ESTIMATION OF GENETIC PARAMETERS FOR WEEKLY LIVEWEIGHTS IN ONE TO ONE SIRE AND DAM PEDIGREE RECORDED JAPANESE QUAIL

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INTRODUCTION

Caron *et al*. (1990) explained the importance, in the context of selection programmes, of genetic parameter estimates for production traits of Japanese quail. There are several published estimates of genetic parameters for liveweights of Japanese quail but few are based on REML procedures using one to one sire and dam pedigree records. Genetic parameters of body weight in Japanese quail were calculated by Kawahara and Saito (1976) but not using REML. Although Toelle *et al*., (1991) used a REML procedure they did not use one to one sire and dam records for each animal. In the studies of Kocak *et al*. (1994) and Aggrey and Cheng (1994) birds from known sires and dams were used but they did not have an extensive pedigree file for the analyses.

The objective of this study was to use animal models to estimate the genetic parameters of weekly liveweight of Japanese quail and genetic correlations between successive liveweights.

MATERIAL AND METHODS

The Japanese quail population used for the present study was reared in the poultry unit of Kafkas University. One male and 1 female adult bird were housed in individual cages for accurate pedigree identification. Each of them was wing-tagged with a numbered aluminum plate. When the eggs were collected, each of them was recorded with sire and dam number. When a chick hatched from a certain egg it was directly wing-tagged and weighted, and recorded with its sire and dam number. Weighing was repeated every weeks until 6 weeks of age. Parent birds were mated without selection for any productive traits but taking special care to avoid inbreeding. Analyses were carried out with the records of 1108 quails having 113 sires and 152 dams.

Statistical analyses. The Minitab (Minitab Release 10 for windows) statistical package was used for preliminary data analysis. A General Linear Model (GLM) was applied to examine the relative importance of the factors influencing quail's weekly weights.

The used model is described below ;

$$Y_{ij} = \mu + a_j + b_j + E_{ij}$$

where Y_{ij} is the observation of animal weight (HW-W6)

μ is the overall mean,

a_j is the effect of sex (i= male and female)

b_j is hatching group (j= 1-26)

E_{ij} is the random error.

Heritabilities and correlations were estimated by MTDFREML (Boldman *et al*., 1995) using an animal model with animals' genetic effect as the only random factor. Standard errors (se) of heritabilities and correlations were calculated as described by Ulutas, (1998). For the univariate analyses, the model was :

$Y_{ijk}=a_i+b_j+c_k+e_{ijk}$,
where Y_{ijk} is the trait,
a_i is the random effect of animal,
b_j is the effect of hatching group,
c_k is the effect of sex,
e_{ijk} is random error.

RESULTS AND DISCUSSION
Descriptive statistics were calculated for all the weights and these are presented in table 1.

Table 1. Descriptive statistics for liveweights

	N	Mean	SE	MIN	MAX	CV %
HW (Hatching Weight)	1108	7.6	0.03	4.6	10.6	13
W1 (Liveweight in 1st week)	1108	19.2	0.12	7.9	36.3	28
W2 (Liveweight in 2nd week)	1108	41.8	0.32	13.5	111.0	27
W3 (Liveweight in 3rd week)	1108	75.0	0.51	26.8	150.1	22
W4 (Liveweight in 4th week)	1108	112.7	0.70	52.6	179.3	18
W5 (Liveweight in 5th week)	1108	146.8	0.71	77.0	220.7	14
W6 (Liveweight in 6th week)	1108	179.1	0.67	122.1	254.7	11

N = Number of observations ; SE = Standard Error ; Min and Max = Minimum and maximum values ; CV% = Coefficient of variation.

Hatching groups significantly affected quail weights ($p < 0.01$). An effect of hatching group on liveweight of Japanese quail was reported by Brah *et al*., (1997), Aggrey and Cheng (1994) and Michalska (1992). As determined in this study, a significant effect of sex on liveweight in Japanese quail was found by Kocak *et al*. (1994), Toelle *et al*. (1991) and Garwood *et al*. (1989). The effect of sex is presented in table 2.

Table 2. Effect of sex on liveweights

	HW	W1	W2	W3	W4	W5	W6
Sex	*	**	**	**	**	**	**
Male N=586	7.5±.01	19.0±.01	41.1±.01	74.0±.02	112.6±.03	145.3±.03	172.0±.03
Female N=522	7.1±.01	19.3±.01	42.5±.01	77.0±.03	117.5±.04	152.4± .04	188.0±.04

(*) = p < 0.05, (**) = p < 0.01.

Heritabilities, genetic correlations and phenotypic correlations for liveweights are presented in table 3. The highest heritability (0.51) was estimated for hatching weight (HW) and the second highest heritability (0.32) was found for liveweight of first week (W1). Heritabilities of second week liveweight (W2), third week liveweight (W3) and fourth week liveweight (W4) were similar, 0.20, 0.21 and 0.20 respectively. Heritabilities of liveweight in fifth week (W5) and sixth week (W6) were close to each other (0.15) and (0.14) respectively. High genetic correlations were observed among the traits. The highest genetic correlation was found between W1 and w3 (0.98). The lowest one was observed between HW and W4 (0.60).

Table 3. Heritabilities on diagonal, genetic correlations above and phenotypic correlations below the diagonal with their (± SE)

	HW	W1	W2	W3	W4	W5	W6
HW	***0.51±.05***	0.71±.08	0.63±.12	0.61±.13	0.60±.12	0.73±.12	0.79±.11
W1	0.15±.08	***0.32±.06***	0.96±.09	0.98±.11	0.94±.07	0.95±.12	0.89±.13
W2	0.13±.02	0.73±.11	***0.20±.05***	0.97±.08	0.90±.06	0.89±.14	0.73±.10
W3	0.20±.04	0.58±.14	0.84±.02	***0.21±.06***	0.90±.08	0.81±.15	0.67±.12
W4	0.16±.06	0.45±.08	0.71±.03	0.82±.05	***0.20±.05***	0.93±.17	0.76±.14
W5	0.18±.05	0.41±.03	0.61±.02	0.72±.07	0.85±.04	***0.15±.04***	0.92±.09
W6	0.25±.07	0.32±.02	0.44±.01	0.53±.05	0.63±.06	0.73±.06	***0.14±.04***

Narayan *et al*. (1996) and Marks *et al*. (1996) reported higher h^2 than that found in this study for 4 -week weight, 0.7 vs. 0.3-0.5 respectively. But Michalska (1994) estimated h^2 for 28 day weight of Japanese quail at 0.3-0.4. Heritability of 34 day weight of the Japanese quail was reported by Toelle *et al*. (1991) as 0.5, and this value is higher than the value found in this study for 5 -week weight (table 3). Heritabilities estimated in the current study for 5 and 6 -week weight were similar to those reported by Kocak *et al*. (1994), with 0.2 for males and 0.3 for females for 38 day weight.

Generally, heritabilities for livewights of Japanese quail, were higher in the literature than in the current study. This might be explained by the fact that higher heritabilities were not based on REML procedure with pedigree records. Namely, differences might be an outcome of the methods used.

Brah *et al*. (1977) reported a genetic correlation between 2 -week weight and 6 -week weight weight of 0.76 which is comparable to that estimated in the present study. However, our estimate of the correlation between 4 -week weight and 6 -week is lower than that reported by Brah *et al*. (1977), (0.76 vs. 0.99). The genetic correlation between 2 and 4 -week weight (0.90) was higher than the estimate (0.76) by Aggrey and Cheng (1994). Kocak *et al*., (1994) reported a weak phenotypic correlation (0.11) between 38 day weight and 58 day weight of Japanese quail. Although it was not based on exactly the same ages, the correlation between late -week weights (4 and 5 -weeks) was higher (0.73) than that reported by Kocak *et al*., (1994). Genetic correlations were higher than phenotypic correlations as expected and reported by Brah *et al*., (1997) for 2, 4 and 6 -week live weights of Japanese quail.

CONCLUSION

Kocak *et al*. (1994) stressed the importance of selecting breeding birds of Japanese quail at an early age. The high genetic correlations observed in the present study suggest that selection on the basis of early body weights is feasible given the high heritability of these weights and the high genetic correlations between them and weights recorded at later ages. The genetic parameter estimates obtained in the present study will be useful as part of strategies to develop index-based selection procedures for Japanese quail, including the use of BLUP to estimate breeding values. The further application of REML in animal models utilising extensive pedigree records would also allow the investigation of additional random effects, e.g. maternal influences on liveweight as carry-over effects from egg weight at laying.

REFERENCES

Aggrey, S.E. and Cheng, K.M. (1994) *Poultry Sci*. **73** : 1822-1826.

Boldman, K.G., Kriese, L.A., Van Vleck, L.D. and Kachman, S.D. (1995) "A manual for use of MTDFREML". USDA-ARS, Clay Center, Nebraska, ABD.

Brah, G.S., Chaudhary, M.L. and Sandhu, J.S. (1997) *Ind. J. Poultry Sci*. **32** : 242-248.

Caron, N., Minvielle, F., Desmarais, M. and Poste, L. M. (1990) *Poultry Sci.* **69** : 1037-1045.

Garwood, V.A., Diehl, J.R. and Haugh, C.G. (1988) *Poultry Sci.* **68** : 1033-1039.

Kawahara, T. and Saito, K. (1976) *Poulry Sci*. **55 :** 1247-1252.

Kocak, C., Altan, O. and Akbas, Y. (1994) *Turkish. J. Vet. Anim. Sci.* **19** : 65-71.

Marks, H.L. (1996) *Poultry Sci.* **75** : 1198-1203.

Michalska, E. (1994) *Proc. 5th WCGALP*.

Michalska, E. (1992) *J. Inst. Genet. Anim. Breeding, Jastrzebiec*. **10** : 27-37.

Minitab (1994) “Minitab reference manual”. Release 10 for Windows.

Narayan, R., Agrawal, SK., Sing, D.P. and Kumar, S. (1996) *Ind. J. Vet. Res.* **5** : 44-46.

Toelle, V.D., Havenstein, G.B., Nestor, K.E. and Harvey, W.R. (1991) *Poultry Sci.* **70** : 1679-1688.

Ulutas, Z. (1998) PhD Thesis, University of Wales, Bangor, UK.