

Genetic interactions involving major genes at the dwarf locus in egg-type chickens

Randolfo William Silvestre Custódio

ABSTRACT

Three egg-type stocks segregating dwarf (dw) and bantam (dw^B) genes in female progeny were produced from the same 18 heterozygous (dw^B/dw) sires used to inseminate dams of three different genotypes: normal (dw^+), dwarf (dw) and bantam (dw^B) dams. The heritability of 8-week body weight estimated from full-sibs of the same phenotype of progeny was 0.40, and that estimated from paternal half-sibs of the same phenotype (dwarf or bantam), and from the same genotype of dam was 0.38. Therefore, maternal and non-additive effects within genotypic classes of dam made little contribution to the genetic variance for 8-week body weight among their progeny. The interaction of sires (S) with genotypes (dw^+ , dw and dw^B) of dam (G) was significant at the 5% level. This indicates that the rankings of the sires within each one of the three genotypes of dam were not the same, probably due to non-additive genetic variation among genotypes of dams. The evidence indicated that in general the genes from individual sires combined differently with each type of dam (G). Those genes which combined well with the genes from normal (dw^+) dams combined poorly with both the genes from the dwarf (dw) and the genes from the bantam (dw^B) dams. The interaction of sires (S) with phenotypes (dwarf and bantam) of progeny (P) was significant at the 10% level. The results indicated a probable gene x genotype interaction for 8-week weight between genes at the dwarf locus (dw and dw^B) and the background genotype (single and/or polygenes). The correlation among paternal half-sibs was influenced more by the S x G than by the S x P interaction, but the effects tended to be cumulative.

INTRODUCTION

Evidence regarding gene x genotype interaction effects (Dickerson, 1962) was presented in chickens by Smith and Fox (1963, 1971), Merat (1959), and with regard to the dwarf locus by Selvarajah *et al.* (1970), Merat (1970), Anthony (1989) and Nir *et al.* (1990), among others. Estimates of correlations can be obtained by using appropriate ratios of variance component estimates and the resultant statistic is called an intra-class correlation coefficient (Snedecor and Cochran, 1969). The notion of intra-class correlations has been developed by several authors (Kempthorne, 1969;

Turner and Young, 1969). Intra-class correlations have been used to calculate genetic parameters (Dickerson, 1969) and the correlation among replicates and repeatability from one test to another in Random Sample Tests (A.R.S., U.S.D.A., 1972). The third bantam allele (dw^B) of the dwarf gene (dw) reported by Custódio and Jaap (1973) in the Z sex-chromosome of the chicken is probably the same sex-linked gene reported by Maw (1935) and Godfrey (1953). Also, this bantam gene (dw^B) may be an allele of the MacDonald dwarf isolate (dw^M) reported by Hsu *et al.* (1975). These dwarfing alleles (dw and dw^B) are suspected to be involved in gene x genotype type interactions with other genes. This question is addressed by using intra-class correlations a) to evaluate genetic variability for 8-week body weight and b) to determine whether

there is a differential interaction of the dw and dw^B gene effects with three sources of background genotypic effects (single and/or polygenes) that control the rate of body growth.

MATERIAL AND METHODS

Three experimental stocks (D4.b, D4.c and D4.d) were produced by mating heterozygous sires (dw^B/dw) to normal (dw^+), dwarf (dw), and bantam (dw^B) dams. The normal (dw^+) dams were strain crosses of White Leghorn commercial layers. The heterozygous sires of both the bantam and dwarf dams came from a 7/8 dw -Leghorn, 1/8 Sebright Bantam flock. From this stock, 18 heterozygous ($k dw^B/k dw$) sires were pedigree-mated to 55 dwarf (dw) and 53 bantam (dw^B) dams from the second backcross generation, together with 49 normal (dw^+) large Leghorn dams to produce, respectively, the experimental stocks D4.b, D4.c and D4.d. Each sire was used to inseminate dams of each of the three genotypes. The average number of normal, dwarf, and bantam dams allocated to each sire was 2.7, 3.0, and 2.9, respectively. In the first hatch there were 1121 chicks with a total of 2280 chicks in two hatches at 2-week intervals. There were 872 and 825 chicks from the dwarf (dw) and bantam (dw^B) dams, respectively. Body weights of females were determined at eight weeks of age. In both hatches individual body weights and shank lengths were recorded at 16 weeks of age for all pullets and these were housed in floor pens. All pullets were transferred from the floor pens to individual cages when those of the second hatch reached 20 weeks of age. At this time the pullets were classified as bantams (dw^B) or dwarfs (dw) on the basis of their 20-week body weight and shank length proportions. The classified bantams had shank lengths equal to or larger than 80 mm, whereas the dwarfs had shanks equal to or shorter than 79 mm. The use of shank length combined with body weight allowed a fairly accurate discrimination between dwarf and bantam phenotypes. Additional information on these stocks was presented by Custódio (in press).

Analysis of variance

The analysis of variance for the 8-week body weight in the experimental stocks which were segregating for dwarf (dw) and bantam (dw^B) genes in female offspring from the same heterozygous sires (dw^B/dw) was carried out using the Least-squares and Maximum Likelihood General Purpose Program (Harvey, 1972). The heterozygous sires and the dams in the bantam (dw^B) and dwarf (dw) groups were considered a

random sample from the 7/8 dw -Leghorn and 1/8 Sebright Bantam population. The normal (dw^+) dams were considered a random sample from a commercial White Leghorn strain. The genotype of dam, hatch, and phenotype of progeny were fixed effects. Therefore, a mixed model with unequal subclass numbers (Harvey, 1970) was appropriate for the analysis of variance. The following hierarchical and cross-classified model represents each observation:

$$Y_{ijklmn} = \mu + s_i + G_j + (sG)_{ij} + d_{ijk} + P_l + (sP)_{il} + (GP)_{jl} + H_m + e_{ijklmn}$$

where Y_{ijklmn} is the 8-week weight of the n th progeny in the m th hatch and l th phenotype belonging to the k th full-sister group of the j th genotype of dam by the i th sire; μ = overall population mean; s_i = effect of the i th sire; G_j = effect of the j th genotype of dam; $(sG)_{ij}$ = effect due to interaction of the i th sire with the j th genotype of dam; d_{ijk} = effect of the k th dam within the j th genotype of dam mated with the i th sire; P_l = effect of the l th phenotype of progeny; $(sP)_{il}$ = effect due to interaction between the i th sire and the l th phenotype of progeny; $(GP)_{jl}$ = effect due to interaction between the j th genotype of dam and the l th phenotype of progeny; H_m = effect common to all individuals in the m th hatch, and e_{ijklmn} = random error characteristic of the n th observation in the m th hatch and l th phenotype belonging to the k th full-sib group of the j th genotype of dam by the i th sire.

The random deviations were assumed to be independent and normally distributed: $e_{ijklmn} \sim N(0, \sigma_e^2)$. There were n_{ijklm} progeny in a given full sib group and the total number of progeny is: $N \dots = \sum_i \sum_j \sum_k \sum_l \sum_m \sum_{n_{ijklm}}$; $i = 1, \dots, s$; $j = 1, \dots, g$; $k = 1, \dots, d_{ij}$; $l = 1 \dots p$ and $m = 1 \dots h$.

The appropriate analysis is basically a split-split plot design (Harvey, 1970). The entire analysis under this model was completed using several separate least-squares analyses which are described by Custódio (1996), where the partitioning of the total variance and formulas for the sums of squares for this analysis in terms of differences in reductions in sums of squares are presented. Also, explanations about procedures needed to obtain correct analysis of variance of mixed models with unbalanced data is shown by Custódio and Macedônio (1995), who presented an example with simulated data. The components of variance and quadratic for the fixed effects that are expected in the mean squares are shown in Table I. The coefficients of the variance components were obtained by method 3 of Henderson (1953).

Table I - Sources of variation, degrees of freedom (d.f.), and expected mean squares of the analysis of variance.

Sources of variation	d.f.	Expectation of mean squares
Sires (S)	s-1	$\sigma_e^2 + k_{12} \sigma_{d:sG}^2 + k_{13} \sigma_{sP}^2 + k_{14} \sigma_{sG}^2 + k_{15} \sigma_s^2$
Genotypes of dam (G)	g-1	$\sigma_e^2 + k_9 \sigma_{d:sG}^2 + k_{10} \sigma_{sG}^2 + k_{11} \delta_G^2$
S x G ^{a/}	a-s-g+1	$\sigma_e^2 + k_7 \sigma_{d:sG}^2 + k_8 \sigma_{sG}^2$
D:SG ^{b/}	b-a	$\sigma_e^2 + k_6 \sigma_{d:sG}^2$
Phenotype (P)	p-1	$\sigma_e^2 + k_4 \sigma_{sP}^2 + k_5 \delta_P^2$
S x P ^{c/}	c-s-p+1	$\sigma_e^2 + k_3 \sigma_{sP}^2$
G x P ^{d/}	d-g-p+1	$\sigma_e^2 + k_2 \delta_{GP}^2$
Hatches (H)	h-1	$\sigma_e^2 + k_1 \delta_H^2$
Remainder	N-t	σ_e^2

^{a/}Number of SG subclasses filled = a; ^{b/}number of DSG subclasses filled = b; ^{c/}number of SP subclasses filled = c; ^{d/}number of GP subclasses filled = d; ^{t/}sum of the d.f. for all effects, including μ .

Intra-class correlations among sibs

Four types of intra-class correlation among full-sisters and among paternal half-sisters were calculated for the progeny of heterozygous sires (dw^B/dw) mated to normal (dw^+), dwarf (dw), and bantam (dw^B) dams. The interpretations of the intra-class correlations were assumed as explained in the following:

a. Intra-class correlation among full-sibs (of the same phenotype). It is assumed that the intra-class correlation among bantam full-sibs is the same as that among dwarf full-sibs. This correlation indicates how the resemblance among full-sibs is influenced by the genetic and environmental variations. The smaller the environmental component, the larger will be the resemblance among the sibs. The intra-class correlation between full-sibs from the same phenotype is the largest correlation possible. This correlation will be the same as that between full-sibs of different phenotypes if the interaction variance component σ_{sP}^2 for each is equal to zero. In other words, the interaction between sires and phenotypes of progeny decreases the intra-class correlation among full-sibs of different phenotypes.

b. Intra-class correlation among full-sibs (of different phenotypes). This correlation measures the correlation among full-sibs of different phenotypes, i.e., dwarf and bantam. Because the interaction between sires and the dwarf phenotype is assumed to be independent from the interaction between sires and the bantam phenotype, the variance of the $(sP)_{il}$ effects does

not contribute to the covariance between the performance of different phenotypes. If the S x P interaction exists, the correlation among full-sibs of different phenotypes (ρ_2) is smaller than the correlation among full-sibs of the same phenotype (ρ_1). These coefficients will be identical if σ_{sP}^2 is zero. Therefore, the difference between the correlation among full-sibs of the same phenotype and that between full-sibs of different phenotypes indicates the relative importance of the sire by phenotype of progeny interaction (S x P). The magnitude of the difference between ρ_1 and ρ_2 is indicative of the extent to which common sires rank the same from one phenotype to the other within the same genotypic class of dam.

c. Intra-class correlation among paternal half-sibs (of the same phenotype and from the same genotype of dam). This is the largest possible correlation between paternal half-sibs. This correlation

coefficient was used for two purposes. First, it provides an estimate of the amount of additive genetic variance existent in the population. In the numerator of this intra-class correlation, the sum of the components $\sigma_s^2 + \sigma_{sP}^2 + \sigma_{sG}^2$ is equal to the variance component for paternal half-sib groups within the P x G subclasses, when the σ_{sPG}^2 three factor interaction is non-existent. The variance component between sires contains one-fourth of the total additive genetic variance of the population ($1/4 \sigma_A^2$). The sum of the variance components in the denominator of the intra-class correlation (ρ_3) equals the total phenotypic variation of the progeny within each genotypic class of dam, averaged over the three classes of dams. Consequently, this intra-class correlation, when multiplied by four, is an estimate of the proportion of the additive genetic variance in a population where the same genotype of dam and phenotype of offspring are present. Since the sires were mated to dams belonging to different genetic groups than the sires, this intra-class correlation is not a true measure of the genetic variation in the population whence the sires came. The second use of this intra-class correlation was in connection with the importance of the combined effects of the S x P and S x G interactions on the ranking of individual sires by the performance of their progeny.

d. Intra-class correlation among paternal half-sibs (of the same phenotype and from different genotypes of dam). Because the interaction between sires and each of the genotypes of dam are assumed to

be independent, the variance of the $(sG)_{ij}$ effects does not contribute to the covariance between the performance of half-sibs from the same phenotype and from different genotypes of the dam. If there is an $S \times G$ interaction, the correlation among half-sibs of different genotypes of dam (ρ_4) will be smaller than the correlation among half-sibs of the same genotype of dam (ρ_3). These coefficients will be identical if σ_{sp}^2 is zero. Consequently, if σ_{sp}^2 is not zero, the difference between the correlation among half-sibs from the same genotype of dam and that among half-sibs of different genotypes of dam indicates the relative importance of the sire by genotype of dam interaction (σ_{sG}^2). The magnitude of the difference $\hat{\rho}_4 - \hat{\rho}_3$ is indicative of the extent to which common sires rank the same from one genotype of dam to another when the ranking is averaged over the two phenotypes of progeny.

e. Intra-class correlation among paternal half-sibs (of different phenotypes and from different genotypes of dam). The interaction between sires and each of the genotypes of dam $(sG)_{ij}$, as well as the interaction between sires and each of the phenotypes of progeny are assumed to be independent. Therefore, neither the variance of the $(sG)_{ij}$ nor the variance of the $(sP)_{ij}$ effects contribute to the covariance between the performance of half-sibs from different phenotypes and from different genotypes of dam. If both effects, $(sG)_{ij}$ and $(sP)_{ij}$, are different from zero, ρ_5 will be smaller than either the correlation among half-sibs of the same phenotype, ρ_4 , or the correlation among half-sibs of the same phenotype and of the same genotype of dam, ρ_3 . All these three coefficients (ρ_3 , ρ_4 , and ρ_5) will be identical if both σ_{sp}^2 and σ_{sG}^2 are zero. Consequently, if both σ_{sp}^2 and σ_{sG}^2 are different from zero, the difference between the correlation among half-sibs from the same phenotype and from the same genotype of dam (ρ_3) and that among half-sibs of different phenotypes and from different genotypes of dam (ρ_5) indicates the relative importance of the combined effects of the $S \times G$ and $S \times P$ interactions.

RESULTS AND DISCUSSION

In the least-squares analysis of variance (ANOVA) of the 8-week body weight of female progeny from normal (dw^+), dwarf (dw), and bantam (dw^B) dams (stocks D4.b, D4.c, and D4.d), the sire (S) source of variation was highly significant ($P < 0.01$) (Table II). This indicates that there were statistically significant differences in the weight at eight weeks between progenies of the same phenotype and from the same genotype

of dam. The G effect was significant at the 5% level. The difference between weight at eight weeks of age of the progeny from the bantam (dw^B) and from the dwarf (dw) dams was equal to 17.8 g. This difference was equivalent to 3.9% the average body weight of bantams (456.7 g). The difference between the weight at eight weeks of the progeny from the normal (dw^+) and the bantam (dw^B) dams was 15.5 g, 3.4% more than the average 8-week weight of bantam females from the normal dams. The largest difference in weight between progenies of the three different genotypes of dam was between the progenies from the normal (dw^+) and the dwarf (dw) dams (33.3 g, or 7.3% more than the bantam daughters of the normal dams). Proudfoot and Hulan (1987) also reported that body weights of progeny from normal dams were significantly higher than those of dwarf hens. On the other hand, Marks (1983) found no differences in 8-week body weight for female progeny from normal and dwarf dams mated to normal males.

Maternal effects

Since the dwarf and the bantam dams were daughters from the same heterozygous sires (dw^B/dw) and the same bantam dams, they should have, on average, an equal sample of genes for rate of growth. Therefore, the differences of growth to 8-weeks of age observed in progenies from the bantam and dwarf dams cannot be explained entirely by differences in the rate of growth of their dams. However, the highly significant differences among egg weights of normal, bantam and dwarf dams (56.8 ± 0.5 g, 53.6 ± 0.4 g and 48.5 ± 0.5 g, respectively) could have contributed to the

Table II - Least-squares analysis of variance for 8-week body weight of progeny from heterozygous sires (dw^B/dw), mated to normal (dw^+), bantam (dw^B), and dwarf (dw) dams.

Source of variation	d.f.	Mean squares	ANOVA line number	F-test ratio with line
Sires (S)	17	21173.4838**	1	1/4
Genotypes of dam (G)	2	61683.1717*	2	2/3
$S \times G$	34	13274.2413*	3	3/4
D:SG	82	7681.7958**	4	4/9
Phenotype (P)	1	970352.6908**	5	5/6
$S \times P$	17	7374.0826 ^{a/}	6	6/9
$G \times P$	2	8010.4469	7	7/9
Hatches (H)	1	76054.0734**	8	8/9
Remainder	597	4702.4370	9	-

d.f. = Degrees of freedom; ^{a/}statistically significant ($P < 0.10$); *statistically significant ($P < 0.05$); **statistically significant ($P < 0.01$); $\hat{k}_3 = 17.1987$; $\hat{k}_6 = 4.7648$; $\hat{k}_7 = 6.1188$; $\hat{k}_8 = 12.7302$; $\hat{k}_{12} = 6.8310$; $\hat{k}_{13} = 21.5920$; $\hat{k}_{14} = 15.2951$; $\hat{k}_{15} = 41.3419$ (see Table I).

observed differences in body weight. Environmental maternal effects due to average differences in egg size among the three genotypes of dam could cause different rates of growth among the progeny of normal, dwarf, and bantam dams. The postulate of Mohammadian and Jaap (1972) that dw^+/dw broiler-type sons were smaller at 8 weeks of age because of their smaller egg size of their dw dams was corroborated by Khan *et al.* (1973). The regression of rate of growth of progeny on dam egg weight is larger than in crosses (Merrit and Gowe, 1965; Khan *et al.*, 1973). As the broiler-type female progeny weight reported by Khan *et al.* was 1.6 kg, the expected increase of 8.6 g in 8-week body weight is equivalent to 0.5% of the average female weight. Converting this 0.5% figure in grams, the 8-week body weight of the progenies from the normal, dwarf and bantam dams would be expected to increase by 2.1 g for each 1 g increase in egg weight of their dams. The percentage of the difference in rate of body growth between the progenies of the normal and the bantam dams, between the normal and the dwarf dams, and between the bantam and the dwarf dams, which could be explained by differences in egg weight of the dams, are 43%, 52%, and 60%, respectively. These results imply that at least part of the difference in rate of growth between the progeny of different genotypes of dam could be explained by maternal effects due to egg size. The remaining part of the difference in growth rate among the progeny of the normal, bantam or dwarf dams could be due to differences in the additive genetic composition of the dams.

Gene effects

The difference between the rate of growth of the bantam females (dw^B) and their dwarf (dw) sisters was 80.5 g (444.8-364.3 g) and highly significant ($P < 0.01$). The percent reduction in body weight attributable to the dwarf gene was 18%. This figure is smaller than that presented by Mohammadian (1971) for the 8-week body weight of dwarfs in relation to normal Leghorn pullets (26.5%) and for 9-week body weight in Plymouth Rock females (37.4%) reported by Knizetova (1993). Also, a smaller difference between the rate of growth of bantams and dwarfs than between dwarfs and normals would be expected if the bantam and the dwarf gene were alleles (Custódio and Jaap, 1973). The observed reduction is probably due to the presence of the dw^B allele instead of the normal allele, plus the effects due to the smaller size and slower growth.

Mohammadian (1971) indicated that the reduction in 8-week body weight of larger dwarf Leghorn pullets was lower than the reduction in smaller dwarf

Leghorns reported by Bernier and Arscott (1960) and by Merat (1970). These results are in line with those of Reddy and Siegel (1977) who reported that the effect of dwarfism was more severe in a low weight line compared with a higher weight line. Therefore, the effects of the dwarf allele seem to diminish in larger pullets and this could account for the discrepancy between the published results. These effects seem to fall in the category of gene \times genome or background genotype interactions involving the dwarf gene and major and/or poligenes. Several characters influenced by the dwarf gene are modified by the background genome. For instance, significant genotype \times line interactions were found for egg shell and yolk traits (Anthony, 1989 and Anthony *et al.*, 1989), several embryo traits (Nir *et al.*, 1990), whole body protein turnover (Muramatsu *et al.*, 1990) and antibody titres (Mauldwin *et al.*, 1981).

Genetic variance

In a comparison of sire and dam components of variance in the hierarchical mating system, Thomas *et al.* (1958) and Siegel (1962) indicated that maternal effects are important in the early growth rate of chickens. In our case, the variation among individual dams within the SG subclasses (D:SG) was highly significant ($P < 0.01$), and the dam component of variance was slightly larger than the sire component (9% larger). Since the heritability estimated from full-sibs was slightly larger than that from paternal half-sibs (0.40 vs. 0.38) it seems that both maternal and non-additive effects within genotypic classes of dam were relatively small.

The mean heritability estimates obtained by Mohammadian for both sexes from normal and dwarf sires were 0.57 and 0.68, respectively. Khan (1972) has found that the heritability estimates for 8-week body weight from full-sib variance components in broiler-type birds were higher for the dwarfs (0.39 ± 0.05) than for the normals (0.27 ± 0.05). Marks (1995) found evidence that, under high energy diets, dwarfs showed a higher genetic variation than normal chickens. For Marks (1983), however the heritability estimates observed in dwarfs was smaller than in normals. Whether the additive genetic variance in bantams is larger or smaller than that from dwarfs could not be verified in our experiments.

Correlations

Variance components, obtained in this study by equating mean squares with their expectations, were

used to calculate intra-class correlations (Table III). The intra-class correlation among paternal half-sibs of the same phenotype and belonging to the same genotype of dam (Table III) yields an estimate of heritability for 8-week body weight of 0.38. This estimate of heritability for 8-week body weight is in the range of those that have been reported for White Leghorn chickens (Kinney Jr., 1969).

G x P interaction

Interactions of this kind seem to have been found for other traits when comparing dwarf and non-dwarf chickens (Anthony *et al.*, 1989, Nir *et al.*, 1990, Muramatsu, 1990 and Mauldwin *et al.*, 1981). In the present paper, however, the G x P effects were not significantly different (Table II).

S x G interaction

The interaction between sires (S) and genotypes of dam (G) was significant at the 5% level (Table II). Robertson (1959) has shown that an interaction can be significant either because the genetic correlation between performances in different environments is less than one, or because the genetic variance for the trait varies among environments, or both. The S x G interaction indicates that in general, the genes from individual sires which combined well with the genes from individual normal dams (dw^+) combined poorly with those coming from dwarf (dw) and bantam (dw^B) dams. These specific interaction effects of the individual crosses were larger than those due to the S x P interaction effects. The observed differences, $\hat{\rho}_3 - \hat{\rho}_4 = \hat{\rho}_6 - \hat{\rho}_5 = 0.063$ (Table III), indicate that the σ_{sG}^2 component diminishes the intra-class correlation among the progeny of different genotypes of dam. Therefore, the S x G interaction may influence the ranking of sires by the average 8-week body weight of their progeny, and these would vary across genotypic classes of dams. Differences in rankings of means of sires may then be manifestations of the S x G interaction, which is related to non-genetic variance among dam genotypes.

S x P interaction

The interaction (S x P) between sires (S) and phenotypes of progeny (P) was significant at the 10% level (Table II). The observed difference between the intra-class correlation coefficients: $\hat{\rho}_1 - \hat{\rho}_2 = \hat{\rho}_3 - \hat{\rho}_6 =$

Table III - Intra-class correlations among sibs descending from heterozygous sires (dw^B/dw), and from normal (dw^+), dwarf (dw) and bantam (dw^B) dams, and variance components.

Genetic groups to which the sibs belong	Intra-class correlation	
	Full-sibs	Paternal half-sibs
Same phenotype and same genotype of dam	$\hat{\rho}_1 = 0.202$	$\hat{\rho}_3 = 0.096$
Different phenotypes and same genotype of dams	$\hat{\rho}_2 = 0.176$	$\hat{\rho}_6 = 0.070$
Same phenotype and different genotypes of dam	-	$\hat{\rho}_4 = 0.033$
Different phenotypes and different genotypes of dam	-	$\hat{\rho}_5 = 0.007$

Variance components: $\hat{\sigma}_s^2 = 39.0$; $\hat{\sigma}_{sG}^2 = 372.8$; $\hat{\sigma}_{d:sG}^2 = 625.3$; $\hat{\sigma}_{sP}^2 = 155.3$; $\hat{\sigma}_e^2 = 4702.4$.

$\hat{\rho}_4 - \hat{\rho}_5 = 0.026$ (Table III) indicates that the σ_{sP}^2 component diminishes the intra-class correlation among paternal half-sibs of different phenotypes. The S x P interaction affected the rankings of sires. The difference between the intra-class correlations, 0.063 and 0.026, indicates that the correlation among the paternal half-sibs was influenced more by the S x G interaction than by the S x P interaction. The percent reduction in full sibs of different phenotypes (dw and dw^B) compared with those of the same phenotype (dw or dw^B) was 13%, when both kinds of full-sibs came from the same genotype of dam. However, comparing similar intra-class correlations ($\hat{\rho}_4$) with progenies of different genotypes of dam ($\hat{\rho}_3$) resulted in a reduction of 66% in half-sibs. This observation is in agreement with the significance observed for S x P ($P < 0.05$) in the analysis of variance. The observed differences, $\hat{\rho}_3 - \hat{\rho}_5 = 0.089$, indicate how the correlation between paternal half-sibs is affected by the cumulative action of the σ_{sP}^2 and σ_{sG}^2 interaction components.

It seems evident that two kinds of genetic interactions were found (S x G and S x P). The S x G interaction, which showed to be higher than the S x P, indicates heterosis mainly due to dominance or epistasis among genes of the sires and genes from the dams. However, the S x P interaction may indicate that genes (major or poligenes) from the sires are lightly interacting with genes at the dw locus (dw and dw^B). This adds more information to the literature regarding interactions of single genes with the residual genotype or environment in chickens which were presented by Merat (1959), Smith and Fox (1963, 1971) and Merat (1970). More recently, it was shown for traits other than 8-week body weight, that the influence of the dwarf gene can be modified by the background genotype (Mauldwin *et al.*, 1981; Anthony *et al.*, 1989; Muramatsu *et al.*, 1990; Nir *et al.*, 1990). The effects of variation in the background or residual genotype on the expression of differences between the effects of alleles at a locus

(epistasis) usually are considered under the heading of gene x genotype interaction (Dickerson, 1962). It is clear, however, that the statistical detection of a gene x genotype interaction does not specify whether or not it has any biological importance (Robertson, 1959).

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RESUMO

Três plantéis segregando os genes dwarf (dw) e bantam (dw^B) em progênie fêmea foram produzidos a partir de galos heterozigotos. Galinhas de genótipos normal (dw⁺), dwarf (dw) e bantam (dw^B) foram inseminadas artificialmente com galos dw^B/dw. Herdabilidades do peso juvenil foram obtidas a partir de coeficientes de correlação intra-classe entre irmãos germanos e meios irmãos paternos. A herdabilidade estimada de irmãos germanos de mesmo fenótipo (dw, ou dw^B) foi igual a 0,40. A herdabilidade do peso juvenil estimada de meios irmãos paternos do mesmo fenótipo e do mesmo genótipo de mãe foi igual a 0,38. Portanto, foi pequena a contribuição de efeitos maternos e não aditivos dentro de classes genóticas de mães, para a variância genética do peso juvenil na população. As interações de galos (S) com genótipos (G) de mãe (dw⁺, dw e dw^B) e com fenótipos (dwarf e bantam) da progênie (P) foram significativas aos níveis de 5% (P < 0,05) e 10% (P < 0,10), respectivamente. As evidências indicam que, em geral, os genes que combinaram bem com os genes de mães normais (dw⁺) combinaram mal com os de mães dwarf (dw) e bantam (dw^B). As correlações entre meios irmãos paternos foram mais influenciadas pela interação S x G, mas os efeitos tenderam a ser cumulativos. Os resultados indicam a existência de interações do tipo gene-genótipo para peso juvenil em galinhas poedeiras, envolvendo alelos do gene dwarf (dw) ligado ao sexo.

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