Phenotypic and Genetic Parameter Estimates for GrowthTraitsin Local Guinea Fowl. Genetic and phenotypic correlations.

Abstract

The objective of this work was to estimate genetic and phenotypic correlations among growth traits of the local Guinea fowlin Ghana. The study was conducted at the Poultry Section of the Animal farm of the Department of Animal Science Education, Faculty of Agriculture Education, Akenten Appiah- Menka University of Skills Training and Entrepreneurial Development Mampong-Ashanti campus, Ghana, from 2015 to 2018. The data used in this study were obtained from six hundred keets (300 males and 300 females) produced from randomly selectingand mating 110 dams and 22 sires and consisted of 780 records collected over a period of 3 years. Estimates of genetic and phenotypic correlations among the traits were obtained using the Arithmetic method and Pearson's product moment correlation for genetic and phenotypiccorrelations.Genetic correlations among weight and growth rate rangedfrom low to high (0.03 to 0.92), whilst their phenotypic correlations were low to medium (0.01 to 0.49) in both males and females.Genetic correlation in males was low between hatch weight and FI (0.02) and moderate between hatch weight and FCR (0.31). Phenotypic correlation between hatch weight and FI and FCR in males were all negatively low (-0.18 and -0.24 respectively). Phenotypic correlation between hatch weight and FI and FCR in females on the other hand, were all low (0.23 and 0.12 respectively). Genetic correlation between four-month weight FI and FCR were high in both males (0.72 and 0.67 respectively) and females (0.64 and 0.78 respectively). Phenotypic correlation between four-month weight FI and FCR in males and females were moderate (between 0.31 and 0.34). Moderate to high positive genetic correlation between SMWT, DOC and SVV were recorded. To conclude, discoveries of this study were in general agreement of what pertains to the Guinea fowl and other farm livestock species.

Keywords: Guinea fowl, hatch weight, feed intake, feed efficiency, survival, phenotypic and genetic correlation

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1. INTRODUCTION

The expectation of global demand for animal products to double by 2050, due to the irresistible growth of the world population, increasing incomes and further urbanization [1], makes establishment of animal genetic improvement programmes a priority to most animal scientists. In Ghana one of the most developmental projects since independence is Guinea fowl production. [2]outlined numerous advantages these birds have over the other domestic animals.

Table 1: **Distribution of Data used for Estimating Parameters in Local Male Guinea Fowls**

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Parameter	Acronym	Number of records	Mean	Range	Standard deviation
Hatch weight, g	HWT	300	25.95	23.4-28.5	1.06
2- month body weight, g	TMWTG	286	461.09	409.1-528	31.84
4- month body weight, g	FMWT	286	815.59	637.67-1070.2	71.73
6-month body weight, g	SMWT	286	1578.76	1420.3-1773.3	61.19
8- month body weight, g	EMWT	286	1759.69	1505-1955	58.85
Daily gain from 1-2 months, g/day	TMWTG	286	7.35	3.9-9.94	0.95
Daily gain from 2-4 months, g/day	FMWTG	286	7.67	5.18-9.98	0.60
Daily gain from 4-6 months, g/day	SMWTG	286	12.71	11.32-14.20	0.72
Daily gain from 6-8 months, g/day	EMWTG	286	4.26	1.32-10.64	0.88
Antibody response to SRBC (ABR)	SRBC	144	7.68	4.50-11.50	0.62
Docility score	DOC	288	2.91	1.20-3.60	0.44
Dressing percentage, %	DRESSP	104	64	57-78	0.06
Feed intake, g/day	FI	124	56.73	46.72-69.25	2.24
Feed conversion ratio	FCR	124	4.03	2.38-5.49	0.41

Knowledge of the phenotypic and genotypic characteristics of the indigenous Guinea fowls will immensely aid the achievement of the genetic improvement programme the country is embarking on. Estimates of heritability and phenotypic and genotypic correlations among traits are required inputsfor designing breeding programmes and for many methodsof genetic evaluation [3]. Works done in the area of genotypic andphenotypic parameter estimates for the indigenous Gunea fowl in the country are insignificant. There are few papers that havereported on phenotypic and genotypic parameters of the indigenous Gunea fowl [4]. The present papercomplements a similar one on co (variance) componentsand heritability of traits of theGunea fowl presented by[5]. The objective of this work was toestimate phenotypic and genotypic correlations amongtraits of the Guinea fowl.

Table. 2 Distribution of Data used for Estimating Parameters of Local female Guinea Fowls

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Parameter	Acronym	Number of records	Mean	Range	Standard deviation
Hatch weight (g)	HWT	300	26.88	23.2-28.9	1.09
2-month weight (g)	TMWTG	292	456.77	408.75-573.5	34.28
4-month weight (g	FMWT	292	828.45	534-987	49.93
6- month weight, (g)	SMWT	292	1583.19	1398.5-1699.5	49.34
8- month weight, (g)	EMWT	292	1810.21	1590-2132	53.41
Daily gain from 1-2 months (g/day)	TMWTG	292	7.82	6.19-9.67	0.56
Daily gain from 2 -4 months, (g/day)	FMWTG	292	7.03	4.98-9.91	0.68
Daily gain from 4-6 months, (g/day)	SMWTG	292	12.66	13.15-10.12	0.45
Daily gain from 1-2 months, (g/day)	EMWTG	292	4.18	1.73-11.37	0.78
Survival	SVV	144	7.48	4.00-10.40	0.61
Docility score	DOC	288	3.07	1.20- 3.90	0.44
Dressing percentage (%)	DRESSP	104	63	49-74	0.03
Feed intake (g/day)	FI	124	57.47	47.17-67.57	2.43
Feed conversion ratio	FCR	124	4.21	2.43-6.90	0.61
Age at first egg (days)	ATFE	292	210.22	185-235	5.41
Egg weight (g)	EGGWT	168	41.06	37.8-49.2	1.24
Hen-day egg production (%)	HDEP	168	71.06	55- 79.8	5.57
Percentage fertility (%)	FERT	168	59	36-73	0.03
Percentage hatchability (%)	HATCH	168	48	10-71	0.03

2. MATERIALS AND METHODS

The animals, location, experimental procedure and traits have been described in a companion paper [4]. Briefly, the study was conducted at the Poultry Section of the Animal farm of the Department of Animal Science Education, University of Education, Winneba, Mampong-Ashanti campus, now Akenten Appiah-MenkaUniversity of Skills Training and Entrepreneurial Development, Asante Mampong campus, Ghana, from 2015 to 2019. Asante Mampong lies in the transitional zone between the Guinea savanna zone of the north and the tropical rain forest of the south of Ghana along the Kumasi-Ejuraroad.Mampong lies on latitude 07˚ 03' N and longitude 01˚ 24'Wwith an altitude of 289.7 m above sea level. The rainfall pattern is bimodal, with the major rainfall season occurring from April to July with 1000mm of rainfall while the minor season occurs from August to November with 350 mm of rainfall. The average daily temperature is between 25°C and 30°C and the average relative humidity of the area is 70% [6].

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The records used in the present experiment were collected from six hundred keets (300 males and 300 females) produced from randomly selecting and mating 110 dams and 22 sires of this base population, between May, 2015 to July, 2018. Seven hundred and eighty (780) records were collected from the keets during this period. The chicks were then taken to a brooding room immediately for brooding. The Guinea fowl keets were kept at a temperature of 35°C with adequate drinker and feeder spaces provided. Light was provided for 24 hours during brooding to avoid pilling and death. The temperature was reduced gradually at the rate of 3.50°C on weekly basis as brooding progressed [7]. The chick phase lasted for 4 weeks (28 days). At the end of the chick phase they were randomly distributed and raised on a slated wooden floor pen partitioned into 20 compartments with each compartment measuring 3 m x 4 m and housing 30 keets. Each sex was kept separately [8].

2.1 Estimate of Genetic correlation:

Estimate of genetic correlations among the traits were obtained using the Arithmetic method below [8]

Genetic correlation:

$$r_G = \frac{COVx_1y_2 + COVx_2y_1}{\sqrt{COVx_1y_1 + COVx_2y_2}}$$

Where:

$r_{G\,=}$ genetic correlation

$^{cov}x_1z_{2=}$ covariance of trait 1 in parent and trait 2 in offspring

$^{cov}x_2z_{1=}$ covariance of trait 2 in parent and trait 1 in offspring

$^{cov}x_1z_{1=}$ covariance of trait 1 in parent and trait 1 in offspring

$^{cov}x_1z_{2=}$ covariance of trait 1 in parent and trait 1 in offspring

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Approximate standard error (S.E.) of the genetic correlation was obtained using the following formula (Falconer, [9]:

$$S.E.\ ({}^{r}{}_{G}) = \frac{1-r_G^2}{2}\sqrt{\frac{S.E.\ (h^2{}_1)\quad S.E.\ (h^2{}_2)}{h^2{}_1\, h^2{}_2}}$$

2.2 Estimate of phenotypic correlation:

Phenotypic correlations among traits were estimated using Pearson's product moment correlation (Ayizanga and Ahunu, 2013) below:

$$r = \frac{COVxy}{SxSy}$$

Where:

r =Phenotypic correlation,

Sx = Standard deviation of variable x

Sy = Standard deviation of variable y

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The standard error of the phenotypic correlation coefficient (S.e.), was calculated using:

$$S.e. = \sqrt{\frac{1-r2}{n-2}}$$

Correlations were classified as low (0.10 – < 0.30), medium (≥ 0.30 – < 0.50) and high (≥ 0.50 – 1.00), regardless of sign [11].

3. RESULTS

The results of genetic and phenotypic correlations are presented in Table 3 (for males) and Table 4 (for females). In males, hatch weight (HWT) was highly correlated genetically with TMWT (0.56) but was lowly correlated with EMWT (0.18). It correlated negatively low with SMWT (-0.17) but there was no genetic correlation between HWT and FMWT. In females, HWT lowly correlated genetically with TMWT (0.13) and lowly negatively correlated with FMWT (-0.01) and EMWT (-0.02) but the genetic correlation between HWT and SMWT was negatively high (-0.75). Phenotypically, HWT was moderately correlated with TMWT (0.33), correlated negatively low with FMWT (-0.2) and SMWT (-0.29) but positively low with EMWT (0.01) in the males. However, in females, HWT correlated positively low with TMWT (0.05) and EMWT (0.29) but negatively low with FMWT (-0.26) and SMWT (-0.23) phenotypically.

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Two month weight (TMWT) in males was highly correlated genetically with SMWT (1.3) and EMWT (1.02) but not important with FMWT. While, in females TMWT moderately correlated genetically with FMWT (0.44), highly correlated with SMWT (0.75) but lowly correlated genetically with EMWT (0.05). Two month weight

(TMWT) in males lowly correlated phenotypically with the weights of the other ages whereas in the female TMWT was moderately correlated phenotypically with SMWT (0.37) but lowly with FMWT (0.24) and EMWT (0.01). Four month weight (FMWT) showed similar trend in both males and females with respect to genetic and phenotypic correlations. It was highly correlated genetically with SMWT and EMWT but moderately correlated phenotypically with SMWT and EMWT. Six month weight (SMWT) in males was highly correlated genetically with EMWT (1.03) but phenotypically, the correlation was low (0.26) while in females SMWT highly correlated genetically with EMWT (1.2) but moderately correlated phenotypically with EMWT (0.42)

Genetic correlation between HWT and SMWTG was low (0.26) but those between HWT and all other body weight gain were high (0.54, 0.64 and 0.78) in males while this correlation in females was low between HWT and TMWTG (0.11) and negatively low between HWT and FMWTG (-0.12) but negatively moderate between HWT and SMWTG (-0.46) and moderate between HWT and EMWTG (0.35). Phenotypic correlation between HWT and SMWTG was moderate (0.38) whereas between HWT and TMWTG, EMWTG were low and negatively zero between FMWTG (0.12, 0.2 and -0.00 respectively) in males. However, in females, phenotypic correlation existed between HWT and all of the weight gains were low (0.07, 0.15 and 0.21) except FMWTG which was not important.

Genetic correlation between TMWT and FMWTG was high (0.83) but between TMWT and SMWTG was low(0.25) and not important with EMWTG in males but in the females, genetic correlation was between TMWT and FMWTG (0.23) and SMWTG (0.15) and negatively moderate between EMWTG (-0.32). Phenotypic correlation in both males and females were moderate between TMWT and FMWTG (0.49 and 0.46 respectively) and low between TMWT and TMWTG (0.11 and 0.09 respectively) and negatively low between TMWT and EMWTG (, -0.28, and -0.04 respectively) and negatively low between TMWT and SMWTG (-0.23) in males and positively low between TMWT and SMWTG (0.02) in females.

FMWT correlated genetically negatively moderate with SMWTG (-0.37) and high with EMWTG (1.2) in males whereas genetic correlation between FMWT and EMWTG was high but low with SMWTG (0.66 and 0.05 respectively) in the females. Phenotypic correlation between FMWT and EMWTG showed similar trend in both males and females (0.34 for males and 0.36 for females). However, phenotypic correlations between FMWT and SMWTG in both males and females (-0.25 and -0.02 respectively) were negatively low.
In males, high genetic correlation existed between SMWT and EMWTG (0.92) whereas in females, this correlation was negatively high (-1.2). Phenotypic correlation between SMWT and EMWTG (0.26) was low in the males whereas in the females, phenotypic correlation was negatively low between SMWT and EMWTG (-0.16).

In males, two month weight gain (TMWTG) was highly correlated genetically with SMWTG (0.82) and EMWTG (0.64) but the genetic correlation between TMWTG and FMWTG was negatively moderate (-0.43). This was different in the females. Genetic correlation between TMWTG and FMWTG (-0.53) was negatively high, between TMWTG and SMWTG was high (1.4) but between TMWTG and EMWTG showed no genetic correlation. Phenotypic correlation in males, between TMWTG and FMWTG was moderate (0.49), negatively low between TMWTG and SMWTG (-0.25) and negatively moderate between TMWTG and EMWTG (-0.30) whereas in the females phenotypic correlation between TMWTG and FMWTG was also moderate (0.42) but was negatively low between TMWTG and SMWTG (-0.02) as well as between TMWTG and EMWTG (-0.02).

Table 3: Genetic (above Diagonal) and Phenotypic (below Diagonal) Correlations among 14 Traits (Sire-son Regression)

	HWT	TMWT	FMWT	SMWT	EMWT	TMWTG	FMWTG	SMWTG	EMWTG	SVV	DOC	DRESSP	FI	FCR	
HWT			0.56	.	-0.17	0.18	0.54	0.64	0.21	0.78	-3.73	-1.81	-1.15	-0.13	-0.07
SE			0.23	.	0.34	0.41	0.31	0.34	0.42	0.21	0.49	1.25	0.4	0.46	0.39
TMWT	0.33	0.33		.	1.34	1.02	1.02	0.83	0.25	-	1.3	-0.32	-2.65	-0.51	-0.63
SE	0.19	0.19		.	0.32	0.02	0.02	0.2	0.47	-	1.03	0.41	0.55	0.39	0.27
FMWT	-0.2	-0.2	0.29		0.93	1.3	-	-	-0.37	1.2	0.75	-0.49	0.95	0.72	0.67
SE	0.2	0.2	0.19		0.05	0.33	-	-	0.43	0.26	0.27	0.34	0.05	0.25	0.24
SMWT-0.29		-0.29	0.23	0.35		1.03	0.39	0.85	0.6	0.92	0.97	-0.67	-0.35	0.51	0.4
SE	0.19	0.19	0.19	0.14		0.03	0.21	0.19	0.52	0.1	0.04	0.26	0.51	0.41	0.39
EMWT0.01		0.01	0.19	0.39	0.26		0.53	0.19	-0.06	0.74	0.65	-0.54	-0.03	0.78	0.91
SE	0.2	0.2	0.2	0.13	0.14		0.45	0.78	0.31	0.38	0.45	0.41	0.7	0.26	0.1
TMWTG0.12		0.12	0.11	-0.2	0.11	0.03		-0.43	0.82	0.64	1.7	0.4	-0.01	0.89	0.65
SE	0.2	0.2	0.2	0.19	0.2	0.2		0.68	0.21	0.64	1.54	0.5	0.73	0.14	0.34
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FMWTG-0.04		0.004	0.49	0.39	0.44	0.18	0.49		-0.16	-0.49	0.79	-0.28	0.02	0.48	0.14
SE	0.18	0.18	0.17	0.18	0.18	0.2	0.17		0.83	0.77	0.4	0.72	0.94	0.69	0.75
SMWTG	0.38	0.38	-0.23	-0.25	0.07	-0.19	-0.25	-0.24		0.27	0.49	0.13	-0.62	-0.42	-0.66
SE	0.17	0.17	0.19	0.15	0.2	0.15	0.19	0.19		0.74	0.63	0.6	0.45	0.58	0.34
EMWTG	0.2	0.2	-0.28	0.34	0.26	0.31	-0.3	0.18	0.06		0.84	0.43	-0.19	0.7	0.76
SE	0.19	0.19	0.18	0.14	0.15	0.14	0.2	0.2	0.2		0.29	0.59	0.85	0.43	0.3
SVV	-0.21	-0.21	0.27	-0.06	0.07	0.08	0.28	-0.28	0.16	0.03		1.09	-2.52	0.93	0.29
SE	0.19	0.19	0.2	0.15	0.15	0.16	0.19	0.19	0.15	0.15		0.14	0.92	0.12	0.68
DOC	0.18	0.18	0.1	-0.21	-0.24	-0.11	0.09	-0.46	-0.05	0.17	0.2		0.49	0.35	0.24
SE	0.2	0.2	0.2	0.15	0.14	0.15	0.2	0.18	0.16	0.16	1.6		0.51	0.56	0.51
DRESSP	-0.41	-0.41	-0.23	0.1	0.00	-0.01	-0.23	0.36	-0.12	-0.01	-0.18	0.08		0.94	1.4
SE	0.18	0.18	0.19	0.15	0.15	0.15	0.19	0.19	0.19	0.15	0.15	0.15		0.09	0.16
FI	-0.18	-0.18	-0.32	0.33	0.2	0.29	-0.32	-0.01	-0.15	0.17	0.15	0.01	0.04		1.01
SE	0.2	0.2	0.19	0.14	0.15	0.14	0.19	0.2	0.14	0.15	0.15	0.14	0.15		-0.01
FCR	-0.24	-0.24	-0.17	0.33	0.21	0.31	-0.16	0.18	-0.13	0.18	0.13	0.01	0.11	0.23	
SE	0.18	0.18	0.2	0.15	0.15	0.14	0.2	0.2	0.15	0.15	0.14	0.14	0.16	0.14	

Hatch weight (HWT); two month weight (TMWT); four month weight (FMWT); six month weight (SMWT); eight month weight (EMWT); two month weight gain (TMWTG); four month weight gain (FMWTG); six month weight gain (SMWTG); eight month weight gain (EMWTG); survival (SVV); docility score (DOC); dressing percentage (DRESSP); feed intake (FI); feed conversion ratio (FCR) and standard error (SE)

Genetic correlation existed in males, between FMWTG and SMWTG was negatively low (-0.16) and negatively moderate between FMWTG and EMWTG (-0.49) where in females genetic correlation existed between FMWTG and SMWTG was low (0.07) and no genetic correlation existed between FMWTG and EMWTG in the females. Negatively low phenotypic correlation was observed between both FMWTG and SMWTG (-0.24) and between FMWTG and EMWTG (-0.18) in males but in females phenotypic correlation was negatively low between FMWTG and SMWTG (-0.1) and low between FMWTG and EMWTG (0.11). Six month weight gain (SMWTG) lowly correlated genetically with EMWTG (0.27) in males while in females, it was negatively high (-0.80). Phenotypic correlation observed between SMWTG and EMWTG (0.06) was low in males and negatively low in females (-0.03).

Genetic correlation in the males was negative between HWT and SVV (-3.73), DOC (-1.81), DRESSP (-1.15), FI (-0.13) and FCR (-0.07). This was not different from what was observed in the females except FI (0.02) and FCR (0.31) which showed positive correlation with HWT. Apart from HWT and DOC (0.18) which showed positive correlation, Phenotypic correlation between HWT and SVV, FI, FCR and DRESSP (-0.21, -0.18, -0.24 and-0.41 respectively), in the males, were all negative. However, phenotypic correlation between HWT and SVV, DOC, FI, FCR and DRESSP in females on the other hand, were all positive (0.26, 0.01, 0.23, 0.12 and 0.4 respectively).
In the males, twomonth weight (TMWT) was highly correlated genetically with SVV (1.3) and was highly negatively correlated genetically with DRESSP (-2.65), FI (-0.51) and FCR (-0.63) but negatively moderate (-0.32) with DOC. In the females, genetic correlation was positive betweenTMWT and FI (0.25) and negative with SVV, DRESSP, FCR and DOC (-0.16. -0.01, -0.06 and -1.01 respectively).Between TMWT and SVV (0.27) and DOC (0.1) in the males, phenotypic correlation was positive but negative with DRESSP (-0.23), FCR (-0.17) and FI (-0.32). Whilst phenotypic correlation oftwo month weight (TMWT)in females on the other hand, was positive with SVV (0.37) and negative with DOC (-0.35), FI (-0.39), DRESSP (-0.15)andFCR(-0.01).

Table 4: Genetic (above Diagonal) and Phenotypic (below Diagonal) Correlations among 19 Traits (Sire and Dam-daughter Regression)

	HWT	TMWT	FMWT	SMWT	EMWT	TMWTG	FMWTG	SMWTG	EMWTG	Surval	Dscore	Dress %	ATFE	EGGWT	HDEP	FERT	HATCH	FI	FCR
HWT		0.13	-0.003	-0.75	-0.02	0.11	-0.12	-0.46	0.35	-0.47	-0.05	-0.16	2.43	0.53	-0.18	0.03	0.56	0.02	0.31
SE		0.34	0.35	-0.75	0.45	0.47	0.53	0.37	0.54	0.42	0.37	0.44	-1.61	0.20	0.20	0.67	0.38	0.42	0.35
TMWT	0.05		0.44	0.73	0.05	0.75	0.23	0.15	-0.32	-0.16	-1.01	-0.01	0.69	-0.3	0.02	0.17	0.57	-0.25	-0.06
SE	0.21		0.32	0.21	0.50	0.23	0.31	0.52	0.63	0.59	-0.01	0.50	0.19	0.28	0.23	0.74	0.42	0.44	0.43
FMWT	-0.26	0.24		1.1	1.2	-0.89	1.33	0.05	0.66	-0.11	-0.19	0.16	-3.7	0.31	-0.04	0.01	-1.4	0.64	0.78
SE	0.2	0.19		0.10	0.23	0.15	0.48	0.55	0.41	0.63	0.41	0.51	-4.88	0.29	0.24	0.79	-0.62	0.29	0.18
SMWT	-0.23	0.37	0.42		1.2	1.1	1.4	0.19	-1.2	-0.07	-0.32	1	.	-0.53	0.05	-0.02	0.77	0.4	0.55
SE	0.19	0.18	0.14		0.26	0.22	0.49	0.04	0.36	0.72	0.44	0.00	.	0.26	0.27	0.90	0.30	0.47	0.36
EMWT	0.29	0.1	0.43	0.42		0.60	0.51	-0.01	1.10	0.73	-0.35	-0.58	1.15	0.12	-0.59	0.9	1	0.87	0.95
SE	0.2	0.2	0.14	0.14		0.41	0.61	0.59	0.16	0.37	0.48	0.44	0.16	0.40	0.20	0.19	0.00	0.15	0.06
TMWTG	0.07	0.09	-0.32	0.12	0.17		-0.53	1.36	.	.	-0.45	.	.	.	1.30	.	1.77	-0.21	-0.71
SE	0.21	0.19	0.19	0.2	0.2		0.60	0.63	.	.	0.46	.	.	.	0.22	.	-1.85	0.62	0.30
FMWTG	-9.26	0.46	0.35	0.35	0.34	0.41		0.07	.	.	-1.16	.	.	.	-0.14	.	-0.08	0.37	-0.08
SE	0.2	0.18	0.19	0.19	0.19	0.18		0.83	.	.	-0.23	.	.	.	0.35	.	0.97	0.63	0.67
SMWTG	0.15	0.02	-0.02	0.17	-0.03	-0.02	-0.1		-0.80	0.16	-0.11	-3.82	-0.58	.	0.52	.	.	0.10	-0.50
SE	0.2	0.19	0.16	0.15	0.15	0.2	0.2		0.35	0.82	0.57	-9.47	0.34	.	0.23	.	.	0.64	0.45
EMWTG	0.21	-0.04	0.36	-0.16	0.35	-0.02	0.11	-0.03		1.43	-0.52	-2.77	0.37	.	-0.48	.	.	1.57	1.35
SE	0.19	0.2	0.14	0.15	0.14	0.2	0.2	0.15		2.38	0.55	6.10	0.58	.	0.32	.	.	1.25	0.64
Survival	-0.26	0.37	-0.11	-0.01	0.03	0.31	0.47	0.1	-0.1		0.07	-0.8	.	.	0.45	0.34	1.11	0.9	0.75
SE	0.18	0.18	0.16	0.16	0.16	0.19	0.18	0.15	0.15		0.65	0.29	.	.	0.29	1.07	-0.23	0.14	0.30
Dscore	-0.01	-0.35	-0.47	-0.43	-0.41	-0.31	-0.22	0.03	-0.04	-0.1		-0.01	.	.	-0.49	0.19	-0.2	0.58	0.33
SE	0.2	0.19	0.14	0.14	0.14	0.19	0.19	0.15	0.15	0.15		0.54	.	.	0.19	0.79	0.64	0.28	0.43
Dress%	-0.35	-0.15	0.23	0.07	-0.03	-0.14	0.47	-0.24	-0.15	-0.11	-0.19		.	.	.	.	.	-0.82	1.31

Table 4 Continued

SE	0.19	0.2	0.15	0.14	0.14	0.2	0.18	0.14	-0.15	0.15	0.17		.	.	.	.	.	0.20	0.40
ATFE	0.42	0.24	-0.2	-0.23	0.06	0.16	0.11	-0.2	0.19	0.49	0.14	0.07		-0.32	0.25	-0.15	-0.48	.	.
SE	0.18	0.19	0.19	0.19	0.2	0.2	0.2	0.15	0.15	0.17	0.2	0.19		0.26	0.21	0.71	0.46	.	.
EGGWT	0.35	-0.07	0.36	-0.25	0.00	-0.07	0.11	0.19	-0.19	0.16	-0.15	0.12	0.07		0.42	0.88	0.48	0.73	.
SE	0.19	0.18	0.19	0.7	0.17	0.2	0.2	0.15	0.15	0.18	0.18	0.15	*0.19*		1.75	-0.49	1.62	0.30	.
HDEP	0.23	0.06	-0.09	0.04	-0.27	0.36	0.1	-0.17	0.08	0.08	-0.25	0.08	-0.13	0.15		0.73	-0.53	0.56	0.73
SE	0.18	0.2	0.19	0.2	0.19	0.19	0.2	0.15	0.15	0.2	0.19	0.15	*0.2*	*0.09*		0.99	1.53	0.44	0.12
FERT	0.25	0.09	-0.01	-0.24	0.39	0.47	-0.09	0.19	-0.25	0.09	-0.12	-0.04	0.08	0.19	0.2		-0.57	0.05	0.01
SE	0.25	0.2	0.17	0.19	0.18	0.18	0.2	0.15	0.14	0.19	0.2	0.15	*0.2*	*0.08*	*0.08*		1.44	0.63	0.85
HATCH	0.25	0.12	-0.2	0.17	0.12	0.04	-0.19	0.11	-0.13	0.21	-0.02	0.17	-0.2	-0.01	0.02	-0.02		-1.2 -	-0.43
SE	0.19	0.2	0.18	0.2	0.2	0.2	0.2	0.15	0.15	0.18	0.2	0.15	*0.2*	*0.09*	*0.08*	*0.09*		0.28	0.57
FI	-0.23	-0.39	0.34	0.27	0.38	-0.32	-0.01	-0.09	0.2	0.16	0.14	-0.09	0.1	0.3	0.27	0.37	-0.33		0.91
SE	0.19	0.18	0.14	0.15	0.14	0.19	0.2	0.15	0.18	0.15	0.16	0.15	0.18	0.18	0.19	0.17	0.19		0.11
FCR	-0.12	-0.01	0.31	0.19	0.03	0.04	-0.01	-0.13	0.18	0.19	0.05	0.1	0.06	0.05	0.23	0.2	-0.13	0.19	
SE	0.2	0.2	0.15	0.14	0.15	0.2	0.2	0.15	0.18	0.15	0.15	0.15	0.2	0.21	0.19	0.2	0.19	0.15	

Hatch weight (HWT); two month weight (TMWT); four month weight (FMWT); six month weight (SMWT); eight month weight (EMWT); two month weight gain (TMWTG); four month weight gain (FMWTG); six month weight gain (SMWTG); eight month weight gain (EMWTG); survival (SVV); docility score (DOC); dressing percentage (DRESSP); age at first egg (ATFE); egg weight (EGGWT); hen day egg production (HDEP); percent fertility (FERT); percent hatchability (HATC); feed intake (FI); feed conversion ratio (FCR) and standard error (SE).

Genetic correlation between FMWT and SVV, DRESSP, FI and FCR in males, were positively high (0.75, 0.95, 0.72 and 0.67 respectively) but negative between DOC (-0.49) whereas in females genetic correlation between FMWT and SVV and DOC were negative (-0.11 and -0.19 respectively) butpositivewith DRESSP (0.16), FI (0.64) and FCR (0.78). Phenotypic correlation between FMWT and SVV and DOC (-0.06 and -0.21 respectively) in the males and SVV (-0.11) and DOC (-0.11 and-0.47 respectively) in females were all negative but positive between DRESSP (0.1 and0.23), FI (0.33 and 0.34). and FCR(0.33 and0.31) respectively in the males and females.

Positive genetic correlation existed between SMWT and SVV (0.95), FI (0.51) and FCR (0.4) but negative genetic correlation was recorded between SMWT and DOC (-0.67) and DRESSP (-0.35) in the males. However, in the females, genetic correlation observed between SMWT and SVV (-0.07) and DOC (-0.32), was negative but this was positive between DRESSP,FI and FCR(1, 0.4 and 0.55 respectively). Phenotypic correlation recorded between SMWT and SVV, FI and FCR in the males, were all positively low (0.07, 0.2 and 0.21 respectively) and negatively low between SMWT and DOC (-0.24) but zero between SMWT and DRESSP (0.00) while in the females, SMWT negatively correlated phenotypically low with SVV (-0.01) and negatively moderate with DOC (-0.43) but low with DRESSP (0.07), FI (0.27) and FCR (0.19).

In males, genetic correlation recorded was positive between EMWT and SVV (0.65), FI (0.78), and FCR (0.19) but negative DOC (-0.54)and DRESSP (-0.03).In the females, genetic correlation recorded was also positive EMWT and SVV (0.65), FI (0.87), and FCR (0.95) but negative with DOC (-0.35) and DRESSP (-0.58). Phenotypic correlations that existed between EMWT and SVV (0.08) FI (0.29) and FCR (0.31) in the males were all positive butEMWT and DOC (-0.11) EMWT and DRESSP (-0.01) correlated negatively whereas in the females similar phenotypic correlation trend was recorded between EMWT and SVV (0.03), FI (0.38), FCR (0.03), DOC (-0.41) and DRESSP (-0.03).

Genetic correlation between HWT and ATFE, EGGWT, FERT and HATCH were positive (2.43. 0.53, 0.03 and 0.56 respectively) but negative with HDEP (-0.18). HWT and FERT. Phenotypic correlation on the other hand, was positively moderate between HWT and ATFE (0.42), EGGWT (0.35) but positively low between HWT and HDEP, FERT and HATCH (0.23. 0.25 and 0.25 respectively).
Two month weight (TMWT) correlated positively genetically with ATFE (0.69),HDEP (0.02), FERT (0.17) and HATCH (0.57) but negatively with EGGWT (-0.30)whereas TMWTcorrelated positively phenotypically with ATFE (0.24), HDEP (0.06), FERT (0.09) and HATCH (0.12) but negatively with EGGWT (-0.07).

Genetic correlation existed between FMWT and ATFE (-3.7) and HATCH (-1.4) were negative. However, positive genetic correlation existed between FMWT and EGGWT (0.31) and FERT (0.01) and negative genetic correlation was also recorded between FMWT and HDEP (-0.04). Phenotypic correlation between FMWT and these egg characteristics, on the other hand, were all negative - (ATFE (-0.2), HDEP (-0.09), FERT 9-0.010 and HATCH (-0.2) except FMWT and EGGWT which was positively moderate (0.36).

No genetic correlation existed between SMWT and ATFE but negative genetic correlation (-0.53) and (-0.02) were recorded between SMWT and EGGWT and between SMWT and FERT in that order. Again, genetic correlation existed between SMWT and HDEP(0.05) and SMWT and HATCH (0.77) were positive. Phenotypic correlations recorded between sixmonth weight (SMWT) and HDEP (0.04) and Hatch (0.17) were positive but negative with ATFE (-0.23), EGGWT (-0.25) and FERT (-0.24).

Positively high genetic correlation was observed between EMWT and ATFE (1.15), FERT (0.9) and HATCH (1) but between EMWT and EGGWT was positively low (0.12) and negatively high between EMWT and HDEP (-0.59).Phenotypic correlations observed between EMWT and ATFE (0.06), HATCH (0.12) and FERT (0.39) were all positive but between EMWT and EGGWT was zero (0) and negative between HDEP (-0.27).

4. Discussion

The higher genetic correlations between body weights at different ages than their respective phenotypic correlations have been reported by several others [12,13].The moderate to high positive genetic correlations obtained among traits observed in the current studies indicate that genetic improvement in anyone of them can improve the other [14]. The high genetic association between body weights at early ages with body weights at later ages could indicate that selection for body weight at early ages would improve body weight at later (maturity) ages [7].The observation also means that selection for SVV can improve higher HDEP and earlier ATFE and selection for higher FERT could also improve hatchability [14] The association between body weight and egg weight was similar to the findings of [15] who observed a fairly high association between egg production and weight gain in the Black and Pearl Guinea fowl. This means that point of lay does not terminate live weight increases in the Guinea fowl [15].

Similar results to this work on genetic correlations have been reported in other livestock species. [13] and [7] reported high genetic correlations between body weights at different ages in Japanese quails. [16] reported high positive genetic correlations between 4-month weight and 8-month weight in the grasscutter. [3] also reported medium to high positive genetic correlations among body weight and growth traits in beef cattle. The realization of these results could be attributed to the fact that many of the body weights and gains were measured at different ages [3]. On the other hand, genetic correlation higher than 1 as obtained among some of the traits (e.g. between FMWT and EMWT) is exceeding parametric range. [17] and [18] also recorded values greater than 1 for genetic correlation between body weights in Japanese quails and in feed efficiency in indigenous chicken in Kenya respectively. This may be due to problems associated with small data size, sampling error and data imbalance (unequal group sizes) which could indicate very high genetic correlations between traits involved, which sometime could be outside parametric range [7].

The moderate to high negative genetic correlations observed among some of the traits on the other hand, indicate that genetic improvement in any of them will decrease the development of the other. Specifically, the high negative genetic correlation between HWT and SMWT means that heavy mothers lay small eggs. This may be the reason why poultry layers are usually light weight. [19] also reported high negative (-1.726) genetic correlation between 5th and 20th week body weight in female colored synthetic broiler breeder chicken of Odisha, India.

The moderate to high positive phenotypic correlations recorded between some of the traits in this experiment means that any of these traits can be used to measure the other in a selection programme whereas those showingmoderate negative phenotypic correlations could mean that the traits involved cannot be used as measures for each other and selection cannot bring about correlated response in them [20].

5. CONCLUSION

The discoveries in this study are notdifferent from values from similar studies conducted by other scientists in indigenous Guinea fowls. In Guinea fowl selection breeding programmes,the results could be used in defining breeding objectives,estimating breeding values, and calculating annual rate of genetic gain.

ETHICAL APPROVAL

Experimental protocols used in this study strictly conformed with the internationally accepted standard.

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Comment [KDA12]: Bold and you have to write references with journal system

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