DIVERGENCE OF STRAINS AND STRAIN CROSSES USED TO DEVELOP NEW REFERENCE POPULATIONS FOR QTL STUDIES IN POULTRY

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Abstract
A study was carried out to estimate the divergence of important traits in broilers originated from two experimental lines TT and CC, as well as their crosses, used to generate new reference populations for quantitative trait loci (QTL) studies. Approximately 100 chicks from each genetic group TT, CC, TC and CT were reared as broilers. Body weight (BW41), lung and heart weights were measured at 41d, and blood samples were collected at slaughter to determine the hematocrit values. The genetic groups differed from each other for BW41, which was highly significant for the organs weight. There were significant differences among genetic groups for hematocrit values and for lung weight adjusted for BW41. CC and TT diverged in most of the evaluated traits, indicating that the reference populations created by crossing these lines will be useful for QTL poultry studies. The crosses CT and TC differed significantly for BW41 suggesting that these reciprocal populations can be used for gametic imprinting studies on body weight and other economically important related traits.

Keywords: broiler, reference population, QTL

Introduction
The probability of detecting QTL depends on the amount of linkage disequilibrium between the marker and the QTL. Linkage disequilibrium can be generated by crossing divergent lines. The amount of disequilibrium depends upon genetic differences between lines (van Arendonk et al. 1994). Populations specifically designed for QTL studies have been used in several species. In poultry, six QTL which had influence on growth, body weight, feed intake and carcass traits were detected using a population generated by crossing two different broiler dam lines (van Kaam et al. 1999). To validate known QTL regions and identify additional ones, new reference populations have been created by crossing reciprocally two divergent lines of poultry: a broiler (TT) and a layer line (CC). These new reference populations can also contribute to elucidate differences in gene expression and QTL effects due to differences in weather and management conditions, as well as to allow studies on gametic imprinting. To achieve enough power to detect association between markers and QTL, many animals need to be genotyped and performance tested. To help decide which traits to maintain in evaluation, and whether to keep both reference populations TCxTC and CTxC, a study was carried out to investigate the divergence of particular traits from the strains used to generate the reference populations, as well as their crosses.

Material and Methods
Two experimental lines, TT and CC, were used to create two F1 populations CT and TC. F2 animals have been generated by crossing F1 individuals. Before producing F2 populations, approximately 100 chicks from each of the genetic groups CC, TT, TC and CT were produced by random mating of non-related animals and reared as broilers. Body (BW41), lung (LW) and heart (HW) weights were measured at 41d. A blood sample was taken during slaughter for hematocrit analysis, which is related to the incidence of ascites in broilers. The analysis of variance included genetic group effect for all traits. The BW41 was used as covariate for LW and HW and removed from hematocrit analysis.

Results and Discussion
BW41 differed significantly among genetic groups (Table 1). TT was almost fivefold heavier than CC at 41d. This was expected due to the different specialization of these lines. The phenotypic divergence
between lines is important to trace back the origin of genetic markers from F2 segregating populations, allowing the identification of genomic regions containing QTL. CT was around 380g heavier than its reciprocal TC. This suggests that the female line has more effect on body weight than the male line, which can be due to maternal, cytoplasmic and sex-linked effects, as well as gametic imprinting. This implies that if broiler dam lines are heavily selected for egg production (which is negatively correlated to body weight), they will contribute with significant reduction in their progeny’s body weight.

LW and HW were higher in lines that had higher BW41, being BW41 highly significant for these organs’ weights. When LW and HW were adjusted for BW41, there were significant differences among genetic groups only for LW (Table 1). Hematocrit values differed among genetic groups, but BW41 did not significantly influence such trait. Higher hematocrit values indicate a larger demand of oxygen during the bird’s metabolism, which can led to ascites.

Table 1. Estimated means and standard errors for BW41, LW and HW, and hematocrit values for the different genetic groups.

<table>
<thead>
<tr>
<th>Genetic Groups</th>
<th>BW41(g)</th>
<th>LW(g)</th>
<th>HW(g)</th>
<th>Hematocrit(%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>CC</td>
<td>513.7±37.9</td>
<td>9.63±.54  a</td>
<td>9.19±.41</td>
<td>32.25±.50    a</td>
</tr>
<tr>
<td>TT</td>
<td>2399.0±38.5  b</td>
<td>12.19±.53  c</td>
<td>8.17±.40</td>
<td>33.74±.52    b</td>
</tr>
<tr>
<td>CT</td>
<td>1573.4±38.2  c</td>
<td>10.94±.32  b</td>
<td>8.44±.24</td>
<td>31.40±.52    a</td>
</tr>
<tr>
<td>TC</td>
<td>1193.3±38.2  d</td>
<td>11.39±.33  bc</td>
<td>8.58±.26</td>
<td>32.52±.49    ab</td>
</tr>
<tr>
<td>Mean</td>
<td>1470.25</td>
<td>10.97</td>
<td>8.59</td>
<td>32.12</td>
</tr>
</tbody>
</table>

Means followed by the same letter did not differ significantly (P>.05)

Divergence between CC and TT was found in most of the studied traits suggesting that the reference populations generated by crossing these lines will be useful for QTL studies in poultry. The F1’s TC and CT showed significant differences in BW41, indicating that these reciprocal populations provide good material for gametic imprinting studies on body weight and other related traits. The female genotype seemed to influence progeny’s body weight more than the male genotype.

References