GENETIC AND PHENOTYPIC PARAMETERS OF GROWTH AND CARCASS
TRAITS OF A MALE LINE OF BROILERS RAISED IN TROPICAL CONDITIONS

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INTRODUCTION
Genetic and phenotypic parameters are essential for genetic improvement programs in any
species, and have to be continuously estimated, preferentially in the same population and
environmental conditions where genetic evaluation is being carried out and are used in the
predictions of breeding values and response to selection in broilers (Ledur et al., 1994). The
broiler industry has to work close to market conditions and trends and genetic improvement
programs will be defined based on benefits that they will cause in the whole production system
or chain, from reproduction to processing plants (Schmidt et al., 1992). Environmental and
market conditions changes are common in broiler industry and genetic improvement programs
and selection tools have to be updated continuously (Yang et al., 1999).
Broiler industry breeding programs and research institutions produced several references to
genetic parameters of traits used (Schmidt et al., 1992; Ledur et al., 1994; Singh and Trehan,
1994; Khan et al., 1994; Kuhlers and Macdaniel, 1996; Le Bihan-Duval et al., 1997; Lopes
and Quaas, 1997; Le Bihan-Duval et al., 1999, Mignon-Grasteau et al., 1999; Yang et al.,
1999).
This research had the objective to estimate genetic parameters of growth and carcass traits of a
selection male line of broilers raised in tropical conditions in Brazil.

MATERIAL AND METHODS
The dataset information came from a male selection line of broilers owned by Agroceres-Ross
Melhoramento Genético de Aves Ltda. and raised in tropical conditions in farm located close
to 22ºS and 48ºW, at altitude around 700 m above sea level.
Growth data came from 27,231 male and female birds submitted to selection and dataset had
information on 5 generations of pedigree, weight at 35 days of age (W35), ultrasound
measurements on breast muscle depth (us1, measured next to middle line, and us2, measured
transversally) and feed conversion (FC).
Carcass data came from 9,463 full sibs of broilers from selection, that were processed at the
experimental slaughterhouse of the Pirassununga Campus of the University of São Paulo.
 Those animals were slaughtered around 42 days of age, from 1999 to 2001 and the traits
measured in this group were live weight at slaughter (LWS), hot carcass weight (HCW),
deboned and skinned chilled breast weight (Breast), and chilled whole leg weight (Legs).
The pedigree dataset had a total of 37,904 animals and all the animals with information were
arranged in contemporary groups, so considered groups born at same week and submitted to
identical environmental conditions.
Statistical analyses. Descriptive statistics were obtained through SAS® procedures and the information was analyzed in single and two traits animal model analysis, by means of REML method, using the software MTDFREML (Boldman et al., 1995) to estimate (co)variance components and genetic parameters for the traits measured. The model considered the fixed effect of contemporary groups and sex, besides the random genetic effects of animals.

RESULTS AND DISCUSSION
Table 1 presents the descriptive statistics for all traits measured.

Table 1. Number of observations (N), mean, minimum (Min.), maximum (Max.), coefficient of variation (C.V.) and standard deviation (s.d.) for growth and carcass traits of broilers

<table>
<thead>
<tr>
<th>Trait</th>
<th>N</th>
<th>Mean</th>
<th>Min.</th>
<th>Max.</th>
<th>C.V. (%)</th>
<th>s.d.</th>
</tr>
</thead>
<tbody>
<tr>
<td>W35, g</td>
<td>24 549</td>
<td>2 434.23</td>
<td>1 100</td>
<td>3 450</td>
<td>11.53</td>
<td>280.74</td>
</tr>
<tr>
<td>Us1, mm</td>
<td>12 259</td>
<td>28.88</td>
<td>16</td>
<td>44</td>
<td>8.67</td>
<td>2.50</td>
</tr>
<tr>
<td>Us2, mm</td>
<td>12 259</td>
<td>29.45</td>
<td>11</td>
<td>49</td>
<td>11.03</td>
<td>3.25</td>
</tr>
<tr>
<td>FC</td>
<td>6 536</td>
<td>1.89</td>
<td>0.95</td>
<td>3.00</td>
<td>13.36</td>
<td>0.25</td>
</tr>
<tr>
<td>LWS, g</td>
<td>9 463</td>
<td>2 487.44</td>
<td>1 236</td>
<td>3 580</td>
<td>13.63</td>
<td>399.08</td>
</tr>
<tr>
<td>HCW, g</td>
<td>9 463</td>
<td>1 738.66</td>
<td>732</td>
<td>2 620</td>
<td>14.14</td>
<td>245.90</td>
</tr>
<tr>
<td>Breast</td>
<td>9 463</td>
<td>484.02</td>
<td>200</td>
<td>780</td>
<td>16.41</td>
<td>79.45</td>
</tr>
<tr>
<td>Legs, g</td>
<td>9 463</td>
<td>594.75</td>
<td>240</td>
<td>940</td>
<td>15.04</td>
<td>89.48</td>
</tr>
</tbody>
</table>

W35 – weight at 35 d ; us1 and us2 – ultrasound measurements of breast depth ; FC – food conversion ; LWS – live weight at slaughter ; HCW – hot carcass weight ; Breast – deboned, skinned and chilled breast weight ; Legs – whole leg weight.

As data came from selected male line of broilers, the information does not represent the average performance of commercial birds raised in similar conditions. Table 2 presents the genetic and phenotypic parameters of traits controlled.

Table 2. Heritability (on diagonal), genetic correlations (above diagonal) and phenotypic correlations (below diagonal) among growth and carcass traits of broilers

<table>
<thead>
<tr>
<th>Trait</th>
<th>W35</th>
<th>us1</th>
<th>us2</th>
<th>FC</th>
<th>LWS</th>
<th>HCW</th>
<th>Breast</th>
<th>Legs</th>
</tr>
</thead>
<tbody>
<tr>
<td>W35</td>
<td>0.45</td>
<td>0.41</td>
<td>0.43</td>
<td>0.24</td>
<td>0.85</td>
<td>-</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>us1</td>
<td>0.53</td>
<td>0.46</td>
<td>0.51</td>
<td>-</td>
<td>0.42</td>
<td>-</td>
<td>0.68</td>
<td>-</td>
</tr>
<tr>
<td>us2</td>
<td>0.56</td>
<td>-</td>
<td>0.51</td>
<td>-</td>
<td>0.43</td>
<td>-</td>
<td>0.67</td>
<td>-</td>
</tr>
<tr>
<td>FC</td>
<td>0.19</td>
<td>-</td>
<td>-</td>
<td>0.22</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>LWS</td>
<td>0.47</td>
<td>0.46</td>
<td>0.46</td>
<td>-</td>
<td>0.33</td>
<td>0.97</td>
<td>0.77</td>
<td>0.87</td>
</tr>
<tr>
<td>HCW</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>0.95</td>
<td>0.34</td>
<td>0.85</td>
<td>0.89</td>
<td>-</td>
</tr>
<tr>
<td>Breast</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>0.83</td>
<td>0.89</td>
<td>0.45</td>
<td>0.59</td>
<td>-</td>
</tr>
<tr>
<td>Legs</td>
<td>-</td>
<td>0.59</td>
<td>0.56</td>
<td>0.89</td>
<td>0.92</td>
<td>0.74</td>
<td>0.34</td>
<td>-</td>
</tr>
</tbody>
</table>

W35 – weight at 35 d ; us1 and us2 – ultrasound measurements of breast depth ; FC – food conversion ; LWS – live weight at slaughter ; HCW – hot carcass weight ; Breast – deboned, skinned and chilled breast weight ; Legs – whole leg weight.
The models used to estimate both genetic and phenotypic parameters achieved convergence criteria without major problems and the results indicate no major data problems that could alter the estimation process.

The analysis of estimates of heritability presented in table 2 indicates that the majority of traits analyzed have enough variation to justify selection and also to expect a significant genetic gain if the population is selected using breeding values. Although birds were raised in tropical conditions, the controlled environment did not affect the estimate of genetic parameters, as the estimates can be compared to several others in literature.

Although heritability for W35 is larger than for LWS, the genetic correlations among LWS and carcass traits are much larger and economic studies should be realized, to identify which one of them are better traits to be used as selection criterion.

Genetic and phenotypic parameters indicate that both breast muscle depth measurements, us1 and us2, have similar genetic variation and correlations with the other traits, indicating that the genes involved in those traits are quite the same and selection should be done based on only one of them. Among all traits, the smaller genetic gain expected is in FC, but the genetic variation for that trait is still available and selection would result in genetic gain, that can be even more important if economic analysis is applied.

Selection can be effective if applied to live weight at slaughter or carcass weight, but will be more efficient when the criterion is LWS, as heritability and genetic correlations indicate. In the case of breast and legs, selection applied to deboned, skinned and chilled breast would cause larger genetic gains.

The analysis of genetic correlations indicate that there are no important antagonism among the traits to be used as selection criteria, however, few genetic correlations are very high. The correlations among ultrasound measurements and breast weight are medium and, as heritabilities of those traits are quite similar, some genetic gain can be achieved if broilers are selected based on one of the ultrasound measurements, that could substitute breast weight as selection criterion.

CONCLUSION

The animal model REML method seemed to be effective to estimate genetic parameters even in data of selected poultry. The growth and carcass traits of the selected male line analyzed can be used as selection criteria, since no important genetic antagonism was observed.

Economic studies should be applied to the traits analyzed, to identify which combination of them would maximize profit. Although the male line studied is a selection line, there is a significant amount of genetic variation to indicate that large genetic gains can be obtained if those traits are used as selection criteria.

As an indicator of carcass merit at slaughter (42 days of age), live weight seemed to be a good and easy to measure selection criterion, that can be widely used, as it has good genetic correlation with the other traits and medium heritability.

ACKNOWLEDGEMENTS

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REFERENCES


