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# Genotype-Environment Interaction in Broilers

## Individual Cage vs. Group housing system

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## ABSTRACT

The effect of housing system on genetic parameters for BW and carcass traits is investigated. Traits were measured on broilers of different ages (48, 63 and 70 d). Birds in groups 48 and 70 d were raised in group housing, whereas birds in the 63 d group were raised in the same housing up to 22 d and in individual cages between 22 and 63 d. Each group consisted of ~2000 individuals from a single group of parents. Carcass, breast meat, and abdominal fat were expressed as percentage of BW. The heritability of BW at 48 d, 63 d, and 70 d was 0.31, 0.26, and 0.19. For carcass traits, heritabilities in the different age groups ranged from 0.41 to 0.58. Genetic correlation between BW at 48 d in individual cage and group housing systems demonstrated a genotype by environment interaction for performance of the birds, which has consequences for design of breeding schemes.

(*Key words*: broiler, genetic correlation, carcass traits, genotype-environment interaction)

## INTRODUCTION

In breeding farms, the birds are evaluated based on their efficiency of production. For such evaluation, birds need to be put into individual cages in order to measure individual feed intake. In commercial farms, however, broilers are kept in group housing systems. In practice, it is assumed that the performance of birds in the cage is an indicator for their performance in the group housing and genotype-environment interaction (G×E) is ignored. However, there is evidence that BW of birds raised in individual cages and in group housing are not the same traits (Tolon and Yalcin, 1997; Van Kaam et al., 1999). There are very few studies on genetic parameter estimation for BW and carcass traits between these environments. The objective of the present study was to estimate genetic parameters for BW and carcass traits at different housing systems to investigate the effect of housing system on genetic parameters.

## MATERIALS AND METHODS

### *Population*

The experimental population was the result of a cross between two genetically different outcross broiler dam lines originating from the White Plymouth Rock breed. After three generation intercrossing, an experiment was conducted on the $F_3$. Measurements were taken from three groups of birds at different ages: 48, 63 and 70 d. There were approximately 2000 individuals in each group of birds. Birds in groups 48 and 70 d were raised in the group housing whereas birds in the 63 d group were raised in the same group housing up to 22 d of age and subsequently housed individually until 63 d. Individual cages were used to enable measurements of individual feed intake. All three groups of birds originated from the same parents, which provide the possibility to estimate genetic correlations between traits measured in different experiments. During the lifetime of the broilers, feed and water were supplied for consumption ad libitum and illumination was 23 h/day. A commercial broiler feed, consisting of crumbled concentrates containing 2,980 Kcal/Kg and 21% protein was used.

### *Traits*

BW and carcass traits were measured on three groups of related birds. In the first group, BW was measured at 48 d ($BW_g48$), in the second group, BW was measured at 48 ($BW_i48$) and 63 days ($BW_i63$), and in the third group, BW was measured at 70 d ($BW_g70$). Birds were slaughtered at 48, 63, and 70 d in the first, second, and third groups respectively. After slaughter, carcass weight was measured on the chilled carcass after removal of feathers, head, lungs, liver, kidneys, gastrointestinal tract and abdominal fat. Carcass (CP), breast meat (BMP), and abdominal fat percentage (AFP) were calculated in relation to live BW. Carcass traits were measured in the 3 days after slaughter. To remove this effect, the data were corrected for day of carcass measurement.

### *Genetic Analyses*

Descriptive statistics, including the test of the normality of the distribution of traits, were obtained from the UNIVARIATE procedure of SAS® (SAS Institute, 1999). An animal model was used to estimate the genetic parameters of carcass-related traits:

$$Y_{ijkl} = \mu + \text{Group}_i + \text{Sex}_j + \text{Day}_k + a_l + e_{ijkl}$$

where $Y_{ijkl}$ is the performance of chicken $l$ in group $i$, of sex $j$ on day $k$; $\text{Group}_i$ is the fixed effect of group ($i$ = 1,2,…,47 for birds in the 48 d group, $i$ = 1,2,…,40 for birds in the 63 d group and $i$ = 1,2,…,42 for birds in the 70 d group); classes were formed based on the age of the dam and the hatching day of the bird; $\text{Sex}_j$ is the fixed effect of sex $j$ ($j$ = 1,2; female or male); $\text{Day}_k$ is the fixed effect of the day $k$ ($k$ = 1,2,3) on which carcass traits were measured after slaughter; $a_l$ is the random direct genetic effect of individual $l$ ; and $e_{ijkl}$ is the random residual effect.The fixed and random effects were identical for all the traits under study. Univariate analyses were used to estimate heritabilities. Bivariate analyses were used to estimate genetic correlations between traits using ASREML software (Gilmour et al., 2000).

## RESULTS AND DISCUSSION

### *Description of Traits*

Descriptive statistics of the traits are summarized in Table1. The average BW and abdominal fat percentages were higher in older birds. The birds weighed around 2,210 g at 48 d, 2,890 g at 63 d, and 3,450 g at 70 d. The average abdominal fat percentage was 2.95% for 48 d birds, 3.26% for 63 d birds, and 4.11% for 70 d birds. The average of other carcass traits hardly changed in different age groups. The effect of group, which was a combination of the age of dam and hatching day of the bird, had a significant effect for all traits. Current results show that the mean values for BW and carcass traits in offspring from groups with older dams were higher than groups with younger dams. Older hens lay larger eggs that hatch into larger chickens and egg weight and hatching weight of chickens are correlated with market weight (Peebles et al., 1999). The effect of sex was significant for all traits at different ages. The mean values for BW and carcass traits were higher in males than in females except for AFP, which was higher in females. The increase in percentage of total body fat and abdominal fat is much higher in females than in males (Edwards et al., 1973; Fisher, 1984; Leenstra, 1986; Le Bihan-Duval et al., 1998). Phenomena such as greater competition between males, different nutritional needs, and greater impact of hormones in females could be involved. The effect of day of measurement ($d_k$) was significant for some traits, i.e. $BMP_g48$, $AFP_g48$, and $CP_g70$. The mean value for these traits was higher on the first day than on the second and third day after slaughter. Extra bleeding and loss of water would influence the weight of carcass parts on day 2 or 3 after slaughter.

### *Effect of Housing System*

Genetic correlations in different housing systems ranged from 0.74 ($CP_g48$-$CP_i63$) to 0.98 ($BW_i48$-$BW_i63$) (Table 2). The genetic correlation between $BW_g48$ and $BW_i63$ (0.79) was lower than genetic correlation between $BW_g48$ and $BW_g70$ (0.92). In addition, genetic correlation between $BW_i48$ and $BW_g48$ (0.80) was lower than genetic correlation between $BW_i48$ and $BW_i63$ (0.98) (figure 1). For carcass traits, genetic correlations followed the same pattern ; for example, the genetic correlation between $CP_g48$ and $CP_i63$ (0.74) was lower than genetic correlation between $CP_g48$ and $CP_g70$ (0.92). The present results revealed that genetic correlations for traits, measured in the same environment, were higher than those measured in different environments. In addition, genetic correlation of BW48 between two different environments (0.8) demonstrated a genotype-environment interaction (G×E) for performance of birds in individual cages and in the group housing system. The methods for estimating the magnitude of G×E, as genetic correlations, have been described by Prabhakaran and Jain (1994) and Mathur and Horst (1994). The genetic correlation of the same traits in different environments is expected to be 1 if there are no interactions. The greater the deviations from 1, the higher are the interactions. These results confirmed earlier findings by Van Kaam et al. (1999) who found a QTL for BW at 48 d of age on birds that were reared in the cage. They found a genetic correlation of 0.60 between BW48 in a cage system and group housing. They concluded that the performance of chickens under different housing conditions is different. Tolon and Yalcin (1997) showed that the husbandry system significantly affected BW at 7 weeks in broilers. In group housing, there could be more competition between chickens. Additionally, chickens housed individually can be stressed due to their limited freedom and also due to change in housing at 3 weeks, when they were switched over to individual housing. One of the important problems in the presence of interaction is that of selection. There are reasons to believe that genetic superiority in one environment may not hold for other environmental conditions, leading to a change in the ranking order of the genotypes in different environments. The interaction effect with respect to body weight would influence the feed efficiency of broilers in breeding farms and commercial farms. In conclusion, there is evidence for a genotype-environment interaction for BW48 in group housing and individual cages. This has consequences for the design of broiler breeding schemes.

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TABLE 1. Means, standard deviations, minimum, and maximum and the result of the analysis of variance of carcass traits measured at 48, 63, and 70 d

| Trait[1] | Number | Mean | SD | Min | Max | Group[2] | Sex[3] | Day[4] |
|---|---|---|---|---|---|---|---|---|
| $BW_g48$ (g) | 1,964 | 2,210 | 335 | 1,220 | 3,023 | *** | 361.8*** | NS |
| $CP_g48$ (%) | 1,963 | 67.42 | 1.83 | 53.87 | 74.76 | *** | 0.43*** | NS |
| $BMP_g48$ (%) | 1,957 | 13.36 | 1.28 | 5.57 | 17.68 | *** | 0.14** | ** |
| $AFP_g48$ (%) | 1,931 | 2.95 | 0.90 | 0.17 | 6.38 | *** | –0.86*** | * |
| $BW_i48$ (g) | 2,080 | 2,190 | 327 | 1,088 | 3,132 | *** | 328.4*** | NS |
| $BW_i63$ (g) | 2,007 | 2,890 | 423 | 1,630 | 4,090 | *** | 501.9*** | NS |
| $CP_i63$ (%) | 1,786 | 67.33 | 1.96 | 54.85 | 75.25 | *** | 1.01*** | NS |
| $BMP_i63$ (%) | 1,784 | 13.31 | 1.33 | 8.32 | 21.47 | *** | 0.2** | NS |
| $AFP_i63$ (%) | 1,759 | 3.26 | 1.12 | 0.22 | 6.82 | *** | –1.26*** | NS |
| $BW_g70$ (g) | 1,913 | 3,450 | 546 | 2,030 | 4,880 | * | 702*** | NS |
| $CP_g70$ (%) | 1,801 | 69.52 | 1.95 | 61.20 | 75.31 | *** | 1.38*** | * |
| $BMP_g70$ (%) | 1,799 | 14.76 | 1.31 | 10.24 | 23.30 | * | 0.56*** | NS |
| $AFP_g70$ (%) | 1,761 | 4.11 | 1.27 | 0.10 | 9.22 | * | –1.48*** | NS |

[1]CP = carcass percentage; BMP = breast meat percentage; AFP = abdominal fat percentage; g = group housing; i = individual cage; and 48, 63, and 70 show the age (in days) at which that trait was measured. [2]Group = combination of the age of dam and the hatching day of the bird; because of large effects of group, only the significance of this effect is shown. [3]In the analysis, the effect of female sex was fixed at zero. [4]Day = the day of carcass traits measurements after slaughter; because of more than 2 effects of day, only the significance of this effect is shown. *$P \leq 0.05$; **$P \leq 0.01$; ***$P \leq 0.001$.

TABLE2. Estimation of genetic correlations with their approximate standard errors (in parentheses) of BW and carcass traits measured in different environments

| Trait[1] | $r_g$ | Trait[1] | $r_g$ | Trait[1] | $r_g$ |
|---|---|---|---|---|---|
| $BW_g48$-$BW_i48$ | 0.80 (0.07) | $CP_g48$-$CP_i63$ | 0.74 (0.10) | $AFP_g48$-$AFP_i63$ | 0.84 (0.06) |
| $BW_g48$-$BW_i63$ | 0.78 (0.08) | $CP_g48$-$CP_g70$ | 0.92 (0.07) | $AFP_g48$-$AFP_g70$ | 0.97 (0.02) |
| $BW_g48$-$BW_g70$ | 0.92 (0.08) | $CP_i63$-$CP_g70$ | 0.83 (0.06) | $AFP_i63$-$AFP_g70$ | 0.96 (0.02) |
| $BW_i48$-$BW_i63$ | 0.98 (0.02) | $BMP_g48$-$BMP_i63$ | 0.89 (0.06) | | |
| $BW_i48$-$BW_g70$ | 0.82 (0.10) | $BMP_g48$-$BMP_g70$ | 0.98 (0.05) | | |
| $BW_i63$-$BW_g70$ | 0.89 (0.07) | $BMP_i63$-$BMP_g70$ | 0.93 (0.05) | | |

[1]CP = carcass percentage; BMP = breast meat percentage; AFP = abdominal fat percentage; g = group housing; i = individual cage; and 48, 63, and 70 show the age (in days) on which that trait was measured.

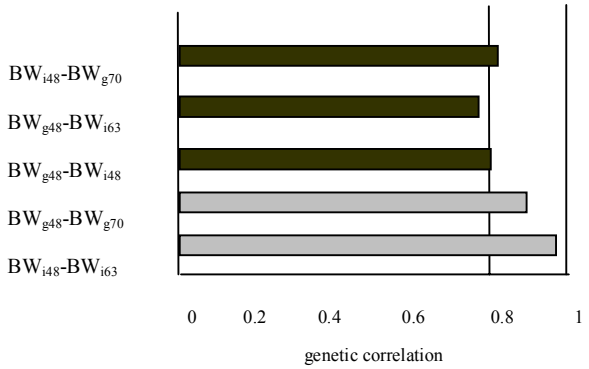


Figure 1. Genetic correlations of BW at different housing systems (g= group housing, i= individual cage. 48, 63, and 70 indicate the age of measurement)