Egypt Poult. Sci. Vol (26) (IV): (1487-1496)

HETEROSIS FROM LINE CROSSES OF TWO SELECTED LINES OF JAPANESE QUAIL:
I- GENETIC VARIANCE COMPONENTS

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Received: **10/8/2006** Accepted: **13/11/2006**

Abstract: *The statistical methods for estimating the variance components based on examination of* F_2 *and backcrosses of a cross between two selected lines of Japanese quail (one was selected for increase egg production and the other was selected for high 6-wk body weight) were used for some productive traits. The aim was to understand the genetic basis of the studied traits. Insignificant additive genetic variances* (σ^2A) *were estimated being 0.0026, 0.2358, 1.7432, 2.0882, 2.066, 4.271, 0.3424 and 0.0032 for body weights at hatch (W0), 2 weeks (W2), 4 weeks (W4), 6 weeks of age (W6), body gain from 2-6 weeks of age (BG2-6), body weight at sexual maturity* (BW_{SM})*, age at sexual maturity (ASM) and egg weight (EW), respectively. Significant additive genetic variances 0.5175 and 59.6 were estimated for egg number (EN) and total egg mass (EM) at the 1st 90 d of production, respectively. The dominance genetic variances* (σ^2d) *for all the studied traits appear to be larger than additive ones. Significant dominance genetic variances (27.8092, 19.0929 and 36.0387) were found for W2, BG2-6 and ASM, respectively. Otherwise, the significant epistatic relations such as additive x additive type of epistatic variances (* σ^2i *) were 0.246 and 16.803 for W0 and BG2-6, respectively. While the significant additive x dominance gene interaction variances* (σ^2j) *were 1.7972, 2.9184, 2.7015 and 88.1 for W4, W6, BG2-6 and EM, respectively. Also, the significant dominance x dominance gene interaction variances (0.067, 44.5755, 2.435, 110.902 and 0.0822) were estimated for W0, W4, W6, body weight at sexual maturity and EW, respectively. These results suggest that selection would be effective for both egg number and total egg mass, and crossing would be effective for improving the rest of the studied traits.*

INTRODUCTION

Partitioning the genetic variance for economic traits into additive, dominance and epistatic components and attempting to determine the relative contribution of different kinds of genes to these components has become a primary focus for poultry research. Numerous studies have documented that crossing among divergently selected lines of the same breed may result in greater non-additive genetic variance for both body weight and egg number traits (Barbato and Vasilotos-Younken, 1991; Ranz *et al*., 2004). Others found that the additive nature of genetic variation had resulted improvement of body weight in Japanese Quail (Nestor *etal*., 1982; Marks, 1990). Although, Lerner (1958) reported that long-term selection scheme reduces the amount of additive variation and increases the proportion of non-additive genetic variation. Ledur *et al*. (2002) found that non-additive, environmental and phenotypic variances increased with age advancing for all traits. Kinghorn (1983) concluded that only additive x additive epistatic interaction would provide an adequate general description of epistatic variance. Hagger *et al*. (1986) and Fairfull *et al*. (1987) found significant additive x dominance effects for different traits in laying hens. Cockerham (1954) and Goodnight (1988) reported that additive x additive epistatic variance can contribute to selection responses by its conversion to additive genetic variance. The frequent lack of response to selection for certain performance traits in two lines of Japanese quail under long-term of selection had led to alternative methods of breeding to exploit both additive and non-additive genetic variations. The original generation means procedures proposed by (Hayman, 1958; Jinks and Jones, 1958) were used in this paper to estimate the components of generation means. So, this experiment has involved crosses between two long-term selected lines of Japanese quail, F_2 and backcrosses to understand the genetic architecture of some economic traits.

MATERIALS AND METHODES

The experimental data were collected at the Nucleus Breeding Quail Farm, Poultry Research Center, Faculty of Agriculture, Alexandria University, Egypt. The parental lines of Japanese quail utilized in this experiment derived from long-term selection (>22 generations). The parental line P_1 was established by selection for increase egg number at 90 d of production, whereas the parental line P_2 was established by selection for high 6-wk body weight.

***Experimental Design and Management*:** Reciprocal crosses were done between the two parental lines (P_1 and P_2) to produce F_1 hybrids. Then intercrossing was conducted using F_1 offspring to form F_2 generation. Backcrosses were conducted to each parent using the males of F_2 generation to form backcrosses (Bc_1 and Bc_2). Such method allowed to estimate the components of variance from the means of the parents, F_1, F_2, Bc_1 and Bc_2 generations. Five hatches per generation were obtained. Management conditions were mainly similar as possible throughout the experiment. The chicks were fed *ad libitum* a starter ration contained 28 % CP with 2819 Kcal ME/Kg of feed up to 2 weeks of age and grower ration 26 % CP with 3213 Kcal ME/Kg. of feed thereafter up to 6 weeks. During the production period a ration contained 21 % CP and 2609 Kcal ME/Kg. of food was used.

Measurements and Analysis**:** The measured traits included some growth traits, body weight g at hatch (W0); at 2 wk of age (W2); 4 wk of age (W4); at 6 wk of age (W6); body gain from 2 to 6 wk of age, g (BG2-6) and egg production traits, age at sexual maturity, d (ASM); body weight at sexual maturity, g (BW_{SM}); number of eggs at 1st 90 d of production (EN); egg weight (EW) and total egg mass, g (EM) throughout the same period. The data were first analyzed using SAS software (SAS Institute, 1997). The genetic analysis started by scaling tests to test the null hypothesis of no epistatic effects (Mather, 1949; Hayman and Mather, 1955). Under the null hypothesis a model of Hayman (1958) was used to describe the components of generation means and variances. When epistasis was absent a model comprising three parameter was used to estimate the components of generation means and variances (Jinks and Jones, 1958).

RESULTS AND DISCUSSION

Phenotypic Analysis: The phenotypic variances have demonstrated the presence of genetic variability among generations for a number of the traits studied. Data presented in Table 1 reflected that F_1 generation have much larger variances than F_2 generation in all studied traits. Moreover, P_1 had the highest variances among generations for W0, ASM, EN, EW and EM, while P_2 variances were the highest among generation variances for W2, W6 and BW_{SM}. In addition, most estimates of backcross variances showed superiority when compared with F_2 variances. Such results may fit the hypothesis that parental epistasis was present. The same result was reported by Sheridan (1986). Also, F_1 variance for BG2-6 (1.654) was the highest among generation variances for this trait. A possible explanation for these results that interaction between and within loci may be responsible for the genetic variability among generations. The same findings were reported by Melchinger (1987); Lynch and Walsh (1998); Adams *et al.* (2003); Gibson *et al.* (2004) and Ranz *et al.* (2004).

Genetic Analysis: It is notable that, adequate scales were found for W0, W4, W6, BG2-6, BW_{SM}, EN, EW and EM traits. Such results indicate that epistasis would be common in the inheritance of these traits. This conclusion agreed with findings of Whitlock *et al.* (1995); Cheverud (2000) and Carlborg and Haley (2004). Contrarily, W2 and ASM showed in adequate scales, what ruling out the presence of epistatic effects for these traits. Data presented in Table 2 reflected negative estimates of additive (*A*) and dominance (*d*) effects for W0, W6, BW_{SM} and EW. Such results could be due to the fact that the variance of non-segregating generation (F1) was larger than that the segregating one (F_2). The same finding was confirmed by Hoffman *et al.* (1993). Former results agreed with those listed in Table 3 which showed insignificant additive ($\sigma^2 A$) and dominance ($\sigma^2 d$) variance components for the previous traits. Moreover, low estimates of heritability h^2 (0.01, 0.02, 0.02 and 0.01), and low ratio of dominance to additive variances $\sigma^2 d$ / $\sigma^2 A$ (3.2, 3.3, 3.3 and 2.9) for W0, W6, BW_{SM} and EW traits were shown in Table 3. On the bases of the above results it could be concluded that epistasis effects were controlling the inheritance of these traits. The same conclusion was stated by Melchinger (1987).

Estimated additive x additive (*i*) epistatic effects seemed to be small in the three traits of W6, BW_{SM} and EW (-34.7, -35.4 and -1.8) compared with dominance x dominance (*l*) epistatic effects (18.3, 28.2 and 1.3, respectively). While the estimates of additive x dominance (*j*) epistatic effects were 16.0, 1.3 and -0.25 in the same manner. The components of variance did not deviate from the previous results.It was noticed from Table 3 that significant differences were observed for dominance x dominance epistatic mean square $\sigma^2 l$ (2.435, 110.902 and 0.082) for W6, BW_{SM} and EW traits, and insignificant differences in additive x dominance $\sigma^2 j$ for BW_{SM} and EW traits (6.589 and 0.528). These results disagreed with those reported by Kinghorn (1983); Hagger *et al.* (1986) and Fairfull *et al.* (1987). While $\sigma^2 j$ had highly significant differences in W6 (2.918). However, this result confirmed by Hagger *et al.* (1986) and Fairfull *et al.* (1987) who found significant additive x dominance effects in laying hens for different traits. Negative estimates of *A*, *d*, *j* and *l* epistatic effects (-0.087, -0.188, -0.017 and -1.325) were observed for body weight at hatch, (Table 2) while the estimated *i* epistatic effects (0.622) indicated that additive x additive epistatic interaction may provide an adequate description of genetic variations of this trait. The same finding was reported by Kinghorn (1983). Also, the components of variance presented in Table 3, showed highly significant differences for both $\sigma^2 i$ and $\sigma^2 l$ epistatic mean squares (0.246 and 0.067). The low estimates of $\sigma^2 d$ / $\sigma^2 A$ ratio and h^2 (3.2 and 0.01) indicated that non-allelic interaction was the major source of variations in W0.

Large positive dominance effects are common in both W2 and ASM (45.09 and 61.38), and highly significant differences due to $\sigma^2 d$, and insignificant differences due to $\sigma^2 A$ were shown in Table 2. Moreover, the high estimates of $\sigma^2 d$ / $\sigma^2 A$ ratio (10.9 and 10.3) and low estimates of h^2

(0.01 and 0.01 Table 3) indicated that dominance effects were more important in the inheritance of these traits. These results agree with that reported by Lerner (1958). The estimates of *A* components were positively higher than *d* effects for both W4 and EM (0.89 and 45.5). Although, it seemed to be very small when compared with *j* effects (15.63 and 84.94). Also, the estimated *l* epistatic effects were 14.69 and 47.1 in the same trend. The estimates of the components of genetic variance for W4 showed insignificant differences of σ^2A, σ^2d and σ^2i (Table 3). On the contrary, highly significant differences for σ^2j and significant differences for σ^2l were found. These results reflected that epistatic effects were controlling the inheritance of this trait. The same finding was reported by Lamkey *et al.* (1995). The highly significant differences additive and additive x dominance mean squares for EM trait (59.6 and 88.1). Moreover, the low estimates of h^2 (0.02) and σ^2d / σ^2A ratio (3.2) indicated that EM trait would be widely affected by both epistatic and environmental factors. Regarding BG2-6, it was noticed from Table 2 that negative estimates of *A* and *l* were found (-0.19 and -328.84, respectively). While positive estimates (141.18, 138.06 and 7.92) were observed for *d*, *i* and *j* epistatic effects, respectively. The results presented in Table 3 showed insignificant estimates of σ^2A and σ^2l for BG2-6 trait. While σ^2d, σ^2i and σ^2j epistatic variances showed highly significant differences in the same trait. These results indicate that non-additive genetic variations would explained the genetic variance in this trait. Concerning EN, in contrary, additive effects (5.9) was the major component among generation means. Also, highly significant differences for σ^2A compared with insignificant differences for the remaining components of genetic variance indicate that σ^2A was more important in the inheritance of EN trait. This result was confirmed by Goodnight (1988); Willis and Orr (1993); Cheverud and Routman (1995) who found that additive variance can increase if there was epistasis.

CONCLUSION

In general, the relatively significant additive components of genetic variance for both egg number and total egg mass suggest that selection would be effective for these traits. Non-additive types of genetic variability were large in magnitude for the other traits studied indicating that dominance and epistatic variances were the most important types of genetic variance. Thus, crossing would be effective for improving these traits.

Table (1): Variance ± SEM of generations from a cross between two selected lines of Japanese Quail

Traits	Generations					
	P_1	P_2	F_1	F_2	Bc_1	Bc_2
W0	.003±.05	.002±.05	.002±.04	.0009±.03	.001±.04	.001±.04
W2	.379±.62	.563±.75	.228±.48	.156±.39	.183±.43	.247±.49
W4	.698±.84	1.548±1.21	3.397±1.84	.544±.74	.485±.69	.773±.88
W6	1.26±1.1	2.061±1.4	1.849±1.4	.764±.87	.757±.87	1.331±1.2
BG2-6	1.11±1.1	1.428±1.2	1.654±1.3	.534±.73	.747±.86	1.319±1.2
BW_{SM}	3.89±1.9	5.378±2.3	2.204±1.5	1.529±1.2	2.065±1.4	2.206±1.5
ASM	.732±.86	.638±.79	.497±.71	.160±.40	.299±.55	.317±.56
EN	.639±.79	.369±.61	.471±.69	.155±.39	.296±.54	.221±.47
EW	.005±.09	.004±.06	.003±.06	.0006±.02	.002±.04	.001±.04
EM	73.9±8.6	40.1±6.3	64.4±8.0	18.4±4.3	33.9±5.8	25.7±5.1

SEM = (MS / number of observations $)^{0.5}$ **,** W0 = Body weight at hatch, W2 = Body weight at 2 weeks of age, W4 = Body weight at 4 weeks of age, W6 = Body weight at 6 weeks of age, BG2-6 = Body gain from 2 to 6 weeks of age, BW_{SM})= Body weight at sexual maturity, ASM = Age at sexual maturity, EN = Egg number at 1st 90 d. of laying, EW = Egg weight, EM = Egg mass, P_1 = Parental line 1, P_2 = Parental line 2, F_1 = F_1 crosses, F_2 = Second generation, Bc_1 = Backcross 1, Bc_2 = Backcross 2.

Table (2): Components of generations means from a cross between two selected lines of Japanese Quail

Traits	Components					
	(*A*)	(*d*)	(*i*)	(*j*)	(*l*)	(*m*)
W0	-0.087	-0.188	0.622	-0.017	-1.325	7.32
W2	-4.16	45.09	-	-	-	54.57
W4	0.89	-24.045	-28.46	15.63	14.69	111.21
W6	-0.29	-31.34	-34.74	16.04	18.28	171.82
BG2-6	-0.19	141.18	138.06	7.92	-328.84	121.15
BW_{SM}	-2.66	-20.69	-35.44	1.3	28.22	216.38
ASM	-3.085	61.38	0-	-	-	61.52
EN	5.9	-5.3	-5.0	-13.4	-1.4	26.3
EW	-0.35	-1.065	-1.82	-0.25	1.33	11.03
EM	54.5	-82.45	-98.12	84.94	27.1	289.07

(*m*) = general mean, (*A*) = Additive effects, (*d*) = Dominance effects, (*i*) = Additive x Additive, (*j*) = Additive x Dominance, (*l*) = Dominance x Dominance, types of epistasis.

Table (3): Variance components from a cross between two selected lines of Japanese Quail

Traits	Variance Components						
	$(\sigma^2 A)$	$(\sigma^2 d)$	$(\sigma^2 i)$	$(\sigma^2 j)$	$(\sigma^2 l)$	$(\sigma^2 d/\sigma^2 A)$	h^2
W0	0.0026^{NS}	0.0274^{NS}	0.246^{**}	0.0039^{NS}	0.067^{**}	3.2	0.01
W2	0.2358^{NS}	27.8092^{**}	-	-	-	10.9	0.01
W4	1.7432^{NS}	17.6682^{NS}	13.73^{NS}	1.7972^{**}	44.5755^{*}	3.2	0.02
W6	2.0882^{NS}	23.259^{NS}	20.58^{NS}	2.9184^{**}	2.435^{*}	3.3	0.02
BG2-6	2.066^{NS}	19.0929^{**}	16.803^{**}	2.7015^{**}	50.753^{NS}	3.0	0.02
BW_{SM}	4.271^{NS}	46.081^{NS}	41.55^{NS}	6.5896^{NS}	110.902^{**}	3.3	0.02
ASM	0.3424^{NS}	36.0387^{**}	-	-	-	10.3	0.01
EN	0.5175^{**}	5.280^{NS}	4.556^{NS}	0.7698^{NS}	13.6613^{NS}	3.2	0.02
EW	0.0032^{NS}	0.02746	0.022^{NS}	0.528^{NS}	0.0822^{**}	2.9	0.01
EM	59.6^{**}	625.7^{NS}	532.8^{NS}	88.1^{**}	1619.6^{NS}	3.2	0.02

$(\sigma^2 A)$ = additive mean square, $(\sigma^2 d)$ = dominance mean square, $(\sigma^2 i)$ = additive x additive mean square, $(\sigma^2 j)$ = additive x dominace mean square, $(\sigma^2 l)$ = dominance x dominance mean square, h^2 = heritability estimates, Ns = in significant differences, * = significant differences, ** = highly significant differences.

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الملخص العربي

قوة الهجين الناتجة عن الخلط بين خطان منتخبان من السمان الياباني:

١- مكونات التباين الوراثي

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استخدم في هذه الدراسة بعض الطرق الإحصائية الخاصة بتقدير مكونات التباين الوراثي علي أساس بيانات الجيل الثاني والهجن الرجعية للخليط الناتج من تزاوج خطين منتخبين من السمان الياباني الخط الأول منتخب لتحسين إنتاج البيض والخط الثاني منتخب لزيادة وزن الجسم عند عمر ٦ أسابيع وذلك بهدف تفهم طرق توريث بعض الصفات الاقتصادية من جيل إلي جيل كي يسهل

وضع برامج تربية ملائمة لها. ولقد أوضحت النتائج أن التباين الوراثي التجمعي كان غير معنوي بالنسبة لصفات أوزان الجسم عند الفقس ، ٢ ، ٤ ، ٦ أسابيع من العمر و الزيادة في الوزن من عمر ٢ إلي ٦ أسابيع ، وزن الجسم عند النضج الجنسي، العمر عند النضج الجنسي و متوسط وزن البيضة. في حين كان التباين الوراثي التجمعي معنويا في صفتي عدد البيض وكتلة البيض.

كما أوضحت النتائج أن قيم التباين الراجع إلي تأثير السيادة كان أعلي من مثيله الراجع لتأثير العوامل الوراثية المضيفة وذلك في جميع الصفات المدروسة. حيث كان التباين الراجع لتأثير عوامل السيادة معنويا بالنسبة لصفات وزن الجسم عند عمر أسبوعين ، الزيادة في الوزن من عمر ٢ إلي ٦ أسابيع و العمر عند النضج الجنسي.

ومن جهة أخري أوضحت النتائج أن التباين الراجع إلي تأثير التفوق من نوع مضيف x مضيف كان معنويا بالنسبة لصفتي وزن الجسم عند الفقس و الزيادة في الوزن من عمر ٢ إلي ٦ أسابيع وكان التباين الراجع لتأثير التفوق من نوع مضيف x سيادة معنويا بالنسبة لصفات أوزان الجسم عند عمري ٤ و٦ أسابيع ، الزيادة في الوزن من عمر ٢ إلي ٦ أسابيع و كتلة البيض. أيضا كان التباين الراجع لتأثير التفوق من نوع سيادة x سيادة معنويا بالنسبة لصفات أوزان الجسم عند الفقس ، عند عمر ٤ أسابيع ، عند عمر ٦ أسابيع ، وزن الجسم عند النضج الجنسي و متوسط وزن البيضة.

وعموما يمكن القول أن الانتخاب قد يكون فعالا في تحسين صفتي عدد البيض وكتلة البيض في حين أن الخلط قد يكون فعالا في تحسين باقي الصفات المدروسة.