Original Scientific paper 10.7251/AGRENG2202123H UDC 636.594 EFFECTS OF PLUMAGE COLOR MUTATIONS ON GROWTH, FEED EFFICIENCY, AND CARCASS CHARACTERISTICS IN JAPANESE QUAIL

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ABSTRACT

The aim of this study is to determine the performance traits of the quail plumage color mutants (Golden, Italian, Black, White, and Wild) with the Gompertz growth function. A total of 100 birds from plumage color mutants (Golden, Italian, Wild, White, Black) with mixed sexes were used in the study. All quails were wing banded and then weighted weekly hatching to six weeks of age. The feed consumption of quails was determined on a weekly basis, and they were slaughtered at six weeks of age. It was determined that the difference in body weight between plumage color mutation groups first appeared between the 14-21st days and continued to exist until the end of the trial. The higher live weight (197.64 g) on day 42 is in quail with the golden color mutation than mean values (163.33-177.31 g) of other genotypes (P<0.05). Although similar results were observed in terms of carcass weight and abdominal fat weight (P<0.05), there was no difference between genotypes in terms of feed efficiency (P>0.05). As a result, it was determined that Japanese quails with different feather colors differed in terms of their performance characteristics.

Keywords: Japanese quail, Plumage color, Body weight, Feed efficiency, Carcass

INTRODUCTION

Japanese quail has been increasingly used as a source of animal protein for human consumption in recent years. Quail, which was produced only in small quantities in the past years, was formerly produced for hobby purposes and was used as a model animal in scientific studies. Today, there are herds with high productivity because of genetic improvement studies for meat and egg production. However, almost all of these studies were carried out in wild type Japanese quails. The advantages of quail breeding are many, these are short generation intervals, good feed conversion, disease resistance, high reproductive capacity, keeping a large number of animals in small areas. The widely available Japanese quail, known as the wild type, is a bird that can be sexed based on its grizzled feathers and appearance. Besides, there are many plumage color mutations in the Japanese quails. There are studies indicating that the high egg yield in white genotype, and high body weight on the Golden and Italian genotypes. The growth performance and other economically traits of color mutations reported in quail are very limited. Information on growth, egg production and carcass characteristics of mutations other than wild type feather color is insufficient to evaluate their use in commercial production. The associated effects of Japanese quail plumage genetic variants on performance traits have been studied for only a few mutations. There are reports of the roux mutation that can be used for sex discrimination at the exit, and there is information about the curly mutation associated with high body weight (Minvielle, 1999; Minvielle, 2005). The aim of this study was to determine the growth performance, feed consumption, feed efficiency, slaughter-carcass characteristics of plumage color mutants in Japanese quails.

MATERIAL AND METHODS

This study was performed in the Poultry Research Unit of Namık Kemal University, Turkey. Japanese quail (Coturnix coturnix japonica) were used as animal material. A total of 100 birds from plumage color mutants (Golden, Italian, Wild, White, Black) with mixed sexes were used in the study. All chicks were wing banded and then weighted weekly hatching to six weeks of age. Chicks were housed in heated brooding cages (82.56 cm^2/quail) for first three weeks. Then, they were transferred to grower cages (150 cm^2/quail). The diet was supplied containing 24% CP and 2900 kcal of ME/kg and ad libitum feeding and a 23 h lighting program were applied from hatch to the end of the experiment (Narinç, 2016). The feeds given to the quails were measured as a group for the first three weeks and then individually. In determination of the difference between genotypes in terms of body weight measurements at a time point, profile analysis method was utilized (Alkan, 2012; Narinc, 2010). The Gompertz growth function was used to compare the growth samples of genotypes which is known the best fitted model (Aggrey 2002; Korkmaz & Ückarde 2013; Ückarde , 2013). Expression, growth rate and inflection point coordinates of Gompertz function is presented in Table 1.

Model	Gompertz
Y _T	$\frac{1}{\beta_0} \frac{\alpha_1}{\alpha_1} \frac{\alpha_2}{\alpha_2} \frac{\alpha_2}$
IP _T	$\frac{\operatorname{rom}_{F_1e^{Z_2t}}}{\operatorname{rom}_{F_1}}$
IP _W	21) / / / / / / / / / / / / / / / / / / /

Table 1. Gompertz model expression and coordinates of inflection point

 β_0 parameter is the asymptotic (mature) weight, β_1 is a shape paremeter, β_2 is growth rate parameter. Model parameters were analyzed using with SAS 9.3 software NLIN procedure Levenberg-Marquardt iteration method (Karaman, 2013).

All quails in the experimental groups were sent to slaughter at the end of the sixweek fattening period. Before slaughter, the feed was removed for 4 hours, and the slaughter weight of the quails was determined. All weight measurements during cutting were carried out with a digital scale with a precision of 0.01 g. Following slaughter, wet plucking and evisceration, hot carcass weights were determined, including neck and abdominal fat, excluding edible internal organs.

In the statistical analysis of the continuous data obtained from the study, the variance analysis technique was used for the variables that met the parametric test assumptions, and the Kruskal Wallis test for the variables that did not meet the assumptions, and whether there was a difference between the experimental groups at 0.05 significance level. In case of statistically significant difference between the groups, Duncan multiple comparison test was used for parametric tests and Mann-Whitney U test was applied for non-parametric tests in order to determine from which group or groups the differences originated. All statistical analyzes were performed using SAS 9.3 statistical software.

RESULTS AND DISCUSSION

The results of variance analyses and mean values of performance traits of genotypes are presented in Table 2. As can be seen from Table 2, the highest body weight averages at both five and six weeks of age were found in the Golden genotype, followed by the Italian genotype (P<0.05). White quails have the lowest body weight averages in both weeks. (P<0.05). In terms of feed consumption averages, Golden and Italian genotypes have higher values (P<0.05), while there is no statistical difference between the feed consumption of other genotypes.

		5	motypes a	na genaer			
Genotype		BW 35	BW 42	FI 35	FI 42	FCR 35	FCR 42
Golden		169.91 ^a	201.41 ^a	588.43 ^a	779.34 ^a	3.65	4.05
Italian		160.21 ^b	179.01 ^b	569.18 ^a	721.98 ^b	3.75	4.24
Wild		151.68 ^c	171.24 ^c	496.05 ^b	645.02 ^c	3.45	3.96
White		146.96 ^d	160.32 ^d	515.13 ^b	665.11 ^c	3.72	4.40
Black		150.86 ^c	170.18 ^c	497.55 ^b	642.65 ^c	3.48	3.96
Sex							
Female		163.97	186.85	565.64	729.07	3.65	4.12
Male		147.88	166.01	500.90	652.57	3.57	4.13
Interaction							
Golden	Female	175.81	210.79	595.30	799.69	3.57	3.97
	Male	164.02	192.02	581.57	759.00	3.73	4.12
Italian	Female	176.31	195.94	618.39	773.21	3.69	4.13
	Male	144.11	162.07	519.97	670.75	3.80	4.34
Wild	Female	158.01	179.83	537.19	690.04	3.58	4.05
	Male	145.35	162.65	454.91	600.00	3.31	3.88
White	Female	149.57	168.12	526.47	681.02	3.78	4.32
	Male	144.35	152.52	503.79	649.21	3.66	4.48

Table 2. The mean values of body weight, feed intake, feed efficiency by genotypes and gender

Black	Female	160.14	179.55	550.84	701.41	3.63	4.11
	Male	141.58	160.81	444.26	583.90	3.32	3.81
SEM		1.87	1.87	8.49	9.07	0.05	0.06
Variation So	urce	P Value					
Genotype		0.001 0.000 0.001 0.000 0.253 0.068					
Sex 0.000 0.000 0.000 0.000 0.422 0				0.907			
Interaction 0.173 0.478 0.223 0.430 0.466				0.479			

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As can be seen in Table 2, there was no statistically significant difference between genotypes at the ages of five and six weeks in terms of cumulative feed efficiency (P>0.05). The results of the profile analysis carried out to determine the effects of the plumage color mutation are presented in Table 3.

Tuble 5. Trome analysis results for qualit with anterent pruntage color						
Time (day)	P value					
1-7	0.865					
7-14	0.785					
14-21	0.034					
21-28	0.001					
28-35	0.001					
35-42	0.002					
Wilks' Lambda	0.001					

 Table 3. Profile analysis results for quail with different plumage color

Different results have been obtained in studies carried out to determine the live weights of Japanese quails with different feather colors. Minvielle et al. (1999), Genchev et al. (2008), O uz and Minvielle (2001) and Marks (1990) reported that the difference in quail feather color had a significant effect on body weight and wild type quails had higher body weights. According to Tarhyel et al. (2012) determined that the white color mutation causes lower body weight, while Nasr et al. (2017) reported that white colored quails had a higher body weight. The results of this study were found to be consistent with the findings reported by Tarhyel et al (2012).

According to the MANOVA test statistic (Wilks' Lambda) in the corresponding Table 3, genotype profiles do not show parallelism (P<0.05). As a result of the analyzes carried out, it was determined that the difference in body weight between plumage color mutation groups first appeared between the 14- 21^{st} days and continued to exist until the end of the trial. The difference in favor of females in terms of body weights of female and male quails is species specific and emerged from the third week due to reverse dimorphism to other birds. A similar situation has been reported by many researchers (O uz et al. 1996; Toelle et al. 1991; Sezer et al. 2006). Non-linear regression parameters of Gompertz function were presented in Table 4.

		gender			
	0	1	2	IPt	IP_w
	275.42^{a}	3.78	0.064	21.97	101.32 ^a
	240.33 ^c	3.68	0.065	20.76	88.41 ^c
	260.05 ^b	3.74	0.057	24.18	95.67 ^b
	217.42 ^d	3.68	0.069	20.42	79.98 ^d
	244.22 ^c	3.70	0.062	22.46	89.84 ^c
	263.82	3.70	0.061	22.18	97.05
	231.16	3.73	0.065	21.73	85.04
Female	316.59	3.67	0.054	24.51	116.47
Male	234.25	3.90	0.073	19.42	86.17
Female	268.47	3.75	0.063	21.55	98.77
Male	212.18	3.62	0.066	19.96	78.06
Female	269.66	3.72	0.057	23.81	99.20
Male	250.44	3.76	0.057	24.55	92.13
Female	225.54	3.69	0.066	20.52	82.97
Male	209.31	3.68	0.071	20.32	77.00
Female	238.82	3.68	0.066	20.52	87.86
Male	249.63	3.71	0.059	24.41	91.83
	5.98	0.04	0.002	0.56	2.20
Variation Source P Value					
	0.031	0.852	0.254	0.306	0.031
	0.008	0.662	0.208	0.691	0.008
Interaction		0.526	0.078	0.106	0.084
	Male Female Female Male Female Male Male	275.42 ^a 240.33 ^c 260.05 ^b 217.42 ^d 244.22 ^c 244.22 ^c 263.82 231.16 Female 316.59 Male 268.47 Male 269.66 Male 250.44 Female 269.66 Male 250.44 Female 209.31 Female 238.82 Male 249.63 5.98 ource	0 1 275.42^a 3.78 240.33^c 3.68 240.33^c 3.68 240.33^c 3.68 240.23^c 3.74 217.42^d 3.68 244.22^c 3.70 244.22^c 3.70 231.16 3.73 263.82 3.70 231.16 3.73 7 231.16 3.67 3.67 Male 234.25 3.90 3.67 Male 212.18 3.62 Female 269.66 3.72 Male 225.54 3.69 Male 225.54 3.68 Female 238.82 3.68 Female 238.82 3.68 Female 249.63 3.71 5.98 0.04 0.031 0.852 0.008 0.662	012 275.42^a 3.78 0.064 240.33^c 3.68 0.065 260.05^b 3.74 0.057 260.05^b 3.74 0.057 217.42^d 3.68 0.069 244.22^c 3.70 0.062 244.22^c 3.70 0.061 263.82 3.70 0.061 231.16 3.73 0.065 $Female$ 316.59 3.67 0.054 Male 234.25 3.90 0.073 Female 268.47 3.75 0.063 Male 212.18 3.62 0.066 Female 269.66 3.72 0.057 Male 225.54 3.69 0.066 Male 209.31 3.68 0.071 Female 238.82 3.68 0.066 Male 249.63 3.71 0.059 ource $Value$ $Value$ 0.031 0.852 0.254	$_0$ $_1$ $_2$ IP_t 275.42a 3.78 0.064 21.97 240.33c 3.68 0.065 20.76 260.05b 3.74 0.057 24.18 217.42d 3.68 0.069 20.42 244.22c 3.70 0.062 22.46 2231.16 3.73 0.065 21.73 263.82 3.70 0.061 22.18 231.16 3.73 0.065 21.73 Female 316.59 3.67 0.054 24.51 Male 234.25 3.90 0.073 19.42 Female 269.66 3.72 0.066 19.96 Female 269.66 3.72 0.057 23.81 Male 250.44 3.76 0.057 24.55 Female 269.66 3.72 0.057 23.81 Male 225.54 3.69 0.066 20.52 Male 209.31 3.68 0.071 20.32 Female 238.82 3.68 0.066 20.52 Male 249.63 3.71 0.059 24.41 5.98 0.04 0.002 0.56 purce P Value 0.031 0.852 0.254 0.306

Table 4. The mean values of Gompertz growth curve parameters by genotypes and gender

In terms of the $_0$ parameter of the Gompertz growth model, the mean found for the Golden genotype was higher than the others. The mature weight parameter ($_0$) was found between 204 and 281 g in most of the studies examining the growth of Japanese quails with the Gompertz model (Akba and O uz 1998; Kızılkaya et al. 2005; Narinç et al. 2009; Alkan et al. 2009; Narinç et al. 2010b). The results of this study are consistent with previous reports.

In Gompertz model, $_1$ and $_2$ are constants related to the shape of the growth curves were in the range of 3.62 to 3.90, and 0.054 to 0.073, respectively. In current study, age and weight at the point of inflection of Gompertz curve were

determined to be from 19.42 to 24.55 day and 77.00 to 116.47 g for different plumage color grups. Similar results reported by Alkan et al. (2009) who estimated ages and weights at point of inflection using Gompertz model for selected and control lines. They reported that the mentioned parameters in selection line were found 113 g for female, and 108 g for male. Also, 82.3 g for female quail, and 75 g for male were found for control line. However, Kızılkaya et al. (2005) reported that ages and weights at point of inflections of Gompertz model were found between 16.19 and 17.05 day, and from 81.57 to 82.96 g respectively. As shown here, growth curve parameters of quail can be affected from both the selection and environmental conditions. As a result, it was determined that Japanese quails with different feather colors differed in terms of their growth characteristics.

Genotype		СР	BRP	LP	WP	AFP
Golden		66.25 ^b	23.66 ^b	15.47	5.50 ^c	0.98 ^a
Italian		68.17 ^{ab}	25.21 ^a	16.21	5.68 ^{bc}	0.75 ^{ab}
Wild		68.87^{ab}	25.57 ^a	16.96	6.12 ^{ab}	0.61 ^b
White		69.60 ^{ab}	25.96 ^a	16.86	6.55 ^a	0.57 ^b
Black		71.57 ^a	26.76 ^a	16.72	6.25 ^{ab}	0.69 ^b
Sex						
Female		66.74	24.69	15.74	5.95	0.67
Male		71.04	26.17	17.15	6.09	0.77
Interaction						
Golden	Female	65.04	22.52	13.90	5.31	0.78
Goldeli	Male	67.45	24.80	17.05	5.68	1.18
Italian	Female	64.63	23.84	15.58	5.52	0.83
Italiali	Male	71.72	26.58	16.84	5.84	0.67
Wild	Female	67.78	25.49	16.73	6.20	0.64
wild	Male	69.95	25.65	17.18	6.03	0.58
White	Female	68.68	26.24	17.12	6.77	0.52
white	Male	70.52	25.69	16.61	6.33	0.61
Dlash	Female	67.55	25.37	15.38	5.95	0.57
Black	Male	75.58	28.15	18.07	6.56	0.80
SEM		0.53	0.25	0.21	0.09	0.04
Variation S	ource			P Value		
Genotype		0.018	0.002	0.119	0.001	0.006
Sex		0.000	0.004	0.001	0.430	0.190

Table 5. The mean values of carcass characteristics by genotypes and gender

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Interaction	0.156	0.112	0.028	0.300	0.121

Carcass characteristics of different color mutant quails are shown in Table 5. As a surprising result in terms of carcass yield, the average value of the black genotype was higher than the others, while the lowest average was found in the Golden genotype. In addition, it was determined that the Golden feather mutation caused an increase in the abdominal fat rate as expected. No study has been found in the scientific literature investigating the effects of plumage color mutations on carcass characteristics in poultry.

CONCLUSIONS

As a result, it was determined that the plumage color mutation affected many performance traits in Japanese quails. Wild genotype was used in all genetic improvement studies in Japanese quails. However, the breeding performance of the lines obtained according to the plumage color mutation is a matter of interest.

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