USING STEPWISE REGRESSION ANALYSIS TO PARTITION THE VARIABILITY IN GROWTH AND SOME CARCASS TRAITS IN THREE LINES OF JAPANESE QUAIL DIFFERING IN GENETIC BACKGROUND.

Ensaf A. El Full, Bothaina Y. F. Mahmoud, Hanan A. Hassan and E. M. Omar.
Poultry Production Dept., Faculty of Agriculture, Fayoum Univ., Egypt.

ABSTRACT:

Data of blood and/or plasma constituents of three weeks old Japanese quail were used to predict the growth and some carcass traits of 6 weeks old quail. Stepwise regression analysis was performed to partition the variability in growth and carcass traits of three lines of Japanese quail differing in genetic background. The first and second lines were selected over three generations for high six week-body weight (HBW_6) and high 0-6 week growth rate (HGR_{0-6}) respectively, whereas the third randombred control line (RC) was kept in order to facilitate comparison among lines. The results cleared that the most important predictor for live body weight at six weeks of age (LBW_6) in both males of RC and males of HGR was thyroxine (T_4). Both plasma total lipids and total proteins (TL and TP) were the best predictors for LBW_6 for females of RC line. Model 2 which used hemoglobin (Hb) and T_4 was the best model for predicting LBW_6 for males of HBW_6. Whereas, TL was the most important predictor for LBW_6 for females of HBW_6 line. The most important predictors for feed conversion (FC) were TL and T_4 for males of RC line, white and red blood cells (WBC and RBC) for females of RC, T_4 and packed cell volume (PCV) for males of HGR_{0-6}, triglycerides (TG) and TL for females of HGR_{0-6}, TL and WBC for males of HBW_6 and growth hormone (GH) and PCV for females of HBW_6 line. Performance index (PI) was predicted through TL and albumin (Alb) for males of RC, TP and GH for females of RC, T_4 and PCV for males of HGR, TG and TP for females of HGR, TL and ratio of triiodothyronine to thyroxine (T_3/T_4) for males of HBW_6 and TG and T_3/T_4 for females of HBW_6. For predicting dressing% in all studied groups, the most important predictors were T_3/T_4 and TP for males of RC, TP and GH for females of RC, ratio of T_3/T_4 and T_3 for males of HGR_{0-6}, Alb and TP for females of HGR_{0-6}, PCV and RBC for males of HBW_6, Alb and T_3/T_4 for females of HBW_6, respectively. Carcass% for all studied groups could be predicted using these predictors: PCV and GH for males of RC, GH and TG for females of RC, GH and RBC for males of HGR_{0-6}, WBC and T_3 for females of HGR_{0-6}, T_3/T_4 and Hb for females of HBW_6, respectively. The most important predictors for boneless meat% (BLM) were RBC and TP for males of RC, Hb and Alb for females of RC, TG and T_4 for males of HGR_{0-6}, TP and T_4 for females of HGR_{0-6}, T_3/T_4 and Alb for males of HBW_6 and TL and Hb for females of HBW_6, respectively. The major predictor in determining protein% for both males and females of the HBW_6 line was T_3. The most important predictors for fat% were T_3/T_4, TL and TP in a descending order for males and females of the RC line and males of HBW_6, respectively. The predicted traits were insignificantly differed than the actual values or percentages ($P>0.05$). Therefore, results of the stepwise regression analyses revealed that either certain studied hematological values or plasma constituents at three weeks of age in studied lines of both sexes could be used to predict carcass and growth productive traits in Japanese quail with high precision and low error.

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

INTRODUCTION

Genetic variations that are manifested in the variability of tissue composition and metabolic processes between strains provide means of evaluating such physiological developmental changes due to genetic selection (**Stewart and Washburn, 1983**). Thus, it is important to assess the significant contribution of each character to the yield. Knowledge of these interrelationships is highly useful in selection for characters that are not easily observed or their genotypic values are modified.

There is abundant evidence that thyroid hormones are very important for normal growth in birds (**Decuypere *et al.*, 1991**). 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 lipids metabolism in birds (**Williams *et al.*, 1986**). The relatively slower growth rate increased carcass lipid (**Cravener *et al.*, 1989**). However, it seems that little or no information is available of the relationship between hematological parameters, carcass traits and productive traits of Japanese quail.

Stepwise regression analysis, as one of the multivariate methods, helps in partioning 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 it is this feature that distinguishes multivariate data from their univariate ones (**Morrison, 1976**). Stepwise analysis is a powerful technique for formulating an effective selection program including various component characters and determining the characters that contribute to the observed correlations among characters as reported by **Foster (1998)**. The low magnitude of effects of such a character on Y trait would be removed from the model and suggests that the character does not directly or indirectly contribute to the enhancement of this system. In other words, stepwise 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. In order to compare the relative efficiency of various models and to select the most suitable model, the following two criteria were used. One, is the coefficient of determination (R^2) and the other is standard error of the estimate (SEE). A larger value of R^2 and smaller value of SEE indicate best fit of the model. The present study aimed to determine the major predictors of hematological parameters and plasma constituents using stepwise technique to partition and rank the variation in growth system and carcass traits to its main and significant variables.

MATERIALS AND METHODS

Chicks of two selected lines of Japanese quail for high six week-body weight (HBW_6) and high 0-6week growth rate (HGR_{0-6}) of the 1st generation were used to partition the variability of growth and carcass traits. A randombred control (RC) line was kept in order to facilitate comparison among lines and to provide a mean for correcting environmental trends or

fluctuations brought about by artificial selection and to reduce random genetic drift in the control and selected populations used (**Havenstein** *et al.,* **1988**). The development of the three lines of Japanese quail from the base population is described by **Abdel Fattah (2006)**. Mangement practices were kept uniform as possible throughout the experimental period. LBW and feed intake were recorded to calculate FC (feed, g/gain, g) and PI (LBW/FC) according to **North (1981).** Twelve chicks per sex within each line were decapitated and exsanguinated to perform a slaughter test at six weeks of age and estimate both protein% and fat% for the whole carcass. Red blood and white blood cells (RBC and WBC), packed cell volume (PCV) and hemoglobin (Hb) were measured for all sexes by line groups. About 1.5 cm^3 of blood from each chick were collected into dry clean centrifuge tubes containing heparin and immediately centrifuged at 3000 rpm for 20 minutes. The clear plasma were carefully drawn and transferred to dry, clean, small glass bottles and stored at -20ºC in the deep freezer until the time of chemical determinations. Plasma samples assayed for GH, T_3 and T_4 using **ELIZA** for GH and radioimmunoassay for T_3 and T_4. 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, PI during the entire period of growth, BLM%, carcass%, dressing%, fat%, protein% of the carcass, GH, Alb, TG, TL, TP, T_3, T_4 and the ratio of 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)**. 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: Y_{ijk}: Observed value in the ith line of the jth sex and the kth individual, 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. Stepwise regression analyses
     The following linear regression model according to **Steel and Torrie (1980)** for a sample was given as:

$$\hat{Y} = a + b_1X_1 + b_2X_2+ b_3X_3+ \ldots.. +b_kX_k + \varepsilon_i.$$

where $\hat{Y}$: is the expected value or mean of the population of Y's for a specified set of values of the X's, **a**: represents the Y intercept, **b's** represents slopes of Y on X that measures the increase or decrease in Y per unit change of X and ε_i: is a deviation of the observation from the regression line, or a residual.

     Differences between actual and predicted estimates for studied productive traits were tested by Student's t-test (**SPSS, 1999**).

RESULTS AND DISCUSSION
1. Performance of the traits
     Means of productive traits, hematological parameters and plasma constituents in different genetic groups of Japanese quail are presented in Table 1a. Line significantly (P<0.01) affected each of LBW_6, FC, PI, BLM%

and carcass fat%, however, it insignificantly affected dressing%, carcass%, and carcass protein%. The RC line had the lower LBW_6, BLM% and carcass fat% (184.65g, 48.13% and 5.05%, respectively) than selected lines. Birds of HBW_6 line had the higher LBW_6 and PI carcass fat% and better FC(Table 1a). In spite of the highest dressing% and BLM%, birds of HGR_{0-6} line, it showed significantly poorer FC and PI than other lines. Similar trend was reported by **El Full and Omar (2006)**.

Sex significantly affected LBW_6, FC, PI, dressing%, carcass%, and BLM%, whereas it 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 females growth than males at different ages and this difference nay be attributed primarily to the relatively large ovaries, liver and intestines of the females. When these parts excluded, lower carcasses% for females were obtained (**Wilson et al., 1961, Farahat, 1998, Abdel Fattah, 2001** and **El Full and Omar, 2006**).

Statistically, line insignificantly affected all studied hematological parameters. Similarly, sex insignificantly affected PCV% and WBC. On the other hand, several investigators reported that male of Japanese quail had significantly higher PCV% than female (**Atwal et al., 1964, Mihailov et al., 1999 and Abdel Azeem et al., 2001** and **El Full and Omar, 2006**). Lower estimate of 28.28% for PCV% for broilers was reported by **Pakdel et al. (2005)**. However, females had significantly higher RBC than males (Tabl;e 1a). This is expected since females had better performance than males which may be due to higher oxygen demand from the anabolic processes, together with high ME maintenance requirements which may result in the maximum oxygen delivery capacity of the respiratory and cardiovascular system (**Decuypere et al., 2003**). Similar results were reported by **Abou Zeid et al. (2000)** for RBC, PCV% and Hb but higher reported estimate for WBC in Japanese quail than those found in this study.

Except TG, line significantly ($P \leq 0.01$) affected all plasma constituents as shown in Table 1a. Birds of the RC line had the highest GH and the lowest TP, Alb, TL, T_3 and T_3/T_4. This result is in harmony with that reported for GH in broilers by **Stewart and Washburn (1983)**. Whereas, HGR_{0-6} had lower GH and T_3 while had the highest TP, Alb 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, 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**). Whereas, higher TG estimate for Pekin ducks was reported by **Farahat and Chavez (2000)**.

Females had significantly higher TP and Alb than males, however, males had higher T_3 and T_3/T_4 than females as shown in Table1a. Similar results were reported by **Stewart and Washburn (1984), Buyse et al.(1991), Buys et al.(1999)** and **Rahimi (2005)**.

The significant line by sex interactions are presented in Table 1b. Females of the HBW_6 line had the best PI and FC, whereas, males of the RC line had the highest GH. Males of the HGR_{0-6} line had higher dressing% and the poorest FC, whereas males of the HGR_{0-6} line had lower GH. Higher TL was shown for males of the HBW_6 and both females of the HGR_{0-6} and HBW_6 lines, however, females of the RC line had the lowest TL. The highest T_3 and T_4 were found for females of HGR_{0-6}, however, the lowest T_3 and T_4

were obtained for females of the RC and HBW$_6$ lines, respectively as shown in Table 1b.

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

Trait	Line effect@			Sex effect	
	RC	**HBW**	**HGR**	♂	♀
Productive traits at 6 weeks of age					
LBW$_6$	184.65±19^b	200.25±14^a	195.88±13^a	184.94±13^b	202.24±10^a
FC	4.79±0.23^b	4.76±0.75^b	5.49±0.71^a	5.45±0.67^a	4.58±0.35^b
PI	3.34±0.32^b	3.55±0.74^a	3.12±0.41^c	2.94±0.38^b	3.73±0.37^a
Dressing%	78.03±0.80^a	77.82±0.85^a	78.16±0.48^a	78.25±0.72^a	77.76±0.67^b
Carcass%	67.07±1.15^a	67.24±1.31^a	67.39±1.02^a	68.17±0.67^a	66.29±0.66^b
BLM%	48.13±1.78^c	54.06±2.27^b	55.85±2.12^a	53.36±3.38^a	51.99±4.29^b
Protein%	19.85±1.53^a	19.76±0.40^a	19.62±0.52^a	19.78±0.43^a	19.71±0.71^a
Fat%	5.05±4.49^b	6.89±1.11^a	6.56±0.61^a	6.27±1.27^a	6.06±1.51^a
Hematological parameters at 3 weeks of age					
PCV, %	41.17±1.24^a	41.17±1.90^a	41.83±1.09^a	41.17±1.62^a	41.61±1.28^a
Hb, g/dl	12.33±1.37^a	12.59±1.06^a	12.23±1.43^a	12.01±1.53^b	12.76±0.85^a
RBC,10^6/ml	2.70±0.40^a	2.79±0.54^a	2.79±0.56^a	2.47±0.54^b	3.05±0.20^a
WBC,10^3/ml	133.33±49^a	133.33±89^a	183.33±49^a	150.00±67^a	155.56±44^a
Plasma constituents at 3 weeks of age					
TP, g/dl	2.5945±0.69^c	3.1323±0.58^b	3.6467±0.69^a	2.9347±0.90^b	3.3143±0.59^a
Alb, g/dl.	1.2712±0.34^c	1.4675±0.30^b	1.7453±0.29^a	1.3680±0.34^b	1.6213±0.35^a
TL, mg/dl	574.67±67^c	721.67±88^a	660.00±108^b	663.11±111^a	641.11±103^a
TG, g/dl	120.44±26^a	107.50±18^a	124.00±30^a	122.17±25^a	115.33±26^a
GH,ng/dl	0.1600±0.03^a	0.1367±0.03^b	0.1333±0.03^b	0.1456±0.04^a	0.1411±0.03^a
T3, ng/dl	29.17±24^b	51.00±18^a	55.50±32^a	49.89±25^a	40.56±29^b
T4, ng/dl	0.1633±0.06^b	0.1483±0.03^b	0.2100±0.07^a	0.1733±0.06^a	0.1744±0.06^a
T3/T4	168.29±101^b	344.59±121^a	292.29±219^a	307.55±177^a	229.23±156^b

a, b and c: Means having different superscripts within each effect within the same row are significantly different at P≤0.05.

Table 1b. Significant means ± SD for productive traits, hematological parameters and plasma constituents in different genetic groups of Japanese quail (Line by sex interaction effect).

Trait	RC		HBW		HGR	
	♂	♀	♂	♀	♂	♀
FC	4.90±0.25^c	4.68±0.14^c	5.29±0.64^b	4.22±0.38^d	6.16±0.26^a	4.83±0.09^c
PI	3.11±0.29^c	3.56±0.17^b	2.97±0.52^{cd}	4.12±0.37^a	2.73±0.09^d	3.51±0.08^b
Dressing%	77.92±1.10^{ab}	78.15±0.32^{ab}	78.36±0.36^{ab}	77.28±0.86^c	78.48±0.33^a	77.84±0.39^b
WBCx10^3/ml	183.33±49^a	133.33±25^b	133.33±89^b	166.67±65^{ab}	133.33±49^b	166.67±25^{ab}
TL, mg/dl	631.00±18^{bc}	518.33±46^d	753.33±102^a	690.00±60^{ab}	605.00±121^c	715.00±56^a
GH,ng/dl	0.180±0.03^a	0.140±0.08^{bc}	0.137±0.03^{bc}	0.137±0.03^{bc}	0.120±0.02^c	0.147±0.03^b
T3, ng/dl	48.33±20^{ab}	10.06±0.0^c	56.00±12^{ab}	46.00±22^b	45.33±38^b	65.67±22^a
T4, ng/dl	0.183±0.08^b	0.143±0.01^{bc}	0.167±0.03^{bc}	0.130±0.00^c	0.170±0.06^{bc}	0.250±0.06^a

a, b, c and d: Means having different superscripts within the same row are significantly different at P≤ 0.05.

2.Stepwise analyses

Stepwise regression parameters, coefficient of determination (R^2), standard error of the estimate (SEE) for predicted traits (Ŷ) of different lines, by sex are presented in Tables from 2 to 9. For predicting LBW$_6$, the most

important predictor for males of both RC and HGR lines which positively and highly correlated with LBW_6 (0.706 and 0.805, P≤0.01) was T_4 associating with R^2 of 49.9% and SEE of 13.335 for the former group and 64.8% and 3.720 for the later group. Model 2 in the females of RC line that used both TL and TP was the best model for predicting LBW_6. Because the value of R^2 was high and SEE was low (98.2% and 2.687) as shown in Table 2. Model 2 for males of HBW_6 line that used Hb and T_4 was the best model for predicting LBW_6; because the associated R^2 was high and SEE was low (100.0% and $4.89E^{-02}$) and both of them were positively and very highly correlated with LBW_6. Also, TL was the most important predictor for LBW_6 in females of HBW_6 line which was negatively correlated with this trait with R^2 of 45.5% and SEE of 11.490. However, all variables entered were removed in the females of HGR group as shown in Table 2.

Table 2. Stepwise regression parameters, coefficient of determination (R^2), standard error of the estimate (SEE) for predicting live body weight at 6 weeks of age as Ŷ of different lines, by sex.

Line	Sex	Model	Predictor	r	R^2%	SEE	Sig.	Fitted equation
RC	M	1	T_4	0.706	49.9	13.335	**	$Ŷ = 147.153+161.094T_4$
RC	F	1	TL	-0.942	88.8	6.417	***	$Ŷ =384.377-0.370TL$
		2	TL, TP	-0.632	98.2	2.687	***	$Ŷ = 359.563-0.248TL -$
				-0.437			***	$13.167TP$
HGR	M	1	T_4	0.805	64.8	3.720	**	$Ŷ =172.378+81.448T_4$
HGR	F							Variables entered/Removed
HBW	M	1	Hb	1.00	100.0	$6.39E^{-02\#}$	***	$Ŷ =152.621+3.226 Hb$
		2	Hb, T_4	0.820	100.0	$4.89E^{-02}$	***	$Ŷ = 155.482+2.644$
				0.181			***	$Hb+25.356 T_4$
HBW	F	1	TL	-0.675	45.5	11.490	*	$Ŷ = 324.104-0.167 TL$

Sig.: significance, [#]: Scientific notation, *: P≤ 0.05 , **: P≤ 0.01 and ***: P≤ 0.001.

The best accurate model for predicting FC_2 (P≤0.001) in all studied line by sex groups was model 2 which indicated R^2 of 100% and zero SEE. The most important predictors for the model were TL and T_4 for males of RC line, WBC and RBC for females of RC line, TL and WBC for males of HBW_6 line and GH and PCV for females of HBW_6 line, T_4 and PCV for males of HGR_{0-6} line, TG and TL for females of HGR_{0-6} line, respectively as shown in Table 3.

For predicting PI, model 2 was the best model (P≤0.001) in all studied line by sex groups which indicated that TL and Alb for males of RC, TP and GH for females of RC line, T_4 and PCV for males of HGR_{0-6} line, TG and TP for females of HGR_{0-6} line, TL and T_3/T_4 for females of HBW_6 line and both TG and T_3/T_4 for females of this line, respectively were the most important predictors for PI (R^2 of 100% and zero to $2.76E^{-09}$ SEE) as shown in Table 4.

The most important predictors for dressing% were T_3/T_4 and TP for males of RC line, TP and GH for females of the RC line, PCV and RBC for males of HBW_6 line and Alb and T_3/T_4 for females of HBW_6 line, T_3/T_4 and T_3 for males of HGR_{0-6}, Alb and TP for females of HGR_{0-6}, respectively. This model was the best model for predicting dressing% (P≤0.001) in all studied line by sex groups which indicated R^2 of 100% and zero to $6.48E^{-03}$ SEE as shown in Table 5.

Table 3. Stepwise regression parameters, coefficient of determination (R^2), standard error of the estimate (SEE) for predicting feed conversion as $\hat{Y}$ of different lines, by sex.

Line	Sex	Model	Predictor	r	R^2%	SEE	Sig.	Fitted equation
RC	M	1	TL	-0.971	94.4	$6.26E^{-02\#}$	***	$\hat{Y}=13.355-1.339E^{-02}TL$
		2	TL, T_4	-1.958 1.015	100.0	0.000	*** ***	$\hat{Y}=21.347-2.70E^{-02}TL+3.238T_4$
RC	F	1	WBC	-0.986	99.2	$1.34E^{-02}$	***	$\hat{Y}=5.440-5.70E^{-03}WBC$
		2	WBC, RBC	-1.531 0.570	100.0	0.000	*** ***	$\hat{Y}=6.28-5.40E^{-03}WBC-0.300RBC$
HGR	M	1	T_4	-0.945	98.3	$8.94E^{-02}$	***	$\hat{Y}=6.872-4.167T_4$
		2	T_4, PCV	-1.323 0.500	100.0	0.000	*** ***	$\hat{Y}=2.988-5.833T_4+0.100PCV$
HGR	F	1	TG	0.996	99.1	$9.14E^{-03}$	***	$\hat{Y}=4.476+2.975E^{-03}TG$
		2	TG, TL	0.833 0.188	100.0	0.000	*** ***	$\hat{Y}=4.310+2.488E^{-03}TG+3.14E^{-04}TL$
HBW	M	1	TL	-1.000	100.0	$1.70E^{-03}$	***	$\hat{Y}=9.987-6.24E^{-03}TL$
		2	TL, WBC	-1.002 0.003	100.0	0.000	*** ***	$\hat{Y}=9.995-6.25E^{-03}TL+2.50E^{-03}WBC$
HBW	F	1	GH	-0.945	89.3	0.130	***	$\hat{Y}=6.103-13.750GH$
		2	GH, PCV	-1.245 -0.444	100.0	0.000	*** ***	$\hat{Y}=10.459-18.118GH-9.06E^{-2}PCV$

Sig.: significance, #: Scientific notation and ***: significant difference at P< 0.001.

Table 4. Stepwise regression parameters, coefficient of determination (R^2), standard error of the estimate (SEE) for predicting PI ($\hat{Y}$) of different lines, by sex.

Line	Sex	Model	Predictor	r	R^2%	SEE	Sig.	Fitted equation
RC	M	1	TL	0.993	98.5	$3.74E^{-02\#}$	***	$\hat{Y}=-6.906+1.588E^{-02}TL$
		2	TL,Alb	1.331 -0.360	100.0	0.000	*** ***	$\hat{Y}=-9.889+2.129E^{-02}TL-0.352Alb$
RC	F	1	TP	0.998	99.6	$1.05E^{-02}$	***	$\hat{Y}=2.752+0.276TP$
		2	TP,GH	0.859 -0.152	100.0	$2.76E^{-09}$	*** ***	$\hat{Y}=3.283+0.238TP-2.985GH$
HGR	M	1	T_4	0.999	99.8	$4.47E^{-03}$	***	$\hat{Y}=2.454+1.625T_4$
		2	T_4, PCV	1.050 -0.068	100.0	0.000	*** ***	$\hat{Y}=2.648+1.708T_4-5.00E^{-03}PCV$
HGR	F	1	TG	-0.998	99.6	$5.77E^{-03}$	***	$\hat{Y}=3.833-2.723E^{-03}TG$
		2	TG, TP	-1.256 0.266	100.0	0.000	*** ***	$\hat{Y}=3.729-3.427E^{-03}TG+4.94E^{-02}TP$
HBW	M	1	TL	0.999	99.8	$2.13E^{-02}$	***	$\hat{Y}=-0.880+5.12E^{-02}TL$
		2	TL, T_3/T_4	0.927 -0.082	100.0	0.000	*** ***	$\hat{Y}=-0.234+4.75E^{-03}TL-1.09E^{-03}T_3/T_4$
HBW	F	1	TG	0.996	99.3	$3.36E^{-02}$	***	$\hat{Y}=1.974+2.02E^{-02}TG$
		2	TG, T_3/T_4	1.001 -0.086	100.0	0.000	*** ***	$\hat{Y}=2.031+2.03E^{-02}TG-1.882E^{-04}T_3/T_4$

Sig.: significance, #: Scientific notation and ***: significant difference at P< 0.001.

Carcass% for all studied line by sex groups could be predicted with100% R^2 and zero SEE using these predictors: PCV and GH for males of RC line, GH and TG for females of RC line, T_3/T_4 and Hb for males of

HBW_6 line and both Alb and Hb for females of HBW_6 line as shown in Table 6.

Table 5. Stepwise regression parameters, coefficient of determination (R^2), standard error of the estimate (SEE) for predicting dressing% as Ŷ of different lines, by sex.

Line	Sex	Model	Predictor	r	R^2%	SEE	Sig.	Fitted equation
RC	M	1	T_3/T_4	-0.994	98.7	0.132	***	$\hat{Y} = 92.238-5.39E^{-02}T_3/T_4$
		2	T_3/T_4 , TP	-1.327 0.352	100.0	0.000	*** ***	$\hat{Y} = 95.665-7.20E^{-02}T_3/T_4 + 0.607$ TP
RC	F	1	TP	-0.997	99.3	$2.78E^{-02\#}$	***	$\hat{Y} =79.673-0.522TP$
		2	TP, GH	-0.802 0.212	100.0	$9.78E^{-09}$	*** ***	$\hat{Y} = 787.272-0.420TP+7.889 GH$
HBW	M	1	PCV	-1.000	100.0	$7.47E^{-02}$	***	$\hat{Y} =85.784-0.182 PCV$
		2	PCV, RBC	-0.965 -0.040	100.0	0.000	*** ***	$\hat{Y} = 85.608-0.176PCV -3.34E^{-02}RBC$
HBW	F	1	Alb	-0.922	84.9	0.352	***	$\hat{Y} = 84.342-4.291Alb$
		2	Alb, T_3/T_4	-1.807 0.967	100.0	0.000	*** ***	$\hat{Y} = 89.389-8.412+4.89E^{-03}Alb, T_3/T_4$
HGR	M	1	T_3/T_4	-0.916	83.9	0.138	***	$\hat{Y} =78.791-9.713E^{-04} T_3/T_4$
		2	T_3/T_4, T_3	-4.382 3.490	100.0	0.000	*** ***	$\hat{Y} = 78.591-4.648E^{-03}T_3/T_4 +3.049E^{-02} T_3$
HGR	F	1	Alb	-1.000	99.9	$9.53E^{-03}$	***	$\hat{Y} =85.384-3.959Alb$
		2	Alb, TP	-0.986 -0.027	100.0	$6.48E^{-03}$	*** ***	$\hat{Y} = 85.367-3.904Alb-2.31E^{-02}TP$

Sig.: significance, #: Scientific notation and ***: P≤ 0.001.

Table 6. Stepwise regression parameters, coefficient of determination (R^2), standard error of the estimate (SEE) for predicting carcass% as Ŷ of different lines, by sex.

Line	Sex	Model	Predictor	r	R^2%	SEE	Sig.	Fitted equation
RC	M	1	PCV	0.987	97.5	$7.67E^{02\#}$	***	$\hat{Y} = 55.805+0.297PCV$
		2	PCV, GH	1.627 0.659	100.0	0.000	*** ***	$\hat{Y} = 46.313+0.489PCV +8.929GH$
RC	F	1	GH	-0.986	97.2	0.155	***	$\hat{Y} = 80.378-101.533GH$
		2	GH, TG	-1.531 0.570	100.0	0.000	*** ***	$\hat{Y} = 85.997-157.653+1.871E^{-02}GH\ TG$
HBW	M	1	T_3/T_4	-0.985	97.0	0.122	***	$\hat{Y} = 74.019-1.697E^{-02}T_3/T_4$
		2	T_3/T_4, Hb	-0.980 -0.172	100.0	0.000	*** ***	$\hat{Y} = 75.077-1.689E^{-02}T_3/T_4 - 8.91E^{-02}Hb$
HBW	F	1	Alb	-0.943	88.9	0.259	***	$\hat{Y} = 72.348-3.771 Alb$
		2	Alb, Hb	-2.382 1.477	100.0	0.000	*** ***	$\hat{Y} = 55.429-9.523Alb+2.029 Hb$
HGR	M	1	GH	1.000	100.0	$1.59E^{-02}$	***	$\hat{Y} =61.384+56.907GH$
		2	GH, RBC	1.013 0.022	100.0	0.000	*** ***	$\hat{Y} = 61.189+57.641GH+4.192E^{-02}RBC$
HGR	F	1	WBC	-1.000	99.9	$3.08E^{-03}$	***	$\hat{Y} = 67.33-4.542E^{-03}WBC$
		2	WBC, T_3	-0.901 -0.102	100.0	0.000	*** ***	$\hat{Y} =67.290-4.00092E^{-03}WBC-5.29E^{-04}T_3$

Sig.: significance, #: Scientific notation and ***: significant difference at P< 0.001.

The greatest predictors for BLM% were RBC and TP for males of RC line, Hb and Alb for females of RC line, T_3/T_4 and Alb for males of HBW_6 line and TL and Hb for females of HBW_6 line, TG and T_4 for males of HGR_0-

$_6$ line, TP and T_4 for females of HGR_{0-6} line, respectively. Model 2 was the best model for predicting BLM% (P≤0.001) in all studied line by sex groups which indicated R^2 of 100% and zero SEE as shown in Table7.

Table 7. Stepwise regression parameters, coefficient of determination (R^2), standard error of the estimate (SEE) for predicting boneless meat% as $\hat{Y}$ of different lines, by sex.

Line	Sex	Model	Predictor	r	R^2%	SEE	Sig.	Fitted equation
RC	M	1	RBC	-0.992	98.4	0.106	***	$\hat{Y} = 52.249-1.111RBC$
		2	RBC, TP	-0.554 -0.456	100.0	0.000	*** ***	$\hat{Y}= 52.352 - 0.620RBC-0.577TP$
RC	F	1	Hb	-0.979	95.8	0.288	***	$\hat{Y} = 59.048-0.991Hb$
		2	Hb, Alb	-0.568 0.460	100.0	0.000	*** ***	$\hat{Y}=51.770 - 0.575Hb+ 1.607Alb$
HGR	M	1	TG	-0.974	94.9	0.192	***	$\hat{Y} =61.323-4.186E^{-02}TG$
		2	TG, T_4	-0.605 -0.433	100.0	9.39E$^{-09\#}$	*** ***	$\hat{Y}=60.355-2.59 E^{-02}TG-5.913T_4$
HGR	F	1	TP	-0.874	76.4	1.489	***	$\hat{Y} =76.837-5.549TP$
		2	TP, T_4	-5.371 4.371	100.0	0.000	*** ***	$\hat{Y} = 130.281-4.10TP+223.852T_4$
HBW	M	1	T_3/ T_4	-0.995	99.0	0.309	***	$\hat{Y} = 80.30-7.70E^{-02}T_3/ T_4$
		2	T_3/T_4, Alb	-1.034 -0.105	100.0	0.000	*** ***	$\hat{Y}=82.703-8.001E^{-02}T_3/ T_4 -1.091Alb$
HBW	F	1	TL	-0.951	90.4	.363	***	$\hat{Y} = 65.891-1.78E^{-02}TL$
		2	TL, Hb	-2.352 1.435	100.0	0.000	*** ***	$\hat{Y}= 45.353-4.39E^{-02}TL+2.967Hb$

Sig.: significance, $^{\#}$: Scientific notation and ***: P≤ 0.001.

Results presented in Table 8 revealed that T_3 was the most important predictor in determining protein% for both males and females of the HBW_6 line with R^2 of 47.9, 37.2% and low SEEs of 0.327 and 0.316, respectively, indicating that 47.9% and 37.2% of the variation in protein% were explained by T_3. All variables entered were removed for other line by sex groups when predicting protein%.

Table 8. Stepwise regression parameters, coefficient of determination (R^2), standard error of the estimate (SEE) for predicting protein% as $\hat{Y}$ of different lines, by sex.

Line	Sex	Model	Predictor	r	R^2%	SEE	Sig.	Fitted equation
RC	M							Variables entered/Removed
RC	F							Variables entered/Removed
HGR	M							Variables entered/Removed
HGR	F							Variables entered/Removed
HBW	M	1	T_3	0.692	47.9	0.327	**	$\hat{Y} = 18.292+2.51E^{-02}T_3$
HBW	F	1	T_3	0.610	37.2	0.316	*	$\hat{Y} = 19.334+1.05E^{-02}T3$

Sig.: significance, *: P≤ 0.05 , **: P≤ 0.01 and ***: P≤ 0.001.

For predicting fat%, the major predictors according to their associated high R^2 were TL, T_3/T_4 and TP in a descending order (R^2: 90.3, 73.9and 49.9, respectively) for each of males and females of the RC line and males of HBW_6. However, all variables entered were removed from the stepwise

model in both sexes of HGR_{0-6} and females of HBW_6 line which revealing that no predictors from hematological and plasma constituents studied at three weeks of age could be used to predict fat% in these two groups as shown in Table 9. These results are confirmed with the findings of **El Full and Omar (2006)** who used path analysis technique and reported that GH, TG, TL, Alb, TP and T_3/T_4 measured at three weeks of age in both sexes could be used to predict carcass traits and growth productive performance in Japanese quail.

Table 9. Stepwise regression parameters, coefficient of determination (R^2), standard error of the estimate (SEE) for predicting fat% as $\hat{Y}$ of different lines, by sex.

Line	Sex	Model	Predictor	r	R^2%	SEE	Sig.	Fitted equation
RC	M	1	T_3/T_4	-0.859	73.9	0.806	***	$\hat{Y} =22.307-6.35E^{-02} T_3/T_4$
RC	F	1	TL	0.951	90.3	0.497	***	$\hat{Y} =-11.499+3.12E^{-02}TL$
HGR	M							Variables entered/Removed
HGR	F							Variables entered/Removed
HBW	M	1	TP	-0.706	49.9	0.812	*	$\hat{Y} =9.865-0.943TP$
HBW	F							Variables entered/Removed

Sig.: significance, *: P≤ 0.05 , **: P≤ 0.01 and ***: P≤ 0.001.

Differences between predicted traits vs. actual values were subjected to Student's t-test are presented in Table 10. The predicted traits were insignificantly different than the actual values or percentages (P>0.05).

In conclusion, results of the stepwise regression analyses revealed that either certain studied hematological values or plasma constituents measured at three weeks of age in both sexes, by lines could be used to predict carcass traits and growth productive performance in Japanese quail with high precision and low error.

Table 10

REFERENCES

Abdel Azeem, F., Ibrahim, F.A. and Ali, N.G., 2001. Growth performance and some blood parameters of growing Japanese quail as influenced by different dietary protein levels and microbial probiotics supplementation. **Egypt. Poult. Sci. 21: 465-489.**

Abdel Fattah, M.H., 2001. Inheritance of some growth, carcass characteristics and chemical composition of Japanese quail.. **M.Sc. Thesis, Fac. Agric., Fayoum, Cairo Univ., Egypt.**

Abdel Fattah, M.H., 2006. Selection for increased body weight and growth rate in Japanese quail. **Ph. D. Thesis, Fac. Agric., Fayoum Univ., Egypt.**

Abou Zeid, A. E., Isshak, N. S., Badaway, N. A. and Abou Ouf, N., 2000. The potential effect of vitamin C supplementation in quail. **Egypt. Poult. Sci. 20: 817-838.**

Atwal, O.S., McFarland, L.Z. and Wilson, W.O., 1964. Hematology of Couternix from birth to maturity. **Poult. Sci. 43: 1392-1401.**

Buys, N., Scheele, C. W., Kwakernaak, C. and Decuypere, E., 1999. Performance and physiological variables in broiler chicken lines differing in susceptibility to the ascites syndrome:2. Effect of ambient temperature on partial efficiencies of protein and fat retention and plasma hormone concentrations. **Br. Poult.Sci. 40: 140-144.**

Buyse, J., Decuypere, E., Huyghebaert, G. and Herremans, M., 1991. The effect of clenbuterol supplementation on growth performance and on plasma hormone and metabolite levels of broilers. **Poult. Sci. 70: 993-1002.**

Buyse, J., Janssens, G.P. J. and Decuypere, E., 2001. The effects of dietary L-carnitine supplementation on the performance, organ weights and circulating hormone and metabolite concentrations of broiler chickens reared under a normal or low temperature schedule. **Br. Poult. Sci. 42: 230-241.**

Cravener, T.L., Vasilatos-Younken, R. and Wellenreiter, R.H., 1989. Effect of subcutaneous infusion of pituitary-derived chicken growth hormone on growth performance of broiler pullets. **Poult. Sci. 68:1133-1140.**

Decuypere, E., Bruggeman, V., Barbato, G.F., and Buyse, J., 2003. Growth and reproduction problems associated with selection for increased broiler meat production. In: Poultry Genetics, Breeding and Biochemistry, edited by **Muir, W.M. and Aggrey, S. E.. CABI Publishing.UK, PP:13-28.**

Decuypere, E., Leenstra, F.R., Buyse, J., Beuving, J. and Berghman, L., 1991. Temporal secratory patterns of growth hormone in male meat-type chickens of lines selected for body weight or feed conversion. **Br. Poult. Sci. 32:1121-1128.**

Decuypere, E., Vega, C., Bartha, T., Buyse, J., Zoons, J and Albers, G. A. A., 1994. Increased sensitivity to triiodothyronine (T_3) of broiler lines with a high susceptibility for ascites. **Br. Poult. Sci. 35:287-297.**

Duncan, D.B., 1955. The Multiple Range and Multiple F-Test. **Biometrics. 11:1-42.**

El Full, E.A. and Omar, E.M., 2006. Using path analysis to partition the variability in growth and carcass traits in three lines of Japanese quail. **Fayoum J. Agric. Res. & Dev. 20: (In press).**

Farahat, A. and Chavez, E.R., 2000. Comparative performance, blood chemistry and carcass composition of two lines of Pekin ducks reared mixed or separated by sex. **Poult. Sci. 79: 460-465.**

Farahat, G.S., 1998. Estimation of some genetic and phenotypic parameters for growth and reproductive traits of Japanese quail. **M.Sc. Thesis, Fac. Agric., Fayoum, Cairo Univ., Egypt.**

Foster, J.J., 1998. Data Analysis Using SPSS For Windows. **Sage Publications Ltd., London, UK.**

Havenstein, G.B., Nestor, K. E. and Bacon, W. L., 1988. Comparison of pedigreed and non pedigreed randombred control systems for use with artificial selection in the Japanese quail. **Poult. Sci. 67: 357-366.**

Mihailov, R., Lashera, V. and Lashev, L., 1999. Some hematological values in Japanese quails. **Bulga J. Vet. Med. 2:137-139.**

Morrison, D.F., 1976. Multivariate Statistical Analysis. **McGrow-Hill Book Company, NY, USA.**

Nijdam, E., Delezie, E., Lambooij, E., Nabuurs, M.J.A., Decuypere, E. and Stegman, J.A., 2005. Feed withdrawal of broilers before transport changes plasma hormone and metabolite concentrations. **Poult. Sci. 84: 1146-1152.**

North, M.O., 1981. Commercial Chicken Production Manual.**2nd Edition. Avi Publishing Company INC, USA.**

Pakdel, A., Van Arendonk, J.A.M., Versijken, A.L.J. and Bovenhuis, H., 2005. Genetic parameters of ascites-related in broilers:Correlations with feed efficiency and carcass traits. **Br. Poult. Sci. 46: 43-53.**

Rahimi, G., 2005. Thyroid hormones characteristics and hepatic deiodinase enzyme activity in broiler lines selected for growth and feed conversion.. **Int. J. Poult. Sci. 4:482-487.**

SPSS Inc., 1999. User's Guide: Statistics. Version 10. **SPSS Inc., Chicago, IL, USA**.

Steel, R.G. and Torrie, J. H., 1980. Principels and Procedures of Statistics. 2nd Ed. **McGraw Hill Book Co., New York, USA.**

Stewart, P.A. and Washburn, K.W., 1983. Variation in growth hormone, triiodothyronine (T$_3$) and lipogenic enzyme activity in broiler strains differing in growth and fatness. **Growth 47: 411-425.**

Stewart, P.A., and Washburn, K.W., 1984. Characterization of plasma hormone levels and lipogenic enzyme activity in chickens divergently selected for oxygen consumption. **Poult. Sci. 63: 600-606.**

Tona, K., Onagbesan, O.M., Bruggeman, V., Mertens, Jedo, Y. and Decuypere, E., 2004. Composition of feed intake, blood metabolite parameters, body and organ weights of growing broilers originating from dwarf and standard broiler breeder lines. **Int. J. Poult. Sci. 3: 422-426.**

Williams, J., Harvey, S., and Lecercq, B., 1986. Plasma levels of leuteinizing hormone and estradiol from six weeks of age to sexual maturity in two lines of chichens selected for low or high abdominal fat content. **Poult. Sci. 65: 1782-1786.**

Wilson, W.O., Abbott, U.K. and Abplanalp, H., 1961. Evaluation of Coturinx (Japanese quail) as pilot animal for Poultry. **Poult. Sci. 40: 651-657.**

Winer, B.J., 1971. Statistical Principles in Experimental Design. **McGraw Hill Book Co., New York, USA.**

استخدام تحليل الانحدار التدريجي لتجزئة الاختلافات في صفات النمو والذبيحة في ثلاثة خطوط
من السمان الياباني مختلفة في خلفيتها الوراثية

إنصاف أحمد الفل، بثينة يوسف فؤاد، حنان عبد الله حسن وعصمت محمد عمر
قسم إنتاج الدواجن- كلية الزراعة- جامعة الفيوم- مصر

استخدمت بيانات صفات الدم ومكونات البلازما عند عمر ٣ أسابيع للتنبؤ بصفات النمو
والذبيحة عند عمر ٦ أسابيع. وقد أجرى تحليل الانحدار التدريجي لتجزئة الاختلافات في النمو وصفات
الذبيحة في ثلاثة خطوط من السمان الياباني مختلفة في خلفيتها الوراثية. وقد أظهرت نتائج الانحدار
التدريجي أن الثيروكسين(T_4) هو المكون الأهم للتنبؤ بوزن الجسم عند عمر ٦ أسابيع في كل من ذكور
خط المقارنة والخط المنتخب لمعدل النمو العالي(HGR_{0-6}). كما كان كل من الدهون الكلية (TL)
والبروتينات الكلية(TP) للبلازما الدم هما المكونان الأكثر أهمية للتنبؤ بوزن الجسم عند عمر ٦ أسابيع
في اناث RC. وكان الهيموجلوبين(Hb) وT_4 هما المكونان الأكثر أهمية للتنبؤ بوزن الجسم عند عمر ٦
أسابيع في النموذج الثاني في ذكور الخط المنتخب لوزن الجسم العالي(HBW_6). بينما كانت TL
بالبلازما هي الأكثر أهمية للتنبؤ بوزن الجسم عند عمر ٦ أسابيع في اناث خط HBW_6. وقد كانت TL
وT_4 هما الأهم في التنبؤ بمعامل التحويل الغذائي (FC) لذكور خط المقارنة، بينما كانت كرات الدم
الحمراء والبيضاء (WBC and RBC) هما الأكثر أهمية بالنسبة لاناث الخط نفسه، TL بالبلازما
WBC لذكور خط HBW_6 و هرمون النمو(GH) والهيماتوكريت (PCV) لاناث خط HBW_6، T_4 و
PCV لذكور خط HGR_{0-6}، الجلسريدات الثلاثية (TG) وTL لاناث الخط الأخير. وجد أن المكونات
الأكثر أهمية في التنبؤ بدليل الأداء الإنتاجي هى TL والألبيومين (Alb) لذكور خط RC، TP، GH
لاناث نفس الخط، والنسبة بين ثلاثى أيودوثيرونين/الثيروكسين (T_3/T_4) لذكور خط HBW_6
ولاناث ذلك الخط وكذلك TG و T_3/T_4 على التوالى، T_4 و PCV لذكور خط HGR_{0-6}، TG وTP
لاناث الخط السابق• يمكن التنبؤ بنسبة الذبيحة من خلال PCV وGH في ذكور خط المقارنة، GH و
TG لاناث خط المقارنة، T_3/T_4وHb لاناث وذكور خط HBW_6، Alb وHb لاناث خط HBW_6،
GH وRBC لذكور خط HGR_{0-6}، WBC وT_3 لاناث خط HGR_{0-6}. وللتنبؤ بنسبة التصافي لكل
المجموعات المدروسة كانت المكونات الأكثر أهمية للتنبؤ هى نسبة T_3/T_4 و TP بلازما ذكور خط
المقارنة، GH وTP في اناث خط المقارنة، PCV وRBC في ذكور خط HBW_6، وAlb و T_3/T_4
لاناث خط HBW_6،T_3/T_4 وT_3 في ذكور خط HGR_{0-6}،Alb و TP لاناث خط HGR_{0-6}. وكانت
TPوRBC هما الأهم للتنبؤ بنسبة التصافى في ذكور خط لمقارنة وAlb لاناث خط المقارنة،
Alb و T_3/T_4 لذكور خط HBW_6وHb لاناث نفس الخط. وTG وT_4 في ذكور خط HGR_{0-6}، TP
وT_4 في اناث نفس الخط. وقد وجد أن T_3 هو المكون الأكثر أهمية الذى يمكن التنبؤ من خلاله بنسبة
البروتين للذبيحة في كل من ذكور واناث خط HBW_6. كانت أهم المكونات الممكن التنبؤ من خلالها
بنسبة الدهن بالذبيحة مرتبة ترتيبا تنازليا هى نسبة T_3/T_4، TL وTP بالبلازما للمجموعات التالية على
التوالى: ذكور وإناث خط المقارنة، ذكور الخط المنتخب لوزن الجسم العالى. كانت الاختلافات غير
معنوية بين القيم أو النسب الحقيقية وتلك المتنبأ بها. لذلك فقد أظهرت نتائج تحليل الانحدار التدريجى
إمكانية استخدام بعض من مكونات الدم ومكونات البلازما المدروسة المقاسة عند عمر ثلاثة أسابيع في
كلا الجنسين للخطوط المدروسة في السمان الياباني للتنبؤ بصفات النمو والأداء الانتاجى والذبيحة بدقة
عالية وخطأ قياسى منخفض.

Table 10. Accuracy of predicting productive traits of Japanese quail through hematological parameters and plasma constituents.

Line	Sex	Value	LBW$_6$	FC	PI	Dressing %	Carcass %	BLM%	Protein %	Fat %
RC	♂	Actual	176.6867	4.9037	36.232	77.8156	67.972	49.5091	-	5.4330
		Predicted	176.6869	4.9036	36.232	77.9174	67.969	49.5086	-	5.4350
		Significance	0.155	1.000	1.000	0.999	0.999	1.000	-	0.573
			NS	NS	NS	NS	NS	NS		NS
RC	♀	Actual	192.6067	4.6800	41.1605	78.1527	66.1638	46.7480	-	4.6600
		Predicted	192.6784	4.6800	41.1605	78.1527	64.1495	46.7437	-	4.6820
		Significance	0.999	1.000	1.000	1.000	0.269	1.000	-	0.774
			NS	NS	NS	NS	NS	NS		NS
HGR	♂	Actual	186.2242	6.1633	30.2937	78.4787	68.2132	56.1179	-	-
		Predicted	186.2242	6.1631	30.2937	78.4782	68.2132	56.1296	-	-
		Significance	0.202	1.000	1.000	0.999	1.000	0.993	-	-
			NS	NS	NS	NS	NS	NS		
HGR	♀	Actual	-	-	42.5590	77.8411	66.5731	55.5727	-	-
		Predicted	-	-	42.5590	77.8414	66.5884	55.5727	-	-
		Significance	-	-	1.000	1.000	0.894	1.000	-	-
					NS	NS	NS	NS		
HBW	♂	Actual	191.9067	5.2900	36.8059	78.3604	68.3294	54.4674	19.7017	6.7933
		Predicted	196.1289	5.6200	36.8059	77.7451	68.3287	54.4676	19.6976	6.9744
		Significance	0.583	0.630	1.000	0.141	0.999	1.000	0.655	0.750
			NS	NS	NS	NS	NS	NS	NS	
HBW	♀	Actual	208.5833	4.2233	49.6843	77.2844	66.1449	53.6462	19.8150	-
		Predicted	208.8740	4.2230	49.6843	77.2816	66.1461	53.6409	19.8170	-
		Significance	0.066	1.000	1.000	0.997	1.000	0.998	0.964	-
			NS	NS	NS	NS	NS	NS	NS	

NS: Not significant.