for pH measured at 15 minutes after slaughter in broiler was 0.49±0.01 and according Le Bihan-Duval et al. (2003) heritability estimate for pH measured at 20 minutes after slaughter in turkey was 0.21±0.04. The heritability estimates found by Le Bihan-Duval et al. (1999 ; 2001 ; 2003) in chicken for pH measured at 24 hours after slaughter were 0.49±0.11, 0.35±0.03 e 0.16±0.04, respectively. They also reported heritability estimates of 0.75±0.08, 0.50±0.03 and 0.12±0.04 for lightness, 0.81±0.04, 0.57±0.02 e 0.21±0.05 for redness and 0.64±0.06, 0.55±0.04 and 0.14±0.04 for yellowness, respectively. According to Le Bihan-Duval et al. (2001), for drip losses in broiler, heritability estimate was 0.39 ± 0.04.

The objective of this study was to estimate the heritability coefficients for meat quality traits in a single male broiler line.

MATERIAL AND METHODS
Data origin and collecting. In the current study the data of sibs from an elite flock which had undergone selection for development of a male line were used. The use of carcass information of these sibs comprises a sib test program, which intends to help in choosing the best animals during the selection of elite flock. At 44 days of age, from May 2005 to December 2005, each flock of sibs was transported to the Experimental Processing Plant of the University of São Paulo, in Pirassununga, Brazil. The birds were submitted to a minimum of 10 hours of feed withdrawal prior to slaughter. After slaughter, the carcasses were stored at 0°C for 24 hours post mortem and deboned. Data collected from sib test flock were: pH, measured at 15 minutes,
6 hours and 24 hours after slaughter (pH15min, pH6 and pH24, respectively); colour
parameters, measured at 24 hours after slaughter using L*, a* and b* scale from CIELab
System; weep, drip and shrink losses of the meat (WL, DL, SL, respectively), given in
percentage; and shear force of the meat (SF). All data were measured in Pectoralis major
muscle. The descriptive statistics for data used in this research is presented at Table 1.

**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, in Pirassununga, Brazil. Extreme values, outliers, were identified through
box-plot procedure and removed from the data set. The descriptive statistics were calculated by
PROC MEANS of SAS software (SAS Institute, 1999). Variance components estimates and
heritabilities estimates were obtained by restricted maximum likelihood method (REML) using
the animal model and the MTDFREML software (Boldman et al., 1993). The numerator
relationship matrix had 107,154 animals. The mathematical model used in the one-trait analysis
was: 
\[ y = Xb + Zu + e, \]
where \( y \) is the dependent variables vector; \( X \) was the fixed effects
incidence matrix, associating elements from \( b \) to \( y \); \( b \) was the fixed effects vector; \( Z \) was the
random effects incidence matrix, associating elements from \( u \) to \( y \); \( u \) was the genetic value
random effects vector, and \( e \) was the residual effects vector. The fixed effect considered for
pH15min, pH24 and b* was flock, for L*, a* and SF were flock and sex, for pH6, WL, DL and
SL were flock, sex and class of dam age at birth. The significance of these effects was
estimated by PROC GLM of SAS software (SAS Institute, 1999), which were significant
\( (P<0.0001) \). The random effect considered was direct additive genetic effect. Standard errors
for heritabilities were estimated using the delta method and the average
information matrix at convergence (Searle et al., 1992).

**RESULTS AND DISCUSSION**
The descriptive statistics for studied traits are presented at Table 1, as so as the heritability
estimates for the traits studied. The heritabilities estimates obtained indicates that there is an
important genetic factor in the expression of mostly of the meat quality traits studied, in
agreement with Le Bihan-Duval et al. (2001 ; 2003), mainly for pH6, pH24 and L*, which
presented the higher estimates. If necessary the selection for improvement of meat quality in
the broiler line studied, the use of pH6, pH24 and L* as selection criteria could result in
satisfactory genetic progress of these traits, which are, therefore, suggested to that purpose. The
traits a*, DL, SL and SF would also be able to respond to selection, but in lower intensity than
pH6, pH24 and L*. The use of pH15min, b* and WL as selection criterion, on the other hand,
is not indicated, since these traits had low heritability estimates, not to being able to respond to
selection sufficiently in the analyzed line. However, the coefficients of variation of b* and WL
were high, so the variability of these traits might facilitate the selection process despite the
heritability values obtained.

The parameters for trait pH15min were similar to those described by Le Bihan-Duval et al.
(2003) and lower than that described by Le Bihan-Duval et al. (2001). For pH24, L* and a* the
heritabilities estimates were higher than those obtained by Le Bihan-Duval et al. (2003) and
lower than those obtained by Le Bihan-Duval et al. (2001) for these traits. The heritability
estimate for DL was lower than that obtained by Le Bihan-Duval et al. (2001). The divergences between the estimates obtained in this study and those found in literature were
maybe due to differences in line or specie studied.
Table 1. Number of observations (N), observed mean (MEAN), standard-deviation (SD), coefficient of variation (CV), minimum (MIN) and maximum (MAX) values, and heritabilities estimates ($h^2$) of the traits studied

<table>
<thead>
<tr>
<th>Trait</th>
<th>N</th>
<th>MEAN</th>
<th>SD</th>
<th>CV (%)</th>
<th>MIN</th>
<th>MAX</th>
<th>$h^2$±s.e.</th>
</tr>
</thead>
<tbody>
<tr>
<td>pH15min</td>
<td>938</td>
<td>6.12</td>
<td>0.18</td>
<td>3.02</td>
<td>5.64</td>
<td>6.62</td>
<td>0.17±0.07</td>
</tr>
<tr>
<td>pH6</td>
<td>932</td>
<td>5.96</td>
<td>0.18</td>
<td>2.94</td>
<td>5.56</td>
<td>6.45</td>
<td>0.34±0.08</td>
</tr>
<tr>
<td>pH24</td>
<td>2,107</td>
<td>5.80</td>
<td>0.13</td>
<td>2.32</td>
<td>5.44</td>
<td>6.20</td>
<td>0.37±0.06</td>
</tr>
<tr>
<td>L*</td>
<td>2,130</td>
<td>56.06</td>
<td>2.97</td>
<td>5.30</td>
<td>47.62</td>
<td>63.98</td>
<td>0.29±0.05</td>
</tr>
<tr>
<td>a*</td>
<td>2,116</td>
<td>5.35</td>
<td>1.10</td>
<td>20.59</td>
<td>2.26</td>
<td>8.54</td>
<td>0.25±0.05</td>
</tr>
<tr>
<td>b*</td>
<td>2,098</td>
<td>13.60</td>
<td>2.12</td>
<td>15.59</td>
<td>7.77</td>
<td>19.20</td>
<td>0.16±0.04</td>
</tr>
<tr>
<td>WL (%)</td>
<td>2,030</td>
<td>2.06</td>
<td>0.58</td>
<td>28.21</td>
<td>0.30</td>
<td>3.70</td>
<td>0.12±0.04</td>
</tr>
<tr>
<td>DL (%)</td>
<td>2,125</td>
<td>6.46</td>
<td>3.22</td>
<td>49.82</td>
<td>0.40</td>
<td>18.30</td>
<td>0.25±0.05</td>
</tr>
<tr>
<td>SL (%)</td>
<td>2,122</td>
<td>21.26</td>
<td>4.17</td>
<td>19.62</td>
<td>8.80</td>
<td>32.60</td>
<td>0.21±0.05</td>
</tr>
<tr>
<td>SF (kgf/g)</td>
<td>2,113</td>
<td>1.21</td>
<td>0.41</td>
<td>33.94</td>
<td>0.30</td>
<td>2.50</td>
<td>0.22±0.04</td>
</tr>
</tbody>
</table>

ApH15min = pH at 15 minutes after slaughter; pH6 = pH at 6 hours after slaughter; pH24 = pH at 24 hours after slaughter; L* = lightness; a* = redness; b* = yellowness; WL = weep losses; DL = drip losses; SL = shrink losses; SF = shear force.

CONCLUSION

This study indicates the existence of genetic factors in the expression of the majority of traits involved in broiler meat quality, mainly for pH6, pH24 and L*. These results also show that the direct selection would be effective in improving these traits. Therefore, these traits could be efficient if used as selection criterion in the broiler breeding program of the analyzed line.

However, further studies, relating the genetic correlation of those traits with growth and ultrasound traits, selection criteria that are being used by the company that owns the program in Brazil, besides studies on genetic trends of these meat quality traits, can point to the program the correct impact that is being observed in that selection population.

REFERENCES


