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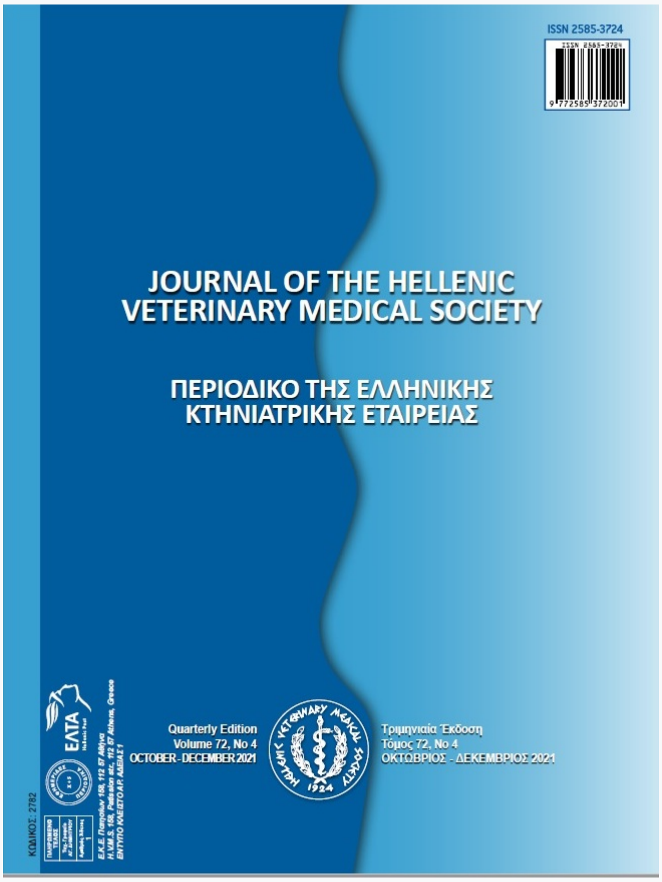

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Research article
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Genetic parameter estimates of chick quality, growth, and carcass characteristics in Japanese quail

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ABSTRACT: The aim of this study was to estimate the heritabilities of chick quality and growth traits and their genetic relationships with some slaughter traits. Chick quality was determined using both Tona and Pasgar score methods. All birds were slaughtered at 8 weeks of age to measure carcass yield (CY), and percentage of breast (BY), leg (LY), wing (WY), abdominal fat (AFY). Heritability estimates for chick quality scores of Tona and Pasgar were found 0.08, and 0.09, respectively. Heritability estimates for growth curve parameters and inflection point coordinates of the Gompertz model were low to moderate, with values ranging from 0.17 to 0.26. Low heritability estimates for CY, BY, LY, and WY were found 0.04, 0.14, 0.09, and 0.07, respectively. Genetic and phenotypic correlations between chick quality and BW-growth traits were determined low and statistically non-significant (P>0.05). Similarly, genetic and phenotypic relationships between chick quality and carcass yield, and between chick quality and percentages of carcass parts were found low and statistically non-significant (P>0.05). As a result, it is possible to say that applying multitrait selection, including chick quality, will not affect other yield characteristics positively or negatively. However, in virtue of the chick quality is a very low heritable trait, environmental improvement of chick quality trait may be considered rather than genetic improvement.

***Keywords*:** Chick quality, Genetic correlation, Heritability, Pasgar score, Tona score

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INTRODUCTION

Thanks to the genetic improvement studies carried out in the last 50 years, there have been significant developments in the rapid growth, muscle development and feed utilization characteristics of the fast-growing genotypes. In the selection studies carried out for many years, more than 25 traits from the ultimate pH of breast meat to angle of sternum have been used for the development of broilers. Environmental improvement such as feed quality, rearing systems, thermal conditions, air quality, equipment technology, and flock management gained importance in this period. Today, all environmental conditions at every stage of broiler production in poultry houses are under control. As a result of all these genetic and environmental improvements, the products with two kilograms of carcass weight at the age of 40 days are obtained and offered on the market. In addition to all these genetic and environmental features, one-day-old chick quality determined by various methods is also important because it directly affects the amount of salable chick (Leksrisompong et al., 2007; Tona et al., 2003). However, chick quality traits have never been incorporated in breeding indexes of applied genetic improvement schemes.

Starting broiler production with chicks of high quality reduces losses and increases profitability during the fattening period. All of the studies in which chick quality is measured by quantitative and qualitative methods are concerned with the effects of environmental factors on yield characteristics, and studies discussing the phenotypic relationships between chick quality and yield traits. Chick quality, like other quantitative characteristics, is affected by both genetic and environmental factors. Environmental factors affecting chick quality can be listed as age, nutrition and health status of breeder flock, egg storage conditions, position, and rotation of eggs, and thermal conditions in incubator. In the literature, there is no study focusing on the heritability of chick quality, and genetic relationships between other yield characteristics and chick quality. This study aims to estimate the heritability of chick quality and genetic correlations between yield characteristics and chick quality. Japanese quail, a commercially important and model animal for other poultry, was used in the study.

MATERIAL AND METHODS

The experiment was conducted at the Animal Science Department, Akdeniz University, Turkey. The care and use of animals were in accordance with laws and regulations of Turkey and approved by the Ministry of Food, Agriculture and Livestock (decision number 22875267-325.04.02-E.3706253) and Animal Experiments Local Ethics Committee of Akdeniz University (decision number B.30.2.AKD.0.05.07.00/59). Japanese quail (*Coturnix coturnix Japonica*) was used as animal material in the research. A total of 42 male and 126 female breeders were used at the Akdeniz University livestock facilities in order to create a base population which had not been selected before. The breeder females were housed in cages with five floors and ten individual compartments on each floor, with a stocking density of 275 cm^2/bird in individual pens. The breeder flock was formed in the family structure. Families consisted of 3 females and 1 male to avoid full and half-sib mating, and males were shifted through the 3 female cages daily. A breeder diet containing 2,800 kcal of ME/kg and 19% CP/kg was given. All adult birds were kept under constant artificial lighting for 18 h/d. Eight hundred and sixty-seven chicks randomly selected from hatchlings obtained from 1200 hatching eggs of the base population were used as experimental animals.

The hatched chicks were kept until dry, and then the wing numbers were attached. Thanks to this process the pedigree records were created, weekly live weights and other measurements were performed by matching the pedigree records during the trial. After 420 h of incubation, all hatched chicks were examined by experienced operators to determine Tona and Pasgar chick quality score of chicks as previously described by Tona et al. (2003) and Boerjan (2002). Tona and Pasgar methods are qualitative scoring systems that assess total score index of 100 and 10, respectively, based on a wide variety of visual parameters, such as activity, appearance, retracted yolk, eye condition, leg and feet condition, navel deformities, and status, remaining egg membrane, beak condition, and remaining yolk (Tona et al., 2003; Boerjan 2002). Quail chicks were housed in brooding cages (90 cm^2/quail) for 3 wk before being feather-sexed, then they were transferred to fattening cages (160 cm^2/quail), and they were housed here until the slaughtering age of 56 days. A grower diet containing 24% CP and 2,900 kcal of ME/kg for the first 21 d, and a fattening diet containing 21% CP and 2,800 kcal of ME/kg were used. Ad libitum feeding, water, and a 23-hours/daylighting program were applied from hatch to the end of the study. The cumulative mortality was found 1.38% in the study.

At 8 weeks of age, the BW of all birds was determined 4 hours after feed withdrawal and slaughtered in an experimental processing plant. The birds were slaughtered, bled out, scalded (55°C, 2 min), defeathered with equipment, manually eviscerated, and the abdominal fat pad (from the proventriculus surrounding the gizzard down to the cloaca) was taken, chilled in an ice-water tank, and drained (Narinç et al., 2014). The next day, after carcass dissection, breast with bone and the remaining abdominal fat on cold carcasses were weighed using an electronic digital balance with a sensitivity of 0.01 g. Slaughter and dissection were performed by the same experienced operators. Cold carcass, breast, leg, wing, and total fat pad yields were calculated in relation to body weight at 8 weeks of age.

To obtain the estimates of individual growth curve parameters, all quail were weighed weekly from hatching to 8 weeks of age. The Gompertz non-linear regression model (1) was used to estimate the growth curve of each quail.

$$y_t = \beta_0 e^{\left(-\beta_1 e^{-\beta_2 t}\right)} \quad (1)$$

where y_t is the weight at age t, β_0 is the asymptotic (mature) weight parameter, β_1 is the scaling parameter (constant of integration) and β_2 is the instantaneous growth rate (per day) parameter (Akbaş and Yaylak, 2000; Narinç et al., 2010b). The Gompertz model is characterized by an inflection point in a manner such that β_0/e of the total growth occurs prior to it and the remainder occurring after. The coordinates of the point of the inflection, age, and weight at inflection point (IPA and IPW, respectively), were obtained as follows:

$$IPA = ln(\beta_1)/\beta_2 \quad (2)$$

$$IPW = \beta_0/e \quad (3)$$

The descriptive statistics and Kolmogorov-Smirnov normality tests of the traits were obtained using UNIVARIATE procedure of SAS 9.3 statistics software.

The restricted maximum likelihood (REML) estimator was used to estimate variance-covariance components for following multi-trait model;

y=Xβ+Zu+e

Where **y**, a vector of observations for the trait; **β**, a vector of fixed effects for the trait; **u**, a vector of random animal effects for the trait; **e**, a vector of random residual effects for the trait; and **X** and **Z** are incidence matrices relating records of the trait to fixed and random animal effects, respectively (Narinç et al., 2014). The sire, dam, and residual variance components and additive genetic and environmental covariance matrices for multivariate analysis were estimated from the mixed-model equations by SAS PROC MIXED. Heritabilities (h_i^2) and genetic correlations ($r_{g(ii')}$) were calculated from the variance and covariance parameters as follows:

$$h_i^2 = \frac{\sigma_{ii}^2}{\sigma_{ii}^2 + \sigma_{ie}^2}$$

$$r_{g(ii')} = \frac{\sigma_{ii'a}}{\sigma_{ii}^2 + \sigma_{i'a}^2}$$

where i and i' represents the trait(s) of interest and σ_{ii}^2 and σ_{ie}^2 are the diagonal elements of $\mathbf{G_0}$ and $\mathbf{R_0}$ matrices, respectively. Also, $\sigma_{ii'a}$ stands for the additive genetic covariance between the traits i and i'. Genetic correlation and heritability estimates and their approximate standard errors of the traits were obtained by SAS interactive matrix language (IML) procedure.

RESULTS

The descriptive statistics of TS, PS, BW6, BW8, β_0, β_1, β_2, IPT, IPW, CY, BY, LY, WY, and AFY are presented in Table 1. In addition, the results of the independent sample t-test conducted to determine the sex effect are also given in Table 1. The significant effects of sex of the birds were not observed for chick quality traits. But, there were significant differences between males and females for traits of BW6, BW8, β_0 parameter, IPT, and IPW, and all slaughter-carcass traits. Females showed higher mean values than males for BW6, BW8, β_0 parameter, IPT, IPW, AFY traits ($P<0.05$ for all mentioned characteristics). The coefficient of determination R2 of the estimated growth curves were found to be above 0.99.

The estimates of genetic parameters (heritabilities and genetic relationships) for chick quality traits and growth characteristics are presented in Table 2. Heritability estimates for slaughter-carcass traits are presented in Table 3. Also, the genetic correlations between chick quality traits and slaughter-carcass characteristics are presented in Table 3. There are phenotypic correlation coefficients between all traits and their statistical significances in Table 2 and Table 3. In the study, the genetic correlation estimates among all characteristics were found higher than the phenotypic correlation coefficients (Table 2 and Table 3).

Table 1. The descriptive statistics and effect of sex on studied traits

Trait	N	Mean	SE	CV %	Min	Max	Sex Effect
TS	855	98.69	0.17	5.14	54.33	100.00	NS[1]
PS	855	9.80	0.02	6.41	5.00	10.00	NS
BW6 (g)	858	114.59	1.25	32.24	35.15	210.43	*
BW8 (g)	855	150.71	1.35	26.43	43.12	234.02	*
β_0[1] (g)	855	253.25	2.45	28.49	54.34	559.83	*
β_1[2]	855	3.25	0.02	17.99	1.81	11.67	NS
β_2[3]	855	0.038	0.001	39.22	0.012	0.126	NS
IPT[4] (d)	855	35.60	0.48	40.10	9.49	119.11	*
IPW[5] (g)	855	93.37	0.92	29.07	19.99	259.75	*
CY (%)	855	74.86	0.21	8.08	61.93	88.74	*
BY (%)	855	28.52	0.14	14.24	20.85	41.14	*
LY (%)	855	17.20	0.08	13.45	2.28	27.91	*
WY (%)	855	5.36	0.02	13.56	3.33	9.28	*
AFY (%)	855	1.08	0.02	53.63	0.08	2.94	*

TS= Tona score; PS= Pasgar score; BW6 and BW8= Body weight at 6 and 8 wk of age; β_0= Asymptotic BW parameter; β_1= Shape parameter; β_2= Instantaneous growth rate parameter; IPT and IPW = age and weight at inflection point, CY= Carcass yield, BY= Breast yield, LY=Leg yield, WY= Wing yield, AFY= Abdominal fat yield.

[1] NS= Non-significance, P>0.05. *=Statistically significance, P<0.05.

Table 2. Heritability estimates (on diagonal), genetic correlation estimates (below diagonal) and SE (in parentheses), phenotypic correlations (above diagonal) and P values (in parentheses) of chick quality and growth traits (N=855 for all traits)

	TS	PS	BW6	BW8	β_0	β_1	β_2	IPT	IPW
TS	0.08 (0.02)	0.81* (0.001)	0.03 (0.388)	0.08 (0.466)	0.00 (0.889)	-0.04 (0.209)	0.00 (0.916)	-0.01 (0.765)	0.01 (0.845)
PS	0.82 (0.01)	0.09 (0.02)	0.02 (0.605)	0.05 (0.315)	0.02 (0.486)	-0.03 (0.367)	-0.01 (0.856)	0.01 (0.879)	0.03 (0.453)
BW6	0.14 (0.03)	0.06 (0.04)	0.46 (0.01)	0.55 (0.001)	0.05 (0.549)	0.02 (0.876)	0.69* (0.001)	-0.60* (0.001)	0.05 (0.225)
BW8	0.13 (0.01)	0.09 (0.01)	0.69 (0.01)	0.51 (0.01)	0.34* (0.005)	-0.18* (0.002)	0.68* (0.001)	-0.61* (0.001)	0.11 (0.091)
β_0	0.38 (0.03)	0.35 (0.02)	0.31 (0.02)	0.35 (0.02)	0.17 (0.02)	0.35* (0.008)	-0.57* (0.001)	0.66* (0.001)	0.99* (0.001)
β_1	0.56 (0.02)	0.28 (0.03)	-0.21 (0.03)	-0.21 (0.03)	-0.08 (0.05)	0.27 (0.02)	-0.08 (0.221)	0.40* (0.001)	0.35* (0.001)
β_2	-0.08 (0.05)	-0.22 (0.03)	0.88 (0.01)	0.84 (0.02)	-0.17 (0.03)	-0.07 (0.04)	0.26 (0.02)	-0.93* (0.001)	-0.58* (0.001)
IPT	0.28 (0.02)	0.32 (0.02)	-0.85 (0.01)	-0.65 (0.02)	0.20 (0.03)	0.33 (0.02)	-0.95 (0.01)	0.26 (0.02)	0.67* (0.001)
IPW	0.39 (0.02)	0.35 (0.01)	0.29 (0.04)	0.43 (0.03)	0.97 (0.01)	-0.06 (0.05)	-0.20 (0.04)	0.24 (0.03)	0.19 (0.02)

TS= Tona score; PS= Pasgar score; BW6 and BW8= Body weight at 6 and 8 wk of age; β_0= Asymptotic BW parameter; β_1= Shape parameter; β_2= Instantaneous growth rate parameter; IPT and IPW = age and weight at inflection point

Table 3. Heritability estimates (on diagonal), genetic correlation estimates (below diagonal) and SE (in parentheses), phenotypic correlations (above diagonal) and p values (in parentheses) of chick quality and slaughter traits (N=855 for all traits)

	TS	PS	CY	BY	LY	WY	AFY
TS	0.08 (0.02)	0.81* (0.001)	-0.03 (0.768)	-0.05 (0.257)	-0.02 (0.816)	0.03 (0.374)	0.03 (0.881)
PS	0.82 (0.01)	0.09 (0.02)	-0.02 (0.254)	-0.03 (0.128)	-0.03 (0.375)	0.01 (0.278)	0.07 (0.554)
CY	-0.05 (0.03)	-0.12 (0.04)	0.04 (0.05)	0.66* (0.001)	0.70* (0.001)	0.38* (0.001)	0.28* (0.000)
BY	-0.11 (0.06)	-0.14 (0.03)	0.14 (0.03)	0.14 (0.03)	0.46* (0.001)	0.11* (0.041)	-0.07 (0.356)
LY	-0.12 (0.05)	-0.12 (0.05)	0.78 (0.03)	0.42 (0.03)	0.09 (0.03)	0.32* (0.001)	0.13 (0.094)
WY	-0.07 (0.04)	-0.08 (0.03)	0.61 (0.03)	0.10 (0.03)	0.57 (0.03)	0.07 (0.04)	0.12 (0.196)
AFY	0.22 (0.03)	0.31 (0.03)	0.33 (0.04)	0.18 (0.01)	0.33 (0.01)	0.27 (0.01)	0.21 (0.01)

TS= Tona score; PS= Pasgar score; CY= Carcass yield, BY= Breast yield, LY=Leg yield, WY= Wing yield, AFY= Abdominal fat yield.

DISCUSSION

The mean values of Tona score and Pasgar Score (98.69 and 9.80) were in agreement with those reported for broiler chickens by Willemsen et al. (2008), Van de Ven et al. (2012), and Bergoug et al. (2015), which range from 95.6 to 90.4 and 9.84 to 9.52, respectively. In the current study, the mean values of chick quality scores of birds were higher than those published by Tona et al. (2004) and Sözcü and İpek (2015) who reported Tona scores of 90.4-68.9 and Pasgar scores of 8.9-7.1 in broiler chickens. Chick quality varies considerably in studies conducted depending on factors affecting chick quality. In the studies where optimum conditions were provided, the Tona score and Pasgar score were over 90 and 9, respectively. In this study, chick quality scores obtained for Japanese quails were found to be compatible with the averages obtained under optimum conditions in these studies.

The mean values of BW at 6 and 8 weeks of age were detected at 114.59 and 150.71 g, respectively. Comparable results (91.63 to 114.76 g) have been reported for body weight at 6 weeks of age by Aggrey et al. (2003), Tarhyel et al. (2012), Raji et al. (2014), and Rocha et al. (2020). In another study conducted by Daikwo et al. (2013), it was found that the live weight at 8 weeks of age was 133.76 g. However, some researchers (Akbaş and Yaylak, 2000; Balcıoğlu et al., 2005; Narinç et al., 2014b) reported much higher mean values for body weight (170.9-184.4 g) even at six weeks of age in random-bred control lines. Minvielle (2004) reported that discrepancies among studies in the literature are attributed to the adaptation of these birds to cage conditions from immigrant life and the genetic improvement that has been applied. Sex differences for BW6 and BW8 in Japanese quail have been reported previously by Aggrey et al. (2003) and Narinç et al. (2010a), who reported that the body weights of females were heavier.

The mean value of β_0 parameter (253.25 g) was in agreement with the mean values reported by Beiki et al. (2013) and Narinç et al. (2014a). Similarly, the mean values for β_0 parameter of Gompertz function in Japanese quails were estimated in the range of 242-276 g by Karabağ et al. (2017), Hyankova et al. (2001), and Kizilkaya et al. (2005). The estimations of integration coefficient parameter (β_1) of the Gompertz model for growth of Japanese quail were found to be 3.39 and 3.31 by Akbaş and Yaylak (2000) and Narinç et al. (2010a), which is in agreement with the mean value (3.25) of β_1 parameter in this study. The mean value of instantaneous growth rate parameter (β_2) was found to be 0.038 and this value is in agreement with the values (from 0.032 to 0.046) reported by Akbaş and Yaylak (2000), Narinç et al. (2014a), and Alkan et al. (2009). As a result of studies conducted by various researchers (Alkan et al., 2009; Akbaş and Oğuz, 1998; Kaplan and Gürcan, 2018), quite different results (ranged from 15 to 35 days of age) have been found for the age at inflection point of the growth curve. The results for IPW have been reported by Alkan et al. (2009), Kızılkaya et al. (2006), and Kaplan and Gürcan (2018) that ranged from 88.13 to 105.84 g.

The percentages of carcass, breast, leg, wing, and abdominal fat were 74.86, 28.52, 17.20, 5.36, 1.08 %, respectively, which were higher than those previously reported by Narinç et al. (2010c), Lotfi et al. (2011), Narinç et al. (2013), and Raji et al. (2014). The significant effects of the sex of the birds were observed for all slaughter-carcass traits. The average percentages of slaughter-carcass traits (BY, LY, and WY), except AFY, were higher in males compared with females. Similar sex differences for slaughter-carcass characteristic in Japanese quail have already been reported for BY, LY, and WY (Narinç et al., 2010c; Shokoohmand et al., 2007; Khaldari et al., 2010).

Heritability estimates for the chick quality traits measured using Tona and Pasgar methods were found to be 0.08 and 0.09, respectively (Table 2). There are no studies on scientific literature for the genetic structure of chick quality traits of poultry species. In terms of chick quality, 4.06 % of the phenotypic variance for the Tona score and 4.48% of the total variance for the Pasgar score could be explained by genetic factors, while the remaining environmental variance rates were 95.94% and 95.52%, respectively. This situation supports the view reported by Tona et al. (2005) that “although there are many genetic and environmental factors affecting chick quality, environmental factors have a larger share”.

Heritabilities for BW at 6 and 8 weeks of age were estimated at 0.46 and 0.56, respectively (Table 2). Consistent with the findings in the current study, many researchers found high heritabilities (0.40-0.69) for both traits (Akbaş and Yaylak, 2000; Narinç et al., 2010b; Sezer 2007; Taraco et al., 2019; Sarı et al., 2011). The estimates of heritability for the Gompertz model parameter β_0 (0.17), β_1 (0.27), β_2 (0.26), and live weight (0.26) and age (0.19) at an inflection point of growth function were close to those reported in a previously published study in Japanese quail (Akbaş and Yaylak, 2000). Akbaş and Yaylak (2000) reported that the heritability estimates for β_0, β_1, β_2 parameters and point of inflection coordinates (IPT and IPW) of Gompertz model were low to moderate (0.18, 0.33, 0.32, 0.32 and 0.18, respectively).

The current estimate (0.04) of the heritability of carcass percentage (Table 3) was close to previously reported low estimates for Japanese quail which range from 0.12 to 0.21 (Lotfi et al., 2011; Sarı et al., 2011; Daikwo et al., 2013; Akbernejad et al., 2015). In the present study, heritabilities for BY, LY, and WY were found at 0.14, 0.09, and 0.07, respectively (Tablo 3). These estimates were in agreement with estimates reported by Vali et al. (2005), Akşit et al. (2003), Lotfi et al. (2011) ranged from 0.09 to 0.19. The estimated heritability for AFY (0.21) was low to moderate. In other studies involving quail, low to moderate heritabilities (0.23-0.29) were also reported for AFY trait (Akşit et al., 2003; Narinç et al., 2010c; Lotfi et al., 2011). However, Narinç et al. (2013) and Le Bihan Duval et al. (1998) reported higher heritability estimates for AFY in Japanese quail and chickens, which range from 0.35 to 0.84.

In the present study, the genetic correlation coefficients among all characteristics were estimated higher than the phenotypic correlation coefficients (Table 2 and Table 3). Cheverud (1988) reported that genetic correlation estimates were slightly larger than their phenotypic counterparts. The correlation patterns were strikingly similar in all studies using data sets based on appropriate effective sample sizes. Hence, Cheverud (1988) claimed that most of the difference between phenotypic and genetic correlation estimates was the imprecise estimates of genetic correlations.

The coefficients of phenotypic and genetic correlation between the Tona and Pasgar chick quality traits were 0.81 and 0.82, respectively. A positive and strong relationship between chick quality scores showed that these measurements were performed consistently and accurately. Positive and strong genetic and phenotypic correlations between weekly live weights (BW6 and BW8) were estimated to be 0.99 and 0.91, respectively (Table 2). These estimates were in agreement with estimates reported by Sezer (2007), Akbaş et al. (2004), and Sarı et al. (2011) and ranged from 0.80 to 0.96. The genetic relationships between the β_0-β_1, β_0-β_2 and β_1-β_2 parameters of the Gompertz model were negatively estimated. The low value of the parameter β_2 and long growing period resulted in high mature weight in birds as a consequence of the correlation between parameters β_0-β_2. These results were in agreement with similar research findings (Akbaş and Oğuz, 1998; Akbaş and Yaylak, 2000; Narinç et al., 2010b). Genetic correlations between parameter β_0, β_2, and weekly live weights were positive, and genetic correlations between β_1 and weekly live weights were negative. These estimates were similar to those reported by Akbaş and Oğuz (1998), Akbaş and Yaylak (2000), and Narinç et al. (2014a). This is the fact that an increase in the asymptotic (mature) body weight results in a decrease in the parameter β_2, which denotes the average rate of maturing. According to Table 2, there were negative genetic correlations (-0.85 and -0.83) between body weight traits and IPT. These results agreed with the estimates of Mignon-Grasteau et al. (2000) who found a strong negative relationship (-0.60) between BW and IPT traits. Genetic correlations between IPT and IPW were estimated to be positive. Similar findings for these genetic correlations Narinç et al. (2010b) have also been reported.

Phenotypic and genetic relationships between chick quality traits determined by Tona and Pasgar methods in one-day-old chicks and yields of cold carcass and carcass parts were found to be low (genetic correlations between -0.14 and 0.13, phenotypic correlations between -0.05 and 0.05) and statistically insignificant. Phenotypic and genetic correlations between whole carcass yield, breast yield, thigh yield, wing yield were generally statistically significant and positive and generally moderate (Table 3). It was determined that the highest phenotypic and genetic correlations were between cold carcass and breast and thigh (0.61-0.78). Lotfi et al. (2011) reported similarly that the genetic relationships between cold carcass yield and percentage of breast and, between cold carcass yield, and the percentage of abdominal fat were 0.46 and 0.43, respectively.

CONCLUSION

Considering the results obtained from the study, it is not possible to say that Tona and Pasgar chick quality scores in Japanese quail have important genetic and phenotypic relationships with most yield characteristics. Since the chick quality is both low heritable trait and low genetic correlated trait with other yield characteristics, there is no requirement to be included directly in the selection index in a poultry breeding scheme, where improvement of the chick quality is also taken into account. In virtue of the chick quality is a very low heritable trait, environmental improvement of chick quality trait may be considered rather than genetic improvement.

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CONFLICT OF INTEREST

The authors declared that there is no conflict of interest.

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