USING PATH ANALYSIS TO PARTITION THE VARIABILITY IN GROWTH AND CARCASS TRAITS IN THREE LINES OF JAPANESE QUAIL.

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ABSTRACT:

Chicks of two selected lines of Japanese quail for high six week-body weight and high 1-6 week growth rate (HBW_6 and HGR_{0-6}) over three generations were used to partition the variability of growth and carcass traits. A randombred control line (RC) was kept in order to facilitate comparison between lines. The RC had the lowest boneless meat% (BLM), fat% and live body weight at slaughter (LBW_6) being 48.13%, 16.09% and 184.65g, respectively. Although HGR had the highest BLM% and dressing%, birds of this line had significantly poorer feed conversion (FC) and performance index (PI) than other lines. On the other hand, birds of the HBW line had the highest LBW_6 and PI but had higher carcass' fat% (200.25g, 3.55 and 20.51%, respectively). Sex significantly affected BLM%, carcass %, dressing%, LBW_6, FC and PI. Although males had significantly higher carcass%, their PI were poorer than females, this may be due to the superiority of females growth than males at different ages of growth and this difference may be attributed primarily to the relatively large ovaries, liver and intestines of the females. When these parts were excluded, lower carcass% for female was obtained. Except triglycerides (TG), line significantly affected all plasma constituents. The RC line had the highest growth hormone (GH) and the lowest albumin (Alb), total lipids (TL), total protein (TP), triiodothyronine (T_3) and ratio of T_3 to thyroxine (T_3/T_4). Whereas, HGR had the lowest GH and the highest Alb, TP, T_3 and T_4. Females had significantly higher Alb, TP and T_3/T_4 than males, however, males had higher T_3 than females. The results of path analyses revealed that the studied plasma constituents measured at three weeks of age in both sexes could be used to predict carcass traits and growth productive performance in Japanese quail. Each of GH, TG, TL, Alb, TP and T_3/T_4 was the first contributors of studied productive traits in line by sex groups indicating direct effects which ranged from 0.530 to 0.763, 0.504 to 0.945, 0.887 to 0.906, 0.513 to 0.990 and 0.609 to 0.892, respectively. Plasma constituents showed higher indirect coefficients of determination for their effects on all studied productive traits than their direct effects. This suggests that a part of the variations in these traits could be attributed to a trait or more, not handled in this study and may diminish the random error variation when considered.

Key words: Path analyses, variability, growth, carcass traits, Japanese quail.

INTRODUCTION

Recently, selection programs in poultry have placed much emphasis on rapid early growth rates and increase body size which resulted in a significant reduction in the number of days required to grow birds to market weight with indirect improvement in feed conversion. However, little is

known, about the physiological mechanisms altered in the course of such genetic improvement. Genetic variations, manifested in the variability of tissue composition and metabolic processes between strains, provide a means of evaluating such physiological developmental changes due to genetic selection (**Stewart and Washburn, 1983**). Growth is controlled by a complex interaction between genotype and environmental factors which are largely translated in hormonal signals by which these factors affect growth processes to improve productivity, productive efficiency and the quality of animal products (**Rahimi, 2005**a). Variation in metabolic rate would be expected to have a major influence on the growth and development of animals. There is abundant evidence that thyroid hormones: Triiodothyronine (T_3) and thyroxine (T_4) are very important for normal post hatch growth in birds which is positively correlated with the rising of circulating T_3 and T_4 (**Decuypere *et al.*, 1991**).A higher metabolic rate is linked to an increased use of thyroxine (**Decuypere *et al.*, 1982**). Differences are also observed between fat and lean broilers divergently selected for abdominal fat weight (**Decuypere *et al.*, 1994**). The growth hormone is considered to have a central role in growth; variations in circulating plasma growth hormone are related to differences in age, sex and strain of birds. Growth hormone has also been reported to affect lipid metabolism in birds (**Williams *et al.*, 1986**). The randombred lines exhibited consistently higher GH levels than the larger, faster growing broiler lines (**Stewart and Washburn, 1983**). No difference in T_3 plasma level between male and female chicks were noted although growth rate differed as reported by **Khun *et al*. (1982)**. The relatively slower growth rate, decreased longitudinal bone growth and increased carcass lipid (**Cravener *et al.*, 1989**). The hormones of the thyroid and GH axes are not only linked to growth and the incidence of ascites but also to protein and fat metabolism in broilers (**Buys *et al.*, 1999**).

The association between carcass traits and plasma constituents could be measured by simple correlations which measure the total association between a pair of characters, however that association does not exist by itself but a complicated interaction pathway is involved (**Sharma *et al.*, 1986 and El Gendy *et al.*, 1997**). Therefore, it is important to assess the direct and indirect contribution of each character to yield. Knowledge of these interrelationships is highly useful in selection for characters that are not easily observed or their genotype values are modified. Path analysis, as one of the multivariate statistical methods, helps in partitioning variability in a complicated system to their related variables. This technique is concerned with handling data obtained of several measurements on the same individual. The common source of each observation generally leads to the dependence or correlation between all measurements, and distinguishes multivariate data from their univariate prototypes (**Morrison, 1976**). Path analysis is a powerful technique for formulating an effective selection program including various component characters and determining the characters that contribute to the observed correlation among characters as reported by **Sharma *et al*. (1986)**. The low magnitude of direct and indirect effects of such a character on Y trait would suggest that the character does not directly or indirectly contribute to the enhancement of this system.

Path analysis is a variant of regression analysis which can establish a logical causal order to independent variables, then can look at their causal influence on each other as well as on the dependent variable (**Wright, 1934**

and Calder and Sapsford, 1996). In other words, path technique can be used to build predictive models and to measure strength of the relationship between the dependent variables and the set of independent variables (**Li, 1975, Babble, 1990 and Foster, 1998**). The path coefficient measures the importance of a given path influence and is defined as the ratio of variability of the considered cause to the total variability when all causes are constant except the one in question and the variability of which is kept unchanged. Consequently, a compensatory variable must exist in the system to diminish the variance of the dependent variable. The square of path coefficient measures the degree of determination of the cause. If the causes are independent of each other, the sum of the squared path coefficients is unity (**Li, 1975**). If the causes are correlated, terms representing joint determination must be recognized. In such, an analysis diagrams will be most helpful as qualitative representations to specify the exact nature of proposed structural relations and according to which the subsequent analysis will be made.

The present study was conducted to assess properties and composition of plasma constituents using path technique to partition the variation in growth performance and carcass traits to its main variables.

MATERIALS AND METHODS

Chicks of two selected lines of Japanese quail for high 42 day-body weight (HBW_6) and high 0-6week growth rate (HGR_{0-6}) of the 3rd generation were used to partition the variability of growth and carcass traits. A randombred control (RBC) line was kept in order to facilitate comparison between lines and to provide a mean for correcting environmental trends or fluctuations attributed to artificial selection and to reduce random genetic drift in the control and selected populations used **(Havenstein *et al.*, 1988)**. This study lasted for three generations after establishing the base population in order to study the response to selection in certain carcass traits and plasma constituents. The development of the three lines of Japanese quail from the base population was described by **Abdel Fattah (2006)**. After establishing the lines, all measurements were taken at the same age in the studied lines. Each line was propagated by three hatches, one week apart, of approximately 300 quail using 30 sires each mated to two dams. Hatches were considered as replications. Management practices were kept uniform as possible throughout the experimental period**.** Twelve chicks per sex within each line were decapitated and exsanguinated at 3 weeks of age in the morning before feeding. About 1.5 cm^3 of blood samples from each chick were collected into dry clean centrifuge tubes containing heparin and immediately centrifuged at 3000 rpm for 20 minutes. The clear plasma samples were carefully drawn and transferred to dry, clean, small glass bottles and stored at -20 °C in the deep freezer until the time of chemical determinations. Plasma samples were assayed for GH, T_3 (ng/dl) and T_4 (ng/dl) using **ELIZA** for the former and radioimmunoassay for the latter. Plasma constituents: Alb, TG, TL and TP were analyzed by enzymatic colorimetric tests using kits (STANBIO Laboratory INC., Texas, USA). The traits under study were: live body weight at slaughter (LBW_6), FC during the entire period of growth, BLM%, carcass%, dressing%, carcass fat%, carcass protein%, PI according to **North (1981)**, GH (ng/dl), Alb (g/dl), TG (mg/dl), TL (mg/dl), TP (g/dl) and the ratio of the T_3/T_4.

Statistical analyses

1. Performance of the traits

All percentages were transformed to their corresponding angles for statistical analysis according to **Winer (1971)** as the follows:

Arc-sin transformation = $\sqrt{}$ (1X/100+0.03) where:X is the measure taken as %.

Whenever the hatch effects were significant, these effects were corrected before analysis. So, data were subjected to one way analysis of variance to test hatch effect for the data using the following model:

$$Y_{ij} = \mu + H_i + e_{ij}$$

where: Y_{ij}: observed value in i^{th} hatch, **μ**: common mean, H_i : hatch effect (i: 1 and 3) and e_{ij} **:** residual error term. Data for carcass traits and plasma constituents were analyzed for line and sex as main effects according to the following model:

$$Y_{ijk}=\mu+ L_i +S_j+LS_{ij}+e_{ijk}$$

where: μ: Overall mean**,** L_i**:** Line effect (**i:** 1 and 3), S_j: Sex effect (**j:** 1 and 2), LS_{ij}: Interaction of line by sex and e_{ijk}: Random error term. Means were compared for effects of line and the Line X Sex interaction by Duncan's multiple range test (**Duncan, 1955**) when significant F value were obtained ($P \leq 0.05$).

2. Path coefficient analysis:

Figure 1 presents the proposed structural relations between each of BLM %, carcass%, dressing%, fat%, protein% and PI, respectively. According to **Wright (1934)**, the following model was used to express the phenotypic value of Y (e.g. BLM) for a specific individual:

$$Y = P_{GH}, BLM\ Y_{GH} + P_{Alb}, BLM\ Y_{Alb} + P_{TG}, BLM\ Y_{TG} + P_{TP}, BLM\ Y_{TP} + P_{TL}, BLM\ Y_{TL} + P_{TP}, BLM\ Y_{TP} + P_{T3/T4}, BLM\ Y_{T3/T4} + P_{U}, BLM.$$

where: Y is the estimated unstandardized **BLM**, P_{GH}**, BLM** is the path coefficient from the concrete variable Y_{GH}, P_{Alb}, P_{TG}, P_{TL}, P_{TP} and $P_{T3/T4}$ represents the other path coefficients for other traits in the model and **U** is the residual variation. Similar models were used for carcass%, dressing%, fat%, protein% and PI.

RESULTS AND DISCUSSION

Performance of the traits: Means of productive traits and plasma constituents in different genetic groups of Japanese quail are presented in Table 1a. Line significantly ($P<0.01$) affected each of BLM%, fat%, LBW_6, FC and PI, however insignificantly affected carcass%, dressing% and protein%. The RC had the lowest BLM%, fat% and LBW_6 (48.13%, 16.09% and 184.65g, respectively). Although HGR had the highest BLM% and dressing%, birds of this line had significantly poorer FC and PI than other lines. On the other hand, birds of HBW line had the highest LBW_6 and PI but were associated with higher carcass fat% (200.25g, 3.55 LBW/FC and 20.51%, respectively). Sex significantly affected BLM%, carcass%, dressing%, LBW_6, FC and PI, whereas insignificantly affected other productive traits. Although males had significantly higher carcass%, their PI were poorer than females, this may be due to the superiority of female's growth than males at different ages of growth. In addition to that, sex difference was attributed primarily to the relatively large ovaries, liver and intestines of the females; when these parts were excluded, lower carcass% for females were obtained (**Wilson *et al.*, 1961** and **Abdel Fattah, 2001**).

Fig. 1

Except TG, line significantly affected all plasma constituents as shown in Table 1a. The RC line had the highest GH and the lowest Alb, TL, TP, T_3 and T_3/T_4. Whereas, HGR had the lowest GH and the highest Alb, TP, T_3 and T_4. Higher estimates of either T_4 or GH and lower T_3 estimates were reported by several investigators for broilers at 3 weeks of age (**Stewart and Washburn, 1983, Stewart and Washburn, 1984, Cravener *et al.*,1989, Buyse *et al.*,1991, Buys *et al.*,1999, Buyse *et al.*,2001, Tona *et al.*, 2004, Nijdam *et al.*, 2005** and **Rahimi, 2005**b). Whereas, higher TG estimate for Pekin ducks was reported by **Farahat and Chavez (2000)**.

There were significant sex differences for Alb, TP, T_3 and T_3/T_4. Females had significantly higher Alb, TP and T_3/T_4 than males, however, males had higher T_3 than females as shown in Table1a. Similar trends of significant sex effect in T_3, T4 and TG were reported by **Stewart and Washburn (1984), Buyse *et al.* (1991), Buys *et al.* (1999**) and **Rahimi (2005b**). The significant line by sex interaction for dressing%, FC, PI, GH, TL, T_3 and T_4 are presented in Table 1b. Males of the HGR had the highest dressing% and poorest FC, whereas, females of the HBW had the best PI and lowest FC. Males of the RBC had the highest GH whereas males of the HGR had the lowest GH. The highest TL was shown for each of males of the HBW and either females of the HGR or HBW lines, however females of the RBC had the lowest TL. The highest T_3 and T_4 was found for females of both HGR and HBW lines however the lowest T_3 was obtained by females of the RBC. Also, females of the HBW had the lowest T_4 as shown in Table 1b.

2. Path coefficient analysis:

Direct and indirect effects estimated by the coefficient of determination (R^2), of GH, Alb, TG, TL, TP and the ratio of T_3/T_4 on BLM%, carcass%, dressing%, fat%, protein% and PI variations are presented in Tables from 2 to 7.

The average determined direct effects of plasma constituents on BLM%, carcass%, dressing%, fat%, protein% and PI ranged from 0.392 to 0.585, 0.360 to 0.510, 0.278 to 0.558, 0.311 to 0.603, 0.404 to 0.519 and 0.353 to 0.579, respectively. The corresponding indirect effects on these traits ranged from 0.416 to 0.609, 0.490 to 0.640, 0.442 to 0.722, 0.397 to 0.689, 0.481 to 0.596 and 0.421, to 0.602, respectively for previously mentioned traits. However, the mean random variation (residual) for these traits ranged from 0.645 to 0.780, 0.699 to 0.800, 0.665 to 0.850, 0.630 to 0.830, 0.694 to 0.772 and 0.648 to 0.804 respectively for BLM%, carcass%, dressing%, fat%, protein% and PI (Tables 2 to 7). It can be concluded that plasma constituents showed higher indirect coefficients of determination for their effects on all studied productive traits than their direct effects. This suggests that a part of the variations in these traits could be attributed to a trait or more, not taken into consideration in this study and may diminish the random error variation when considered.

Results presented in Table 2 revealed that TP caused the largest direct effects on BLM% of males of HGR, both males and females of the RC line(0.699, 0.541 and 0.632, respectively) compared to other constituents. Both TG (for females of HGR and males of HBW) and GH for females of HBW had the greatest contribution in variations of BLM% (0.906, 0.887 and 0.969, respectively).

Table 1a. Means ± SD for productive traits and plasma constituents in different genetic groups of Japanese quail (Main effects).

Trait @	Line effect@			Sex effect	
	HGR	HBW	RC	M	F
Productive traits					
BLM%	55.85±2.12^{a}	54.06±2.27^{b}	48.13±1.78^{c}	53.36±3.38^{a}	51.99±4.29^{b}
Carcass%	67.39±1.02^{a}	67.24±1.31^{a}	67.07±1.15^{a}	68.17±0.67^{a}	66.29±0.66^{b}
Dressing%	78.16±0.48^{a}	77.82±0.85^{a}	78.03±0.80^{a}	78.25±0.72^{a}	77.76±0.67^{b}
Fat%	19.58±2.61^{a}	20.51±3.72^{a}	16.09±4.49^{b}	19.00±3.92^{a}	18.45±4.33^{a}
PI	3.12±0.41^{c}	3.55±0.74^{a}	3.34±0.32^{b}	2.94±0.38^{b}	3.73±0.37^{a}
Protein%	19.62±0.52^{a}	19.76±0.40^{a}	19.85±0.40^{a}	19.78±0.43^{a}	19.71±0.71^{a}
LBW6	195.88±13^{a}	200.25±14^{a}	184.65±19^{b}	184.94±13^{b}	202.24±10^{a}
FC	5.49±0.71^{a}	4.76±0.75^{b}	4.79±0.23^{b}	5.45±0.67^{a}	4.58±0.35^{b}
Plasma constituents					
GH,ng/dL	0.1333±0.03^{b}	0.1367±0.03^{b}	0.1600±0.03^{a}	0.1456±0.04^{a}	0.1411±0.03^{a}
Alb, g/dl.	1.7453±0.29^{a}	1.4675±0.30^{b}	1.2712±0.34^{c}	1.3680±0.34^{b}	1.6213±0.35^{a}
TG, mg/ dL	122.17±25^{a}	107.50±18^{a}	124.00±30^{a}	120.44±26^{a}	115.33±26^{a}
TL, mg/ dL	660.00±108^{b}	721.67±88^{a}	574.67±67^{c}	663.11±111^{a}	641.11±103^{a}
TP, g/ dL	3.6467±0.69^{a}	3.1323±0.58^{b}	2.5945±0.69^{c}	2.9347±0.90^{b}	3.3143±0.59^{a}
T_3, ng/ dL	55.50±32^{a}	51.00±18^{a}	29.17±24^{b}	49.89±25^{a}	40.56±29^{b}
T_4, ng/ dL	0.2100±0.07^{a}	0.1483±0.03^{b}	0.1633±0.06^{b}	0.1733±0.06^{a}	0.1744±0.06^{a}
T_3/T_4	292.29±219^{a}	344.59±121^{a}	168.29±101^{b}	307.55±177^{a}	229.23±156^{b}

@HGR: A line selected for high growth rate , HBW: A line selected for high body weight, RC: Random bred control line, M: Male, F: Female, BLM%: Boneless meat%, GH: Growth hormone, Alb: Plasma albumen, TG: Plasma triglyceride, TL: Plasma total lipids, TP: Plasma total proteins, T3&T4: Triiodothyronine& thyroxine. Means having different superscripts within each effect within the same raw are significantly different at P≤0.05.

Table 1b. Significant interaction effects for line by sex in Japanese quail.

Trait	HGR		HBW		RC	
	M	F	M	F	M	F
Dressing%	78.48±0.33^{a}	77.84±0.39^{b}	78.36±0.36^{ab}	77.28±0.86^{c}	77.92±1.10^{ab}	78.15±0.32^{ab}
FC	6.16±0.26^{a}	4.83±0.09^{c}	5.29±0.64^{b}	4.22±0.38^{d}	4.90±0.25^{c}	4.68±0.14^{c}
PI	2.73±0.09^{d}	3.51±0.08^{b}	2.97±0.52^{cd}	4.12±0.37^{a}	3.11±0.29^{c}	3.56±0.17^{b}
GH	0.120±0.02^{c}	0.147±0.03^{b}	0.137±0.03^{bc}	0.137±0.03^{bc}	0.180±0.03^{a}	0.140±0.08^{bc}
TL	605.00±121^{c}	715.00±56^{a}	753.33±102^{a}	690.00±60^{ab}	631.00±18^{bc}	518.33±46^{d}
T_3	45.33±38^{b}	65.67±22^{a}	56.00±12^{ab}	46.00±22^{b}	48.33±20^{ab}	10.06±0.0^{c}
T_4	0.170±0.06^{bc}	0.250±0.06^{a}	0.167±0.03^{bc}	0.130±0.00^{c}	0.183±0.08^{b}	0.143±0.01^{bc}

Means having different superscripts within the same raw are significantly different at P≤0.05.

Table 2. Means of direct and indirect coefficient of determination (R^2), using path coefficient analysis for the variability in boneless meat%, by line and sex group.

Trait @	R^2	HGR		HBW		RC	
		M	F	M	F	M	F
GH	Direct	0.396	0.742	0.531	0.969	0.428	0.249
	Indirect	0.604	0.258	0.469	0.032	0.572	0.751
Alb	Direct	0.531	0.217	0.567	0.422	0.539	0.111
	Indirect	0.469	0.783	0.434	0.579	0.461	0.889
TG	Direct	0.156	0.906	0.887	0.264	0.524	0.546
	Indirect	0.844	0.094	0.113	0.736	0.476	0.454
TL	Direct	0.492	0.194	0.605	0.275	0.440	0.203
	Indirect	0.508	0.806	0.395	0.725	0.560	0.797
TP	Direct	0.699	0.804	0.553	0.619	0.541	0.632
	Indirect	0.301	0.196	0.447	0.381	0.460	0.368
T_3/T_4	Direct	0.594	0.198	0.364	0.332	0.015	0.607
	Indirect	0.406	0.802	0.636	0.668	0.985	0.393
Average	*Direct*	*0.478*	*0.510*	*0.585*	*0.480*	*0.414*	*0.392*
	Indirect	*0.522*	*0.490*	*0.416*	*0.520*	*0.586*	*0.609*
	Residual	*0.722*	*0.699*	*0.645*	*0.721*	*0.765*	*0.780*

@:As footnoted in Table 1.

Ratio of T_3/T_4 had larger direct effect on carcass% for males of HGR of 0.892 than other constituents. Where TP was the most important constituents causing variability in carcass% for females of HGR. For females of HBW, TL had the largest direct contribution of 0.987 in carcass%. Also, TG showed the major direct effect on the variations in carcass% for both males of HBW and RC line and females of the RC (0.582, 0.713 and 0.892, respectively) as shown in Table 3.

Table 3. Means of direct and indirect coefficient of determination (R^2), using path coefficient analysis for the variability in carcass%, by line and sex group.

Trait @	R^2	HGR		HBW		RC	
		M	F	M	F	M	F
GH	Direct	0.249	0.416	0.559	0.082	0.446	0.063
	Indirect	0.751	0.584	0.441	0.919	0.554	0.937
Alb	Direct	0.660	0.697	0.517	0.280	0.530	0.213
	Indirect	0.340	0.304	0.483	0.720	0.469	0.787
TG	Direct	0.214	0.092	0.582	0.078	0.713	0.892
	Indirect	0.786	0.908	0.418	0.922	0.287	0.108
TL	Direct	0.351	0.381	0.544	0.987	0.463	0.106
	Indirect	0.649	0.619	0.456	0.013	0.537	0.894
TP	Direct	0.507	0.759	0.414	0.125	0.504	0.856
	Indirect	0.493	0.241	0.586	0.875	0.496	0.144
T_3/T_4	Direct	0.892	0.717	0.436	0.619	0.103	0.029
	Indirect	0.107	0.283	0.564	0.381	0.897	0.971
Average	*Direct*	*0.479*	*0.510*	*0.509*	*0.362*	*0.460*	*0.360*
	Indirect	*0.521*	*0.490*	*0.491*	*0.638*	*0.540*	*0.640*
	Residual	*0.722*	*0.699*	*0.701*	*0.799*	*0.735*	*0.800*

@:As footnoted in Table 1.

TL was found to play the most important role in explaining the variation in dressing% for males of HGR, males of HBW and females of the RC line with direct coefficients of determination of 0.800, 0.767 and 0.987, respectively. Dressing% for females of HGR was mainly affected by T_3/T_4 (0.823) whereas this trait was extremely influenced by TP with direct contribution of 0.945 for females of HBW. Lower direct effect of Alb being 0.558 was shown in the variation of dressing% for males of the RC line (Table 4).

Table 4. Means of direct and indirect coefficient of determination (R^2), using path coefficient analysis for the variability in dressing%, by line and sex group.

Trait @	R^2	HGR		HBW		RC	
		M	F	M	F	M	F
GH	Direct	0.666	0.166	0.417	0.169	0.345	0.167
	Indirect	0.334	0.834	0.583	0.831	0.655	0.833
Alb	Direct	0.177	0.175	0.670	0.042	0.558	0.312
	Indirect	0.823	0.825	0.330	0.958	0.442	0.688
TG	Direct	0.310	0.675	0.103	0.499	0.318	0.090
	Indirect	0.690	0.325	0.897	0.501	0.682	0.910
TL	Direct	0.800	0.714	0.767	0.462	0.284	0.987
	Indirect	0.200	0.286	0.233	0.538	0.716	0.013
TP	Direct	0.628	0.797	0.336	0.945	0.041	0.731
	Indirect	0.373	0.203	0.664	0.055	0.959	0.269
T_3/T_4	Direct	0.417	0.823	0.348	0.521	0.119	0.399
	Indirect	0.583	0.177	0.562	0.479	0.881	0.601
Average	*Direct*	*0.499*	*0.558*	*0.440*	*0.440*	*0.278*	*0.448*
	Indirect	*0.501*	*0.442*	*0.560*	*0.560*	*0.722*	*0.552*
	Residual	*0.708*	*0.665*	*0.748*	*0.749*	*0.850*	*0.743*

@:As footnoted in Table 1.

Table 5. Means of direct and indirect coefficient of determination (R^2), using path coefficient analysis for the variability in fat%, by line and sex group.

Trait @	R^2	HGR		HBW		RC	
		M	F	M	F	M	F
GH	Direct	0.416	0.743	0.097	0.536	0.445	0.117
	Indirect	0.584	0.257	0.903	0.464	0.555	0.883
Alb	Direct	0.754	0.056	0.020	0.763	0.463	0.511
	Indirect	0.246	0.944	0.980	0.237	0.537	0.489
TG	Direct	0.617	0.464	0.731	0.430	0.458	0.404
	Indirect	0.383	0.536	0.269	0.570	0.542	0.596
TL	Direct	0.373	0.298	0.566	0.564	0.959	0.563
	Indirect	0.627	0.702	0.434	0.436	0.041	0.437
TP	Direct	0.774	0.009	0.259	0.859	0.579	0.498
	Indirect	0.226	0.991	0.741	0.141	0.421	0.502
T_3/T_4	Direct	0.668	0.297	0.376	0.464	0.175	0.609
	Indirect	0.332	0.703	0.624	0.536	0.825	0.391
Average	*Direct*	*0.601*	*0.311*	*0.342*	*0.603*	*0.513*	*0.450*
	Indirect	*0.399*	*0.689*	*0.658*	*0.397*	*0.487*	*0.549*
	Residual	*0.632*	*0.830*	*0.812*	*0.630*	*0.698*	*0.742*

@:As footnoted in Table 1.

It was found that TP had major effects on the variation of fat% in both males of HGR and females of HBW (0.774 and 0.859). GH was the most important contributor in variability of fat% for females of HGR(0.743). Also, TG had the largest contribution in fat% for males of the HBW (0.731). Whereas, the first largest direct contributors to variability of fat% in males and females of the RC line were TL and T_3/T_4 in a descending order (0.959 and 0.609, Table 5).

In both males of HGR and females of RC line, TG showed the greatest direct effects of 0.551 and 0.938 on protein% as shown in Table 6. Also, GH was the most important constituents causing variability in protein% in these groups: females of HGR, females of HBW and males of the RC line with direct R^2 of 0.513, 0.875 and 0.701, respectively. In males of HBW, it was found that TL had the major direct effect of 0.775 on the variation in protein% (Table 6).

PI in both males and females of HGR was mainly affected by T_3/T_4 with direct R^2 of 0.692 and 0.682 (Table 7). It can be seen that TP was found to be the most important contributor in PI variations for males of HBW and females of RC line (0.790 and 0.881). Also, GH had the largest direct effect on the variation of PI between individuals for females of the HBW (0.781). However, Alb was the most important constituents causing variability in PI for males of the RC line with direct effect of 0.548 as shown in Table 7. In other words, effects of plasma constituents on studied productive traits were not similarly ranked in the different line by sex groups.

In conclusion, TP had the largest contribution in variations of BLM%, carcass%, dressing%, fat% and PI. The contributions of TG were high in explaining the variability in each of BLM%, carcass%, fat% and protein%. GH had the first major influence on variations in BLM%, fat%, protein% and PI. Also, T_3/T_4 was the first contributor to variations of carcass%, dressing%, fat% and PI. Similarly, TL had the major direct effect on the variability in each of carcass%, dressing%, fat% and protein%. Also, Alb was the most contributor in variability of the dressing% and PI for males of the RC line.

Table 6. Means of direct and indirect coefficient of determination (R^2), using path coefficient analysis for the variability in protein%, by line and sex group.

Trait @	R^2	HGR		HBW		RC	
		M	F	M	F	M	F
GH	Direct	0.104	0.513	0.027	0.875	0.701	0.469
	Indirect	0.896	0.487	0.973	0.125	0.299	0.531
Alb	Direct	0.487	0.472	0.277	0.616	0.280	0.740
	Indirect	0.513	0.528	0.723	0.384	0.720	0.260
TG	Direct	0.551	0.430	0.523	0.210	0.544	0.938
	Indirect	0.449	0.570	0.477	0.790	0.456	0.062
TL	Direct	0.507	0.494	0.775	0.092	0.438	0.344
	Indirect	0.493	0.506	0.225	0.908	0.562	0.656
TP	Direct	0.467	0.505	0.563	0.475	0.492	0.621
	Indirect	0.533	0.495	0.437	0.526	0.508	0.379
T_3/T_4	Direct	0.493	0.453	0.258	0.154	0.107	0.001
	Indirect	0.507	0.547	0.742	0.846	0.893	0.999
Average	*Direct*	*0.435*	*0.478*	*0.404*	*0.404*	*0.427*	*0.519*
	Indirect	*0.565*	*0.522*	*0.596*	*0.596*	*0.573*	*0.481*
	Residual	*0.752*	*0.723*	*0.772*	*0.772*	*0.757*	*0.694*

@:As footnoted in Table 1.

Table 7. Means of direct and indirect coefficient of determination (R^2), using path coefficient analysis for the variability in PI, by line and sex group.

Trait @	R^2	HGR		HBW		RC	
		M	F	M	F	M	F
GH	Direct	0.293	0.535	0.487	0.781	0.119	0.277
	Indirect	0.707	0.465	0.513	0.219	0.881	0.723
Alb	Direct	0.251	0.511	0.434	0.699	0.548	0.078
	Indirect	0.749	0.489	0.566	0.301	0.452	0.923
TG	Direct	0.470	0.033	0.579	0.245	0.351	0.641
	Indirect	0.530	0.967	0.421	0.755	0.649	0.359
TL	Direct	0.665	0.075	0.743	0.402	0.530	0.231
	Indirect	0.335	0.925	0.257	0.598	0.470	0.769
TP	Direct	0.433	0.555	0.790	0.256	0.370	0.881
	Indirect	0.567	0.445	0.210	0.744	0.630	0.119
T_3/T_4	Direct	0.692	0.682	0.446	0.016	0.201	0.294
	Indirect	0.308	0.318	0.554	0.984	0.799	0.706
Average	*Direct*	*0.467*	*0.398*	*0.579*	*0.400*	*0.353*	*0.401*
	Indirect	*0.533*	*0.602*	*0.421*	*0.600*	*0.467*	*0.599*
	Residual	*0.730*	*0.776*	*0.648*	*0.775*	*0.804*	*0.774*

@:As footnoted in Table 1.

Results of the present study revealed that the studied plasma constituents measured at three weeks of age in both sexes could be used to predict carcass traits and growth productive performance in Japanese quail with high precision since these constituents were the most important contributors that significantly affected either directly or indirectly these traits.

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استخدام معامل المرور لتجزئة الاختلافات فى صفات النمو والذبيحة فى ثلاثة خطوط من السمان اليابانى

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استخدمت بيانات خطين منتخبين من السمان اليابانى لصفات وزن الجسم العالى عند عمر ٦ أسابيع والآخر منتخب لمعدل النمو العالى فى الفترة من عمر يوم الى ٦ أسابيع من العمر لمدة ٣ أجيال لتحليل الاختلافات فى بيانات النمو والذبيحة لهم. وقد تم الاحتفاظ بخط للمقارنة عشوائى التلقيح لتيسير المقارنة بين تلك الخطوط. كانت الصفات الإنتاجية المدروسة هى: نسبة التشافى، نسبة الذبيحة، نسبة الدهن، نسبة البروتين ودليل الأداء الإنتاجى (جم زيادة بالوزن/ جم علف مأكول). وكانت مكونات بلازما الدم المدروسة هى: هرمون النمو، الألبيومين، الجلسريدات الثلاثية، الدهون الكلية، البروتين الكلى و النسبة بين T_3/T_4 (ثلاثى أيوديد الثيرونين/ الثيروكسين). كان لخط المقارنة نسب التشافى والدهن الأقل وكذلك وزن الجسم (٤٨.١٣%، ١٦.٠٩% و١٨٤.٦٥ جم على التوالى). بالرغم من أن خط HGR كانت له نسب التشافى والتصافى الأعلى إلا أن معامل التحويل ودليل الأداء الانتاجى له كانا الأسوأ عن باقى الخطوط. ومن جهة أخرى فان طيور خط HBW كان لها أعلى وزن جسم و دليل أداء انتاجى لكن أيضا كانت له نسبة دهن أعلى فى الذبيحة (٢٠٠.٢٥جم، ٣.٥٥جم عائد نمو/جم علف مأكول و٢٠.٥١%). كما أثر الجنس معنويا على صفات نسب التشافى، الذبيحة، التصافى، وزن الجسم الحى، معامل التحويل و دليل الأداء الانتاجى. فبالرغم من أن الذكور كان لها نسبة ذبيحة أعلى إلا أن دليل الأداء لها كان أسوأ وربما يعزى ذلك إلى أن الإناث تتفوق على الذكور فى النمو على الأعمار المختلفة وربما يرجع هذا الفرق إلى أن للإناث أوزانا أعلى نسبيا للمبايض والكبد والأمعاء فإذا استبعدت تلك الأجزاء كانت نسبة الذبيحة للإناث أقل. فيما عدا الجليسريدات الثلاثية بالسيرم فان تأثير الخط كان معنويا على كل مكونات البلازما. كان خط المقارنة الأعلى فى تركيز هرمون النمو و الأقل فى الألبيومين، الدهون الكلية، البروتين الكلى T_3 و T_3/T_4. بينما كان خط HGR الأقل فى تركيز هرمون النمو والأعلى فى الألبيومين، البروتين الكلى و T_3 وT_4 . وكانت الإناث الأعلى معنويا فى الألبيومين، البروتين الكلى و T_3/T_4عن الذكور بينما كان للذكور T_3 عن الإناث. وقد أظهرت نتائج Path analyses أن مكوناتالبلازما المدروسة المقاسة عند عمر ثلاثة أسابيع يمكن استخدامها فى التنبؤ بصفات النمو والأداء الانتاجى والذبيحة فى السمان اليابانى. وجد أن كلا من هرمون النمو، الجلسريدات الثلاثية، الدهون الكلية، البروتين الكلى وT3/T4 هى المساهم الأول فى الصفات الإنتاجية المدروسة فى المجموعات المدروسة من الخطوط و الجنسين مبينا أن التأثيرات المباشرة لها تتراوح بين ٠.٥٣٠الى٠.٧٦٣ ،٠.٥٠٤الى ٠.٩٤٥، ٠.٨٨٧الى٠.٩٠٦، ٠.٥١٣الى ٠.٩٩٠، ٠.٦٠٩الى ٠.٨٩٢على التوالى. كما أظهرت مكونات البلازما معاملات تقدير غير مباشرة أعلى من تأثيراتها المباشرة على الصفات الإنتاجية المدروسة. لذا من المقترح أن يكون مرجع ذلك أن جزء من التباين بهذه الصفات ربما يعزى إلى أن هناك صفة أو أكثر لم تشملها الدراسة فان شملتها أدى ذلك إلى تقليل تباين الخطأ العشوائى عند أخذها فى الاعتبار.

Figure 1. Path diagram for the relationships of Y's (BLM%, carcass%, dressing%, fat%, protein% and performance index) with plasma constituents at 3 weeks of age: growth hormone (GH), albumin (Alb), triglycerides (TG), total lipids (TL), total protein (TP) and the ratio of the triiodothyronine to thyroxine (T_3/T_4) and U, where U is the residual, P is the path coefficient and r stands for the correlations.