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Genetic Parameters of Some Productive and Reproductive Traits in Japanese Quail

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ABSTRACT. Dam variance components were higher than those of the sire for body weight (BW) at all ages studied. The same trend was observed for absolute daily gain (ADG) during different growth periods studied except during the period from 4 to 6 weeks of age, since a reverse trend was observed.

Heritability estimates for BW recorded at different ages were moderate to high (0.29 to 0.88) and the h_D^2 was higher than h_S^2. Similar trend was observed for ADG during the different growth periods studied except that from 4 to 6 weeks of age since a reverse trend was observed (0.46 vs 0.11). Heritability for average hatch weight per hen (AHW) was (.79) and (.05) for egg production during the first week and the seventh week (EP1 and EP7) while it was (0.81) for egg production during the first 70 days.

BWs recorded at different ages were positively phenotypically and genetically correlated with each other and the magnitude increased with advance of age. BWs recorded at different ages were negatively phenotypically correlated with HAT%.

BWs were positively genetically correlated with EP1 while a negative phenotypical correlation was observed between BW and EP1 and EP70.

Introduction

The advantage of Japanese Quail production compared with chickens has been summarized by Wilson *et al.* (1961) and discussed by Lepore and Marks (1971); Sefton and Siegel (1974) and others. However, it seems desirable to examine in more details the potentialities of this bird for meat and egg production and to produce additional quantitative information on the suitability of Coturnis as a meat and egg production bird.

The present study was carried out to estimate the genetic parameters of different meat and egg production traits in a flock of Japanese Quail.

Materials and Methods

A total number of 2110 Japanese Quail produced during three consecutive generations was included in the study (Table 1). The system of generating the three generations is shown schematically in Fig. 1. A complete description of management, feeding and breeding practices used was given by El-Fiky (1991).

TABLE 1. Number of sire groups and their offspring used to study growth, carcass, reproductive and egg production traits during three generations.

Generation	Group I				Group II			
	Parents		Offspring		Parents		Offspring	
	S	D	M	F	S	D	M	F
1st	15	30	58	61	60	120	121	242
2nd	29	58	88	86	53	106	103	211
3rd	30	60	84	96	49	98	98	196
Total	74	148	230	243	162	324	324	649

S, D, M and F are sires, dams, males and females, respectively.

Growth performance was assessed through studying individual weekly body weight (BW) from hatch (BW0) until 6 weeks of age (BW6) as well as individual biweekly absolute daily gain (ADG) from hatch to 6 weeks of age. Carcass quality was evaluated through estimating dressing percentage (D%) and the chemical analysis of the meat to estimate protein (P), fat (F) and moisture (M) percentages. Egg production performance was assessed through estimating age at first egg (AFE), fertility (FER) and hatchability (HAT) percentages, egg production during the first week (EP1), the seventh week (EP7) and the first 70 days (EP70) as well as the average hatch weight per hen (AHW).

Prior to statistical analysis, measurements taken as percentages were transformed using arc sin transformation according to Winer (1971).

Body weight, absolute daily gain and carcass traits were analyzed by fitting the following mixed model (Model type 5 of Harvey, 1987) :

$$Y_{ijklm} = \mu + G_i + S_{ij} + D_{ijk} + SX_l + (GSX)_{il} + e_{ejklm}$$

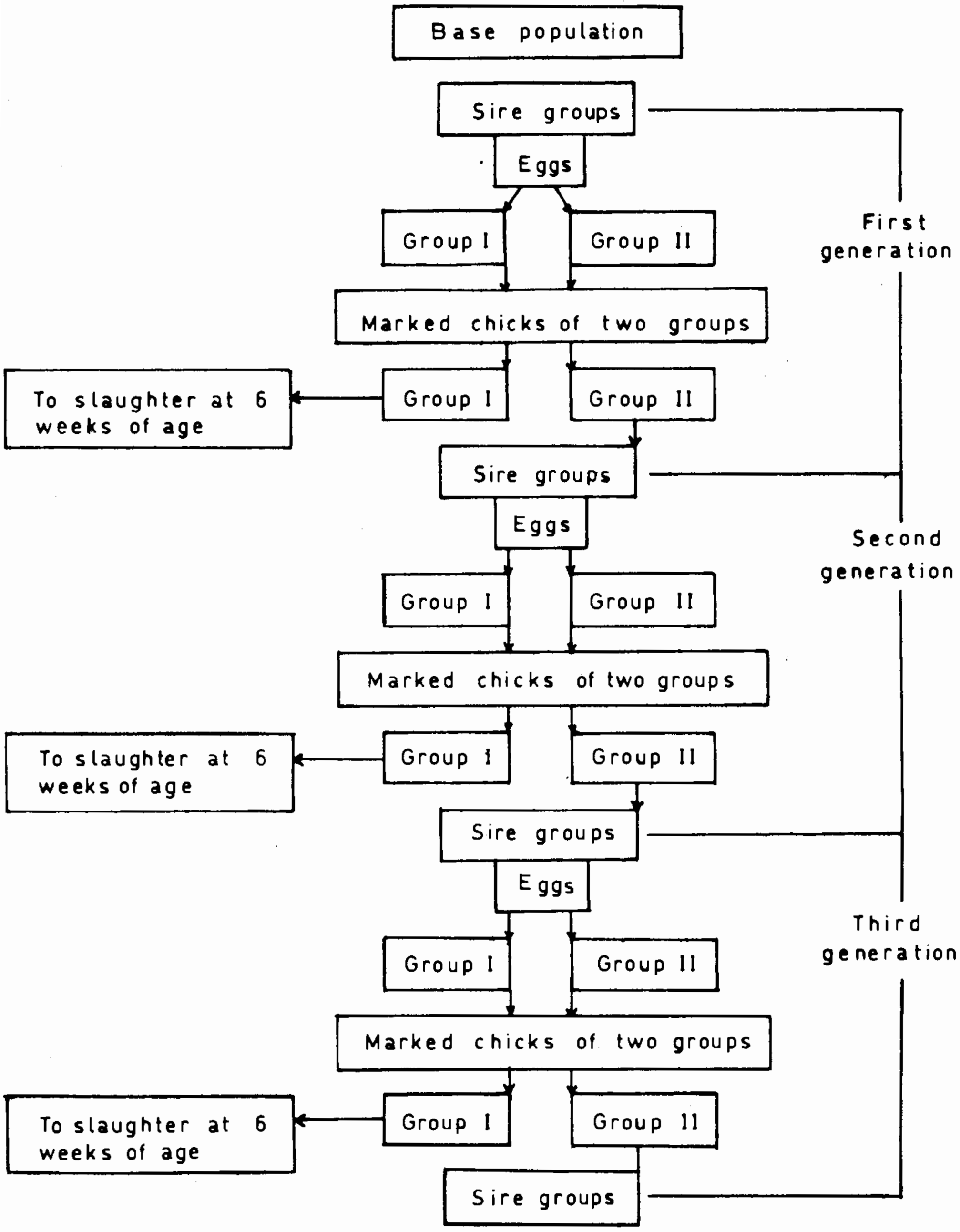

FIG. 1. Schematic illustration of breeding scheme for producing the three generation.

where : Y_{ijklm} = the observation on ijklmth bird; μ = overall mean, common element to all observations; G_i = fixed effect of ith generation; S_{ij} = random effect of jth sire nested within the fixed effect of ith generation; D_{ijk} = random effect of kth dam nested within the random effect of jth sire within the fixed effect of ith generation; SX_l = fixed effect of lth sex; $(GSX)_{il}$ = fixed effect of interaction of ith generation and lth sex; and e_{ijklm} = a random deviation of mth bird of kth dam and jth sire within ith generation. It includes all the other effect not specified in the model.

The assumption reported by Harvey (1970 & 1979) has been imposed. Estimates of the sire, dam within sire and remainder components of variance for each trait and covariances between any two traits were derived by equating mean squares and mean cross-products to their expectations and solving the resulting set of simultaneous equations (Harvey, 1970). The sire's and dam's variance and covariance components were weighted by the average progeny group size (k's) calculated as Becker (1975), and Harvey (1979). Heritability was estimated for growth and carcass traits by paternal and maternal half-sib and full-sib correlations according to Falconer (1983). The standard errors of the estimates were calculated according to Swiger *et al.* (1964) and Becker (1975). The genetic and environmental interpretation of the causal components of variance and covariance were given by Kempthorne (1955), Becker (1975) and Falconer (1983).

Age at first egg (AFE), fertility (FER), hatchability (HAT), average hatch weight (AHW) per hen, first 70 days egg production (EP70), and first and seventh week egg production (EP1 & EP7) were analyzed by fitting the following mixed model (Harvey, 1987).

$$Y_{ijkl} = \mu + G_i + S_{ij} + H_{ijk} + e_{ijkl}$$

where : Y_{ijkl} = the observation on ijklth hen (paternal half sister); μ = overall mean, common element to all observations; G_i = fixed effect of ith generation; S_{ij} = random effect of jth sire nested within the fixed effect of the ith generation; H_{ijk} = random effect of kth daughter (hen) nested within the random effect of jth sire within the fixed effect of ith generation; and e_{ijkl} = a random deviation of lth bird within kth hen within jth sire within ith generation. It includes all other effects not specified in the mixed model.

The assumption imposed and the estimates of the sire, hen within sire and remainder components of variance as well as weighing of the sire's and daughter's variance and covariance components were as in the previous model. Heritabilities were estimated for hen traits by paternal half-sib method, as four times the interclass correlation coefficient between sire groups (Harvey, 1979). The approximate standard errors of heritability were computed from procedures described by Swiger *et al.* (1964). The coefficient of phenotypic correlation (rp) between different traits was obtained according to Harvey (1987). Genetic correlation coefficient between any two traits was computed by dividing the family covariance component for the two traits by the geometric mean of the two families variance components (Becker, 1975; Harvey, 1987). Standard errors of the genetic correlation were estimated approximately by the formula given by Tallis (1959) and Swiger *et al.* (1964).

Results and Discussion

Growth Traits

Body weight (BW)

Sire, dam, remainder variance components and the percentage of variation in body weight due to these components are presented in Table 2.

Heritabilities for BW at different ages from sire (paternal half-sibs) dam within sire (maternal half-sibs) and sire and dam (full-sibs) components are presented in Table 3.

The dam component was much higher and accounted for more variation in BW at different ages than the sire component (Table 2). However, in a nested classification analysis the dam component is expected to be larger in magnitude by the variances due to the dominance deviations and maternal effects.

TABLE 2. Variance component (σ^2) estimates due to random effects of body weight and absolute daily gain recorded at different ages.

Trait	Sire		Dam / Sire		Remainder	
	σ^2S	V%	$\sigma^2D:S$	V%	σ^2e	V%
Body weight at						
Hatch (BW0)	0.078	12.5	0.199	31.8	0.349	55.7
1st week (BW1)	0.058	6.9	1.232	14.5	6.711	78.7
2nd week (BW2)	2.042	5.2	3.668	9.4	33.195	85.3
3rd week (BW3)	3.603	4.5	12.214	15.4	63.712	80.1
4th week (BW4)	9.600	9.6	12.007	12.1	78.212	78.3
5th week (BW5)	8.942	11.1	11.625	14.5	59.679	74.4
1st week (BW6)	13.594	17.7	15.815	20.6	47.436	62.7
Absolute daily gain						
ADG 0-2	0.007	3.8	0.014	7.5	0.165	88.7
ADG 2-4	0.025	8.1	0.032	10.3	0.253	81.6
ADG 4-6	0.042	11.6	0.012	3.3	0.309	85.1
ADG 0-6	0.007	16.3	0.009	20.9	0.027	62.8

Heritabilities computed from the sire component (h_S^2) ranged between 0.18 (BW3) and 0.71 (BW6). They generally fall within the range of estimates reported by Sittmann *et al.* (1966), Kawahara and Satio (1976) and Strong *et al.* (1978), but higher than that of 0.12 and 0.10 reported by Sefton and Siegel (1974) for body weight at 2 and 4 weeks of age, respectively.

Heritabilities computed from the dam components (h_D^2) are generally higher than those from the sire components (Table 3). The range was between 0.38 (BW2) and 1.27 (BW0). This may be due to the large dam variance components obtained (Table 2). Similar estimate of 1.14 for body weight at hatch was reported by Sefton and

TABLE 3. Estimates of heritability (h^2) for body weight and absolute gain recorded at different ages.

Trait	Sire	Dam / Sire	Full-sib
	h^2_S	$h^2_{D:S}$	$h^2_{S+D} \pm SE$
Body weight at			
Hatch (BWO)	0.49 ± 0.08	1.27 ± 0.09	0.88 ± 0.05
1st week	0.27 ± 0.07	0.58 ± 0.08	0.43 ± 0.05
2nd week	0.21 ± 0.06	0.38 ± 0.08	0.29 ± 0.04
3rd week	0.18 ± 0.06	0.61 ± 0.08	0.39 ± 0.05
4th week	0.38 ± 0.07	0.48 ± 0.05	0.43 ± 0.04
5th week	0.44 ± 0.07	0.57 ± 0.08	0.51 ± 0.05
6th week	0.71 ± 0.09	0.82 ± 0.09	0.76 ± 0.05
Absolute daily gain			
ADG 0-2	0.16 ± 0.06	0.30 ± 0.07	0.23 ± 0.04
ADG 2-4	0.33 ± 0.07	0.41 ± 0.08	0.37 ± 0.05
ADG 4-6	0.46 ± 0.08	0.11 ± 0.07	0.29 ± 0.04
ADG 0-6	0.63 ± 0.09	0.82 ± 0.09	0.72 ± 0.05

Seigel (1974) in Japanese Quail. Bias and/or sampling error could be responsible for obtaining heritability estimates larger than one. Here, sampling error probably occurred from the relatively small number of sires and dams used in the analysis. The estimates of h^2_D for BW6 (0.82) was higher than those of 0.63 (Marks and Lepore, 1968); 0.65 (Yoshida and Collins, 1967) and 0.58 (Sefton and Seigel, 1974). However, Seften and Seigel (1974) and Sittmann *et al.* (1966) reported an estimate of 1.44 and 1.48 for heritability of body weight at 5 and 6 weeks of age, respectively. The discrepancy between the present estimates and those reported in the literature might be due to that these estimates are based on different methods of estimation applied, in different flocks under varying conditions and therefore, considerable variability among estimates is expected.

Heritabilities computed from full-sib components (h^2_{S+D}) for BW at different ages fluctuated in magnitude from hatch until 6 weeks of age (Table 3). They ranged between moderate and high in magnitude (0.29 for BW2 and 0.88 for BWO). The estimates obtained for h^2_{S+D} (Table 3) is in good agreement with the estimates ranged between 0.30 and 0.78 reported by Kawahara and Satio (1976); Macha and Becker (1976) and Strong *et al.* (1978) using the same variance component.

In view of the relatively high heritabilities for BW obtained (Table 3), considerable genetic improvement could be attained through individual selection for these traits in this flock and in similar flocks.

Absolute daily gain (ADG)

The dam variance components were higher than the sire's for ADG during different growth periods except for ADG from 4 to 6 weeks of age (ADG 4-6), where a reverse trend was observed (Table 2). The variation due to the sire component ranged between 3.8% for ADG from hatch to 2 weeks of age (ADG 0-2) and 16.3% for ADG from hatch to 6 weeks of age (ADG 0-6). While the percentage due to the dam component ranged between 3.3 and 20.9% for ADG 0-6.

Heritabilities computed from the sire component (h_S^2) ranged between 0.16 for ADG 0-2 and 0.63 for ADG 0-6. The estimate obtained for ADG 0-2 is higher than that of 0.13 reported by Narayan (1976) for the same trait. However, the relatively high value of h_S^2 for ADG 4-6 (0.46) and ADG 0-6 (0.63) indicate that there is a great genetic variability in this trait among the birds of this flock. Therefore, it could be concluded that daily gain could be genetically improved through selection.

Comparing the h_S^2 for BW at different ages, 0.21, 0.38 and 0.71 for BW2, BW4 and BW6, respectively (Table 3) with those from the same components for ADG during the preceding growth periods, 0.16, 0.33 and 0.46 for ADG during the period 0-2, 2-4 and 4-6 weeks (Table 2), it could be concluded that the estimates for ADG were more reasonable than those for the body weight. This was expected since the amount of growth achieved during a certain period is a precise reflection for the additive genetic effect influencing growth than the absolute weight at a certain age.

Heritability estimates computed for ADG during different growth periods from the dam components (h_D^2) are generally higher than those from the sire components except from 4 to 6 weeks of age where the h_S^2 was higher than (h_D^2) (0.46 vs 0.11). The high estimates of h_D^2 is mainly due to the large magnitude of the dam variance component in comparison with that of the sire (Table 2). The range of estimates computed from the dam components was between 0.11 (ADG 4-6) and 0.82 (ADG 0-6). Unfortunately, there is a lack of information concerning the estimates of heritability of ADG in Japanese Quail in the literature. Therefore, the present estimates could not be compared with other estimates.

Heritabilities computed from full-sib components (h_{S+D}^2) are moderate to high in magnitude ranging from 0.23 to 0.72 (Table 3). In poultry, Kinney (1969) reported that the heritability of daily gain computed from full-sib components during different growth periods were moderate to high and ranged from 0.53 to 0.68.

In view of the high heritability of ADG during different growth periods from different components, it seems possible that a long term selection program for such a trait within this flock would lead to a simultaneous improvement in growth rate.

Carcass Traits

Dressing percentage (D%)

The dam variance component for D% was higher than that of the sire (Table 4). The variation in this trait due to the two components in the same order was 10.69 and 6.52, respectively.

Heritability for D% were 0.26 and 0.43 from the sire and dam components, respectively. Higher estimates of 0.69 and 0.35 computed for male and female D%, respec-

TABLE 4. Variance components (σ^2) estimates due to random effects of carcass traits.

Carcass trait	Sire		Dam / Sire		Remainder	
	σ^2S	V%	$\sigma^2D:S$	V%	σ^2e	V%
Dressing %	0.442	6.52	0.691	10.69	5.535	82.79
Protein %	0.009	1.02	0.036	4.09	0.836	94.89
Fat %	1.606	17.34	1.785	19.28	5.869	63.38
Moisture %	1.967	15.38	1.526	11.93	9.299	72.69

TABLE 5. Estimates of heritability (h^2) for carcass traits.

Carcass trait	Sire	Dam / Sire	Full-sib
	h^2S	$h^2D:S$	$h^2S + D$
Dressing %	0.26 ± 0.15	0.43 ± 0.19	0.34 ± 0.09
Protein %	0.04 ± 0.13	0.17 ± 0.18	0.11 ± 0.08
Fat %	0.69 ± 0.20	0.77 ± 0.20	0.73 ± 0.11
Moisture %	0.62 ± 0.19	0.48 ± 0.19	0.55 ± 0.11

tively were reported by Kawahara and Satio (1976).

The estimate computed from the full-sib component (h^2_{S+D}) was 0.34. Similar estimate of 0.35 was reported by Kawahara and Satio (1976) for carcass weight of Japanese Quail.

Chemical analysis

The dam variance components for protein (P) and fat (F) percentages were higher than those of the the sire, while a reverse trend was observed for the moisture (M) percent (Table 4). The variation in P% due to the dam and sire components was 4.09 and 1.02%, respectively. While the two components in the same order accounted for 19.28 and 17.34% of the variation in F% and 11.93 and 15.38% of the variation in M%.

Heritabilities computed from the dam components for P% and F% (0.17 and 0.77) were higher than those computed from sire component (0.04 and 0.64). The reverse was observed for M% (Table 5). The relatively high standard error of the heritability of P% lessens the confidence in the estimates themselves. Statistically the heritability estimate obtained for P% is not different from zero.

Heritabilities for P, F and M% could not be compared with other estimates because the reviewed literature does not include any estimates for heritability of these traits in Japanese Quail.

Reproductive and Egg Production Traits

Age at first egg (AFE)

Sire variance component was higher than that of the daughter where the percentage of variation due to them were 35.5 and 24.9%, respectively. The unrealistic high estimate of heritability from the sire component of variance (h_S^2) for AFE (1.42) lessens the confidence in the estimate itself. Statistically the estimate is beyond the theoretical level. However, it still gives an indication of a possible genetic variability in the flock which render genetic improvement of this trait through selection.

Fertility percent (FER%)

Daughter variance component was higher than the sire's. The percentage of variation due to the two components in the same order were 17.7 and 5.9% (Table 6). The low heritability for FER% (0.07) was expected since this trait is related to fitness where the additive genetic variance is usually extremely low due to natural selection acting on such traits. The relatively high standard error lessens the confidence in the estimate. Statistically the computed heritability is not different from zero.

TABLE 6. Variance component (σ^2) estimates due to the random effects for reproductive and egg production traits.

Trait	Sire		Daughter / Sire		Remainder	
	σ^2S	V%	σ^2D : S	V%	σ^2e	V%
Age at 1st egg (AFE)	7.66	35.5	5.37	24.9	0.53	39
Fertility (FER)	0.01	5.9	0.03	17.7	0.13	76
Hatchability (HAT %)	a	a	0.05	29.4	0.12	70
Average hatch weight per hen (AHW)	0.13	20.0	0.24	36.9	0.28	43
Egg production during :						
1st week (EP1)	0.11	8.5	0.11	8.5	1.07	82
7th week (EP7)	0.01	1.2	0.16	18.6	0.69	80
1st 70 days (EP70)	7.00	20.1	9.13	26.3	18.64	53

[a] Negative estimate of sire component of variance is set to be zero.

In poultry, Crittenden and Bohren (1961) and Gilbreath *et al.* (1963) reported an estimate of 0.01 and 0.02 for the same trait, respectively.

Hatchability percent (HAT%)

Sire variance component was negative (Table 6) which is statistically not different from zero. The variation in HAT% due to the daughter component was 29.4%.

Low heritability for this trait was expected since its variation is mainly due to environmental rather than to genetic factors. However, more estimates from different flocks including greater number of birds are needed to throw more light on the inheritance of this trait.

The present negative estimate for heritability of HAT% (Table 7) is consistent with the same trend reported by Brunson *et al.* (1955) in poultry (– 0.14 to – .05). Davis (1955) reported an estimate of 0.65 for the same trait in poultry.

Average hatch weight per hen (AHW)

The dam variance component was higher than the sire's and the variation due to the two components were 36.9 and 20.0%, respectively (Table 6). The high heritability of AHW per hen (0.79) refer to the possibility of considerable genetic improvement that could be attained through individual selection for this trait in this flock and in similar flocks.

TABLE 7. Estimates of heritability (h^2) for reproductive and egg production traits.

Trait	Sire (h^2S ± SE)
Age at 1st egg (AFE)	1.42 ± 0.21
Fertility (FER%)	0.07 ± 0.15
Hatchability (HAT%)	a
Average hatch weight per hen (AHW)	0.79 ± 0.19
Egg production at:	
1st week (EP1)	0.05 ± 0.17
7th week (EP7)	0.05 ± 0.15
1st 70 days (EP70)	0.81 ± 0.19

a Heritability not determined because the sire variance component was negative.

Egg production

Generally, the magnitude of the sire and daughter components of variance fluctuated during the egg production periods studied (Table 6).

The variation in egg production due to sire component ranged between 1.2% during the 7th week of production and 20.1% during the first 70 days of production. The percentage due to the daughter component ranged between 8.5% (EP1) and 26.3% (EP70).

Heritability for EP70 (0.81) is higher than the estimate of 0.39, 0.26 and 0.36 reported by Marks and Kinney (1964), Strong *et al.* (1978) and Sittmann *et al.* (1966) for the same trait. This high estimate indicates that there is great genetic variability in this trait among the birds of the flock. Thus, it could be concluded that genetic improvement of egg production can be achieved through selection.

The relatively high standard error of heritability of EP1 and EP7 (Table 7) lessens the confidence in the estimates themselves. Statistically, the heritability obtained for EP1 and EP7 is not different from zero.

Phenotypic correlations

The phenotypic correlation (rp) between body weight, reproductive and egg production traits are presented in Table (8).

The rp between BW at different ages was positive and moderate in magnitude. Also, the magnitude of the correlation increased with decreasing time intervals between weights.

The rp between BW and AFE was positive and ranged between moderate to high magnitudes (.35, .46 and .73). This indicates that the correlation between AFE and BW increased in magnitude by decreasing the time interval between AFE and age of recording the weight. Thus, increasing BW beyond a certain limit will delay sexual maturity. However, Kadry *et al.* (1986) found that BW was negatively correlated with age at sexual maturity in Japanese Quail.

The rp between BW and FER% was negative and small in magnitude (Table 8). The same was also observed for the rp between BW at different ages and HAT%. In spite of the very low estimates of these correlations which are almost equal to zero (range – .01 to .1), the results might indicate that improving BW might decrease F% and HAT% to some extent. This should be considered in any breeding plan aiming at increasing BW beyond a certain limit. However, there is a lack of information con-

TABLE 8. Estimates of phenotypic (above diagonal) and genetic (below diagonal) correlations among body weights, reproductive and egg production traits.

Traits	(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)	(10)
1. Hatch weight (BW0)		0.41	0.35	0.35	– .03	– .01	0.26	0.06	– .06	– .05
2. 3-week weight (BW3)	0.78 ± ± 0.19**		0.58	0.46	– .04	– .04	0.43	0.10	– .09	– .11
3. 6-week weight (BW6)	0.73 ± 0.12**	1.01 ± 0.14**		0.73	– .08	.01	0.64	0.16	.06	– .05
4. Age at 1st egg (AFE)	1.03 ± 0.10**	0.88 ± 0.16**	0.79 ± .05*		– .12	– .05	0.51	.14	– .16	– .06
5. Fertility (FER)	0.16 ± 0.56**	0.48 ± 0.84**	– .09 ± 0.46*	– .35 0.53**		0.28	– .05	– .03	0.01	0.04
6. Hatchability (HAT)	a	a	a	a	a		0.01	0.01	0.09	0.17
7. Average hatchability weight / hen (AHW)	0.63 ± 0.15**	0.43 ± 0.01**	0.78 ± 0.07**	0.52 ± 0.10**	– .35 ± 0.22**	a		0.15	0.02	0.03
8. 1st week egg production (EP1)	0.07 ± 0.25	– .09 ± 0.33*	0.30 ± 0.20**	0.16 ± 0.18**	– .16 ± 0.68**	a	0.23 ± 0.22**		0.8	0.41
9. 7th week egg production (EP7)	– .65 ± 0.18**	– .23 ± 0.21**	– .25 ± 0.16**	0.14 ± 0.11**	– .26 ± 0.63**	a	0.16 ± 0.57**	0.78 ± 0.13**		0.55
10. 70 days egg production (EP70)	– .38 ± 0,18**	– .19 ± 0.21**	– .05 ± 0.16	– .01 ± 0.56**	– .38 ±	a 0.16**	0.14 ± 0.17**	0.65 ± 0.13**	0.78 ±	

a Undetermined genetic correlation due to negative estimates of sire components of variance for hatchability.

cerning these correlations in Japanese Quail in the literature.

Positive rp was found between BW and AHW per hen (Table 8). The magnitude ranged between moderate to high. The present estimates could not be compared with others because there is no information available concerning that relationship in Japanese Quail and/or poultry. However, the sign and magnitude of the correlation between these two traits, *i.e.,* the body weight at one hand was expected since biologically the two traits are governed by the same set of genes.

The rp between BW and EP1 was positive while BWs were negatively correlated with EP7 and EP70 (Table 8). The estimates were generally low in magnitude. The correlation between BW and EP1 increased in magnitude with advance in age of recording the weight (0.6, .1 and .16).

Negative rp was found between AFE, FER% and HAT%. The magnitude of the correlation was relatively low (– .12 and – .05). However, the results indicate that early sexual maturity improves fertility and hatchability percent.

Positive rp was found between AFE.and AHW per hen (.51). This indicates that increasing AFE will increase AHW per hen through increasing egg size.

Negative rp were found between AFE and EP1, EP7 and EP70 (Table 8). The magnitude of the correlations were relatively low ranging between – .14 and – .16. However, these estimates are lower than those of – .33 and – .71 reported by Kadry *et al.* (1986) and Bray *et al.* (1960) for the same correlations in Japanese Quail and poultry, respectively. The present results are biologically expected since delayed sexual maturity is always decreasing egg production as reported by Brandsch (1979).

Positive rp was found between FER% and HAT% (.28), while FER% was negatively correlated with AHW per hen (– .05). Except the small negative rp between FER% and EP1 (– .03), the correlations between FER% and EP7 and EP70 were positive and small in magnitude (.01 and .04). Statistically, these estimates are not different from zero. Therefore, the correlation between these traits in Japanese Quail needs further investigation.

Positive rp was found between HAT% and AHW per hen (.01). The rp between HAT% and EP1, EP7 and EP70 were positive but small in magnitude (.01, .09 and .17). The correlation between FER% and HAT% on one hand, and EP during different periods and AHW per hen on the other hand, indicate that improving FER% and HAT% will generally improve different egg production traits.

Positive rp was found between AHW per hen and EP1 and EP70 (.15 and .03), while AHW was negatively correlated with EP7 (– .02). This indicates that if egg production increased and reached the peak at the 7th week, as it is normally the case in Japanese Quail, the AHW per hen decreased.

Genetic correlation

The genetic correlation (rg) between different traits studied are presented in Table (8). Some of the estimates had a relatively high standard error which lessens the confidence in the estimates themselves. Statistically, such estimates are not different from zero. However, the relatively high standard error observed for some estimates might be due to the relatively small number of observations used in estimating the correlation.

The rg between BW at different ages were positive and large in magnitude (Table 8). The estimates ranged between 0.73 ($p < .01$) for the correlation between BW0 and BW6 and 1.01 ($p < .01$) for that between BW3 and BW6. The present estimates agree well with those of .75 and .88 reported by Kadry *et al.* (1986) and Strong *et al.* (1978) for the rg between BW6 and BW12 in Japanese Quail. Generally, the positive and relatively high rg between body weight at different ages was expected and indicates that the possibility of improving body weight at later ages through selection at earlier ages.

The rg between BW at different ages and AFE were positive and relatively high ranging between .75 ($p < .01$) and 1.03 ($p < .01$) for the correlation between AFE and each of BW6 and BW0. These estimates are higher than those reported by Hale and Clayton (1965) and Kadry *et al.* (1986) in Japanese Quail (.35 and .29). The inflation of the rg coefficient between AFE and BW0 over the theoretical limit (1.0) may be due to sampling error. However, the present correlations indicate that the increase in BW will delay AFE. Trehan (1978) and Verma *et al.* (1983) found that BW at different ages was negatively genetically correlated with AFE in poultry. They suggested that early maturing birds are likely to have lighter BW which in turn lead to produce small eggs. The contradicting trends between Japanese Quail and poultry may be due to species differences.

The rg between BW at different ages and FER% was .16 ($p < .01$), .48 ($p < .01$) and – .09 ($p < .05$). El-Ebiary *et al.* (1966) reported an estimate of – .03 for the rg between BW at 100 days of age and FER% in Japanese Quail. Because of the negative sire component of variance for the HAT%, the rg between HAT% and other traits studied were not determined.

The rg between AHW per hen and BW at different ages was .63 ($p < .01$), .43 ($p < .01$) and .78 ($p < .01$). These correlations indicate the importance of considering this trait as a selection criterion for dams in any breeding plans aiming the improvement of meat production in Japanese Quail.

There was no consistent trend for the rg between BW at different ages and EP during different production periods (Table 8). The rg between BW3 and EP during different production periods were negative. They were low ranging between – .09 ($p < .05$) and – .23 ($p < .01$) for the correlation between BW3 and EP1 and EP7. On the other hand, BW was positively correlated with EP1, while it was negatively correlated with EP7 and EP70 (Tabl 8). The rg ranged between .30 ($p < .01$) and – .25 ($p < .01$) for the correlation between BW6 and EP1 and EP7. The negative rg (– .05) between BW6 and EP70 is in agreement with that of (– .15) reported by Strong *et al.* (1978) for the same correlation in Japanese Quail. The present results indicate that increasing BW will generally decrease egg production and vice versa.

The rg between AFE and FER% was – .35, while that between AFE and HAT% was undetermined, because of the negative estimate of sire component of variance for HAT%. The rg between AFE and AHW per hen was moderate and positive .52 ($p < .01$). This indicates that increasing AFE might lead to an increase in AHW per hen. This might be due to that delaying AFE increase egg size which in turn is positively correlated with AHW per hen.

The rg between AFE and EP1 was .16 ($p < .01$), while it was negatively correlated with EP7 and EP70 – .14, ($p < .01$) and – .01 ($p < .05$). This indicates that delaying sexual maturity in Japanese Quail will decrease EP and vice versa. This should be considered in selection programs designed to improve EP in Japanese Quail. Similar trend for the rg between AFE and EP was reported by Kadry *et al.* (1986) in Japanese Quail. The inconsistency in the trend of the rg between age at sexual maturity and EP1, EP7 and EP70 (Table 8) may be due to the high variability in egg laying during the first week of egg production.

The rg between FER% and AHW per hen was – .35 ($p < .01$). Also, the rg between FER% and EP during different laying periods were negative (– .16, – .26 and – .38, $p < .01$). These results indicate that the magnitude of correlation increased with advance in length of laying period.

The rg between EP during different laying periods and AHW per hen were positive and low in magnitude, .23, .16 and .14 ($p < .01$).

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المقاييس الوراثية لبعض الصفات الإنتاجية والتناسلية للسمان الياباني

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المستخلص : أجريت هذه الدراسة على عشيرة من السمان الياباني واشتملت على ٢١١٠ طائر أنتجت خلال ثلاثة أجيال متتالية . ولقد تم دراسة المقاييس الوراثية (المكافىء الوراثي – الارتباط المظهري – الارتباط الوراثي) لبعض الصفات الانتاجية والتناسلية للسمان الياباني مثل وزن الجسم – معدل النمو – نسبة التصافي – نسبة البروتين والرطوبة في اللحم وكذلك العمر عند أول بيضة ونسب الخصوبة والفقس ووزن الكتكوت عند الفقس / دجاجة بالإضافة إلى إنتاج البيض ، وتتلخص أهم النتائج في الآتي : المكافئات الوراثية لوزن الجسم تراوحت ما بين (٢٩, – ٨٨,) ولمعدل النمو ما بين (١١, – ٤٦,) ونسبة التصافي ما بين (٢٦, – ٤٣,) وللخصوبة (٠٧,) ولنسبة الفقس (٠٥,) ولمتوسط وزن الكتكوت عند الفقس / دجاجة (٧٩,) ولإنتاج البيض (١١,) وبالنسبة للارتباط المظهري فلقد ارتبطت أوزان الجسم من الفقس وحتى ٦ أسبوع من العمر ارتباط مظهري موجب مع بعضها ومع العمر عند أول بيضة ومع متوسط وزن الكتكوت ومع إنتاج البيض في الأسبوع الأول . وارتبطت أوزان الجسم ارتباط سالب مع نسبة الخصوبة ونسبة الفقس وإنتاج البيض – والعمر عند أول بيضة ارتبط ارتباطا سالبا مع إنتاج البيض – نسبة الخصوبة ارتبطت موجبا مع نسبة الفقس ، وبالنسبة للارتباط الوراثي ارتبطت أوزان الجسم من الفقس وحتى ٦ أسبوع ارتباطا وراثيا موجبا مع بعضها ومع العمر عند أول بيضة ومع متوسط وزن الكتكوت عند الفقس / دجاجة بينما كان الارتباط الوراثي للعمر عند ٦ أسبوع ونسبة الخصوبة سالبا ، وكان الارتباط الوراثي بين أوزان الجسم وإنتاج البيض سالبا ، كما أن نسبة الخصوبة ارتبطت سالبا مع إنتاج البيض خلال الفترات المختلفة .