

CORRELATION STUDIES ON SIRE BEST LINEAR UNBIASED PREDICTION VALUES AND RANKS OF MEHALLAH 85 TURKEY PERTAINING BODY WEIGHT AND CONFORMATION MEASURES

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ABSTRACT

Data of body weight and conformation measures (i.e. length of keel, KL; shank, SL and breast width, BRW) of 1103 Mehallah 85 turkey offspring were analyzed using Restricted Maximum Likelihood (REML) under Mixed Model Equations. Best Linear Unbiased Estimates (BLUE) included the effects of hatch; sex and hatch X sex interaction along with unrelated 28 sires as a random effect. The respective 16 wk. of age BW, KL, SL & BRW overall Best Linear Unbiased Estimates (BLUE) for Mehallah 85 were 6095.5 g, 131.92 mm, 156.92 mm and 207.65 mm. The Sire model included the following fixed effects: Hatch (H); Sex (S) and Hatch X Sex interaction (H X S). All the fixed effects and their interactions were highly significant ($P \leq 0.0001$) regarding the traits under consideration.

Transmitting ability (TA) estimates of Mehallah 85 turkey at 16 wk. of age ranged from -561.26 to 389.28 g. (range = 950.54 g.) for BW; -3.62 to 3.97 mm. (7.59 mm.) for KL; -7.73 to 7.00 mm. (14.73 mm.) for SL and -8.20 to 6.70 mm. (14.91 mm.) for BRW. The range for the top 30% ranked sires were 270.45 g., 3.54 mm., 5.72 mm. and 5.31 mm. for BW, KL, SL and BRW, respectively. However, the number of sires having positive TA records reached about $\geq 50\%$ from the tested individuals at each of the considered trait.

The product moment correlation coefficient concerning sire transmitting ability and the Spearman correlation coefficient concerning ranks of sire transmitting ability were generally weak and insignificant among all traits except that between BW and BRW where the two correlation sorts were highly significant ($P \leq 0.0001$) being 0.878 and 0.863, respectively.

Heritability estimates were relatively intermediate and ranged between 0.2655 - 0.3751 and the percentage sire variance component (σ_s^2) ranged between 13.27 - 18.76% in the turkey herd under study.

Key words: turkeys, Restricted Maximum Likelihood, Sire transmitting ability.

INTRODUCTION

Paternal genetic effect could be determined by the genes transmitted by the sire to his offspring. Therefore, accurate determination of turkeys' individual breeding values for an economic trait is fundamental for planning and to attain progress in breeding programs. Genetic progress depends to great extent on the correlation between breeding values in addition to that amongst phenotypic ones. Best linear unbiased prediction (BLUP) estimated by different procedures is an approach to predict breeding values of animals and to adjust simultaneously for fixed effects of the model (Lukafahr, 1992). Mixed-model procedures are useful means for getting assessments of genetic parameters identifiable for populations and for scrutinizing and then

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improving industrial selection programs. The majority of the evolution in industrial selection can be accomplished when breeding values are estimated with parameters specific for the population so optimum weight can be given to each trait for specific breeding objectives (Ferraz and Johnson, 1993). Van der Werf et al., 1994 acquainted that prediction of BLUP values has the property of diminishing the error variance.

The objectives of the present study were to estimate sire variance component and to predict the sires' proofs as well as their rank using the mixed model equations (MME) pertaining to body weight (BW) and body conformation (i.e. length of keel, KL; shank, SL and breast width, BRW) measures in Mehallah 85 turkeys. Those, besides studying the correlation among those traits, using Product moment and Pearson coefficients for sire transmitting values and ranks, respectively.

MATERIALS AND METHODS

Herds and data

Data of body weight, g. (BW) and body conformation measures, mm. (i.e. lengths of keel, KL; shank, SL and breast width, BRW) at 16 wk. of age concerning Mehallah 85 turkeys were collected from 1103 individuals sired by 28 toms. These records belong to flocks raised in Mehallet Mousa Turkey Research Station, Ministry of Agriculture, Kafr-El-Sheikh Governorate, which belongs to Animal Production Research Institute, Egypt. Mehallah 85 is an Egyptian synthetic turkey strain (Abd El-Gawad *et al.*, 1993 and Balat *et al.*, 1993). It is originated by crossing White Nicholas toms along with White Holland hens backcrossed afterwards with White Nicholas concentrating the selection on egg production from the formed turkey hens.

Management and feeding

Day-old offspring poults were wing-banded and housed in floor pens provided with feeders and automatic drinkers. They were fed on a starting (up to 8 wk. of age) and a growing (from 9 up to 16 wk. of age) commercial mash diet. Starting diets contained approximately 28% crude protein, 2800 kcal metabolizable energy per kg diet meanwhile the growing diets contained approximately 20% crude protein, 3000 kcal metabolizable energy per kg diet. Feed and water were provided ad libitum.

Statistical analysis: Analysis of variance was performed using LSMLMW program of Harvey (Harvey, 1990) to obtain Best Linear Unbiased Prediction (BLUP) of random effects, (i.e. turkey sire); Best Linear Unbiased Estimators of fixed effects (BLUE) and Restricted Maximum Likelihood Estimates (REML) of variance components using Mixed Model Equations.

The base linear sire model in matrix notation was as follows:

$$Y = X\beta + Zs + e$$

Where:

Y denotes n X 1 vector of observation of body weight (BW) and body conformation measures, mm. (i.e. lengths of keel, KL; shank, SL and breast

width, BRW) traits at 16 wk. of age where n epitomizes number of observations; β denotes $(p \times 1)$ column vector of unknown fixed effects of hatch, sex and hatch*sex interaction, at which p symbolizes the number of levels for fixed effects; s denotes $(q \times 1)$ column vector of unknown sire random effect at which q indicates the number of levels for random effects; X denotes $(n \times p)$ known incidence matrix for fixed effects; Z denotes $(n \times q)$ known incidence matrix for random effects; e denotes $(n \times 1)$ column vector of non-observable residual effects, which includes random environmental and non-additive genetic effects, assuming that these effects are normally and independently distributed $(0, \sigma^2_e)$. Pedigree of sires was not available, therefore the inverse of the relationship coefficient matrix (A^{-1}) was not included in the model. Instead an identity matrix (I) was used. The mixed model equations (MME) of the sire model described above were:

$$\begin{vmatrix} X'X & X'Z \\ Z'X & Z'Z + KI \end{vmatrix} \begin{vmatrix} \hat{B} \\ \hat{s} \end{vmatrix} = \begin{vmatrix} X'Y \\ Z'Y \end{vmatrix}$$

Where:

$K = \sigma^2_e / \sigma^2_s$ and I denotes the identity matrix. The solution to s is called BLUP predictors of s . $V(e) = I \sigma^2_e$ and $V(s) = I \sigma^2_s$.

The linear genetic model employed for the prediction of the sires transmitting abilities, (assuming that dominance and epistasis, which represents intra- and inter-locus interactions respectively were of diminutive significance) was as follows:

$$Y_{ij} = \mu + g_{ai} + e_{ij}$$

Y_{ij} is the record j of the i^{th} animal; μ refers to identifiable non-random (fixed) environmental effects (i.e. the mean performance of the bird under the same management group) and it is assumed to be known; g_{ai} is the sum of the additive genetic values of the genotype of animal i which in turn equals twice the animal transmitting ability; and e_{ij} being the random environmental effects, the remainder of genetic values of the genotype of animal i . It is assumed that Y follows a multivariate normal distribution, implying that traits are determined by infinitely many additive genes of infinitesimal effect at unlinked loci, the so-called infinitesimal model (Bulmer, 1980). Furthermore, it is assumed that the values of $\text{var}(g_{ai})$ and $\text{var}(e_{ij})$ or their proportionality is known, along with that there is no correlation between g_{ai} and e_{ij} ($\text{cov}(g_{ai}, e_{ij})=0$).

The reliability, (r^2) of the predicted breeding values is [$r_{ay} = n / (n + k)$] where, n = number of progeny; k is a constant for any assumed heritability being [$k = (4 - h^2) / h^2$]; a is the sire breeding value and \bar{y} is the mean of single records of n progeny of a given sire. The accuracy (r) of the predicted breeding values is therefore, equals to the square root of the reliability (Mrode, 1996). However, reliability and accuracy approaches unity as the number of progeny enhances.

RESULTS AND DISCUSSION

Means and variations

Number of observation (n), actual means, standard error (SE) and coefficient of variability (CV%) for Mehallah 85 pertaining body conformation measures, mm. (i.e. lengths of keel, KL; shank, SL and breast width, BRW) traits at 16 wk. of age are presented in table 1. These figures were comparable with those reported by many investigators (i.e. Krueger *et al.*, 1972; Mostafa, 1997; Nestor *et al.*, 1997; Mostafa and Nofal, 2000 and Nofal *et al.*, 2001). Phenotypic variability is the main tool for selection.

Percentages of variation (CV%) for body weight (BW) and body conformation measures (KL, SL and BRW) were low and relatively higher in BW compared with body conformation measures, which in turn means that improvement of body weight (BW) in this turkey flock through phenotypic selection is quite possible relative to body conformation measures, especially if it is associated with reasonable heritability (h^2) estimate. For all traits, values of CV% denote that phenotypic variations for body weight (BW) and body conformation measures (KL, SL and BRW) affected with the order of hatch proceeds.

Table (1): Number of observation (N); actual mean; standard error and Coefficient of variability (CV%) for body weight, g. and conformation measures (lengths of shank, keel and breast width, mm.) in Mehallah 85 at 16 wk. of age.

Trait & Effect	N.	Actual mean	Standard Error	CV%
Body Weight (g.):				
Hatch1	312	5893.59	52.75	15.81
Hatch2	403	6113.65	57.65	18.93
Hatch3	388	6423.97	76.51	23.46
Males	570	7188.77	35.02	11.63
Females	533	5060.98	18.07	8.24
Overall	1103	6160.56	37.81	20.38
Keel length (mm):				
Hatch1	312	132.86	0.88	11.65
Hatch2	403	131.39	0.76	11.62
Hatch3	388	133.02	0.86	12.68
Males	570	147.16	0.21	3.44
Females	533	116.57	0.15	3.06
Overall	1103	132.38	0.48	12.02
Shank length (mm):				
Hatch1	312	155.59	0.66	7.47
Hatch2	403	153.30	0.55	7.22
Hatch3	388	163.12	0.74	8.93
Males	570	167.23	0.43	6.11
Females	533	146.89	0.27	4.24
Overall	1103	157.40	0.40	8.43
Breast width (mm):				
Hatch1	312	200.75	1.01	8.85
Hatch2	403	207.68	0.86	8.34
Hatch3	388	216.61	1.18	10.75
Males	570	223.87	0.67	7.12
Females	533	192.81	0.47	5.62
Overall	1103	208.86	0.62	9.92

Non-genetic effects:

Hatch: The hatch effect was significant ($P \leq 0.0001$) on body weight (BW) and body conformation measures, mm. (i.e. lengths of keel, KL; shank, SL and breast width, BRW) traits at 16 wk. of age (table 2). Hatch was one of the most important non-genetic factor affecting body weight (BW) and body conformation measures. An evidence for such considerable hatch effect was recognized in different breed groups in poultry by many investigators (Sabra, 1990 and Abdel-Ghany, 1995). The highest Best Linear Unbiased Estimates (BLUE) regarding body weight (BW) and body conformation measures (KL, SL and BRW) were frequently recorded by individuals hatched from the third hatch, while the inferior body weight (BW) and body conformation measures (KL, SL and BRW) were in general attained by those hatched from the first one. This could be explained by that settled eggs were collected from turkey hens before complete maturation of their body, which in turn could downgrade the performance of their hatched poults. When hens getting older, reaching the convenient phase of autosomal maturity, their hatched poults revealed better performance. In other words, the superiority of the later hatch may be attributable to better pre-ovipositional maternal effects in terms of oviductal factors that exert their effects on egg size, egg weight, shell quality, yolk composition and transmitted immunities (Aggrey and Cheng, 1994 and Khalil et al., 1999) to the hatched chicks relative to that in the earlier hatch. It could be also explained by the changes of circumstances at the time of hatch.

Table (2): Best Linear Unbiased Estimates (BLUE) and test of significance of factors affecting body weight and conformation measures (lengths of shank, keel and breast width, mm.) of Mehallah 85 turkeys at 16 wk. of age.

Factor	N	Traits			
		Body Weight	Keel	Shank	Breast
BLUE ± SE	1103	6095.50±42.45	131.92±0.32	156.92±0.49	207.65±0.88
Hatch (H):		****	****	****	****
1 st	312	-246.28±23.93	0.60±0.18	-1.57±0.28	-7.67±0.50
2 nd	403	-36.87±22.38	-1.17±0.17	-3.96±0.26	-0.68±0.47
3 rd	388	283.15±22.58	0.57±0.17	5.53±0.26	8.35±0.47
Sex:		****	****	****	****
Males	570	1037.86±16.17	15.29±0.12	10.16±0.19	15.36±0.34
Females	533	-1037.86±16.17	-15.29±0.12	-10.16±0.19	-15.36±0.34
Hatch*Sex:		****	****	****	****
1 st H_Males	160	-265.41±23.84	-0.50±0.18	-0.98±0.28	-1.52±0.50
1 st H_Females	152	265.41±23.84	0.50±0.18	0.98±0.28	1.52±0.50
2 nd H_Males	210	-69.98±22.27	-0.64±0.17	-1.43±0.26	-2.70±0.46
2 nd H_Females	193	69.98±22.27	0.64±0.17	1.43±0.26	2.70±0.46
3 rd H_Males	200	335.59±22.49	1.14±0.17	2.41±0.26	4.22±0.47
3 rd H_Females	188	-335.59±22.49	-1.14±0.17	-2.41±0.26	-4.22±0.47

**** = significant at ($P \leq 0.0001$).

Sex: Sex effect presented in table 2, constituted a significant source of variation ($P \leq 0.0001$) on body weight (BW) and body conformation measures, mm. (i.e. lengths of keel, KL; shank, SL and breast width, BRW) at 16 wk. of age. However, males were superior in all studied traits (table 2). This

superiority of males over females in body weight (BW) and body conformation measures (KL, SL and BRW) was observed by many authors (i.e. Kruger *et al.*, 1972; Nestor *et al.*, 1985; Mostafa , 1997; Mostafa and Nofal, 2000 and Nofal *et al.*, 2001).

(Hatch X Sex) interaction comprised a significant source of variation ($P \leq 0.0001$) on all traits studied (Table 2). This may indicate dissimilar response of hatch groups to the effect of sex. These (hatch X sex) interaction significant effects are difficult to comprehend and its interpretation was barely possible. Though, the general trend indicated the reverse response of different sexes in the third hatch compared with that in the first and second hatches.

Variance components (σ^2) and heritability (h^2) estimates. Sire (σ^2_s) and error (σ^2_e) variance components and paternal half sib heritabilities (h^2_s) estimated using restricted maximum likelihood procedure (REML) assuming unrelated sires for body weight (BW) and body conformation measures at 16 wk. of age, were presented in table 3. For all body weight (BW) and body conformation measures, mm. (i.e. lengths of keel, KL; shank, SL and breast width, BRW) traits at 16 wk. of age in Mehallah 85 , heritability estimates (h^2_s) were generally intermediate and ranged from 0.2655 ± 0.1289 to 0.3751 ± 0.1397 . An explanation for these relatively good estimates is that Mehallah 85 turkeys as a new strain have not been subjected yet to an intensive selection programs.

Table (3): Estimates of sire (σ^2_s) and error (σ^2_e) variance components, their percentages along with paternal half-sib heritability (h^2_s) estimates for body weight and conformation (lengths of shank, keel and breast, mm.) measures for Mehallah 85 turkeys at 16 wk. of age.

Trait	Sire Variance		Error		Heritability $h^2_s \pm SE$
	Component	%	Component	%	
Body Weight	63814.27	18.76	276398.55	81.24	0.3751 ± 0.1397
Keel Length	2.47	13.53	15.79	86.47	0.2705 ± 0.1275
Shank Length	15.65	15.33	86.42	84.67	0.3076 ± 0.1320
Breast width	18.54	13.27	121.13	86.73	0.2655 ± 0.1289

Number of sires = 28; K = 6.5340.

This increase of h^2 estimates in Mehallah 85 was greatly due to enlarged magnitude of the sire variance component. The percentages of the sire variance components ranged from 13.27 – 18.76%, revealing high additive variance of these traits, table 3. These h^2 estimates were comparable to those obtained by Krueger *et al.*, (1972); Nestor (1977; 1984 and 1985); Mostafa (1997) and Nofal *et al.* (2001). However, BW achieved the highest h^2 estimates being 0.3751, which indicate that it would respond reasonably with direct selection.

Sire transmitting ability. The breeding value of an individual is an aggregate expression of the information relative to a performance trait, including that

from relatives, designed to predict its genetic potential as accurately as possible. It concerns the genetic merit that an individual transmits to his offspring (Chapman, 1985). BLUP solves for the fixed and random effects simultaneously, and in doing so provides an unbiased method by which phenotypic records can be adjusted for known sources of environmental influences. In addition BLUP also takes into account the presence of genetic trends across generations and also changes in genetic variance caused by gametic phase disequilibrium (Henderson, 1973). Valid evaluation of breeding values of economic traits in turkeys is basic information to be used in constructing breeding policies and managerial decisions. To maximize the genetic progress the best sires have to be selected. Increasing accuracy of selection could be accomplished in part by choosing the right model for the evaluation. Sire effect must be seriously considered in studies on body weight (BW) and body conformation measures (KL, SL and BRW) in turkey, especially those associated with improvement of traits, through selection of sires based on the performance of their progeny. Best Linear Unbiased Prediction (BLUP) estimated by different procedures can be used to predict breeding values (BV) of animals and to adjust simultaneously for the fixed effects of the model (Lukafahr, 1992).

Minimum and maximum body weight (BW) and body conformation measures (KL, SL and BRW) estimates at 16 wk. of age regarding sire breeding values (SBV) are presented in table 4, which revealed that ranges of SBV of Mehallah 85 turkeys were 950 g. for BW, while for KL, SL and BRW they were 7.59, 14.73 and 14.91 mm, respectively. These figures were to great extent correspond with those reported by Nofal *et al.* 2001. However, the data in table 4 exhibited an obvious trend that percentage of sires that possess positive values (% PR) in Mehallah 85 turkeys amounted ≥ 0.50 . From a genetic point of view improvement in animal breeding is achieved through detecting the best animals as parents for the next generation (Chyr *et al.*, 1979). In this respect, sires would be further efficiently selected using SBV when artificial insemination and frozen semen are introduced to turkey farms.

Table (4): Minimum and maximum estimates and the range of sire transmitting abilities (SBV) along with SBV of the superior 30% sires and the number and percentage of sires that possess positive SBV for body weight, g. and conformation (lengths of shank, keel and breast, mm.) measures in Mehallah 85 at 16 wk. of age.

Trait	SBV of all sires used			SBV of the top 30% sires used		Positive Records	
	Min.	Max.	Range	Min.	Range	n	%
Body weight	-561.26	389.28	950.54	118.83	270.45	14	50.00
Keel length	-3.62	3.97	7.59	0.43	3.54	16	57.14
Shank length	-7.73	7.00	14.73	1.28	5.72	15	53.57
Breast width	-8.20	6.70	14.91	1.39	5.31	14	50.00

Correlation analysis: Animal Model Restricted Maximum Likelihood computer programs allow only few traits to be tested for covariance estimation. As number of traits tested increases the sensitivity of the available programs for covariance estimation declines (Youssef, 1998). Adding to this the time-consuming and boring computations using animal model analysis, using mixed model analysis would be more preferable though less accurate. In this respect Calo *et al.*, 1973 reported that genetic correlation between traits could be derived from single trait models by adjusting correlations between expected breeding values (EBVs) for reliabilities. Therefore, correlation studies were introduced here to establish an approximate way for finding out the genetic correlation between actual breeding values generated from a single-trait model analysis. However, the conclusion arrived here need to be tested for efficiency at least using outputs of multi-trait animal model analysis. As noted from the following figures that reliability exceeds 98% and accuracy transcend 99% using mixed model analysis for the studied traits. However, values of reliability and accuracy reported here are to great extent comparable with those reported for Broad Breasted Bronze by Nofal *et al.*, 2001.

Trait	Reliability	Accuracy
Body weight	0.991	0.996
Keel length	0.988	0.994
Shank length	0.989	0.995
Breast width	0.987	0.994

However, Spearman ranking studies propose an idea if the sires which are superior in some trait, how they would be in the other one. In the other hand, product moment correlation coefficient presents valuable knowledge on the sign and magnitude of the genetic correlation between each of the two considered traits.

Across all traits (i.e. body weight, BW and body conformation measures KL, SL and BRW) at 16 wk. of age, the product moment correlation coefficients (SAS, 1988), among sires, according to their values of transmitting abilities, and Spearman correlation coefficients among ranks of sire transmitting abilities presented in table 5, were mostly low and insignificant except that among body weight and breast width. These values ranged from -0.191 to 0.878 and -0.038 to 0.863 in product moment and Spearman correlation coefficients, respectively. A general trend could be deducted from the two types of correlation figures (Table 5) that the respective estimates were to great extent alike in their sign (i.e. positive or negative) and magnitude (i.e. high or low) with a tendency of the product moment coefficient to be slightly higher relative to Spearman coefficient. However, The correlation (either product moment or Spearman) coefficient between body weight and Breast width was positive and the unique, which was high and significant ($P \leq 0.0001$) being 0.878 and 0.863 in product moment and Spearman correlation coefficients, respectively. In this respect, Sadek *et al.* 1993 and Abdel-Ghany *et al.* 1998 verified the same tendency but with other model animals. The present results substantiate the presence of correlated response between these two traits (i.e. body weight and Breast width), which must be carefully considered in selection.

Table (5): The sire transmitting ability's product moment correlation coefficient, (upper diagonal) and sire ranks (according to their transmitting ability) Pearson correlation coefficient, (lower diagonal) as well as their tests of significance ($H_0: \text{Rho}=0$) for body weight, g. and conformation (lengths of shank, keel and breast, mm.) measures in Mehallah 85 at 16 wk. of age.

Trait	Body weight	Keel length	Shank length	Breast width
Body weight		-0.081 ^{ns}	0.371 ^{ns}	0.878 ^{****}
Keel length	-0.038 ^{ns}		0.111 ^{ns}	-0.191 ^{ns}
Shank length	0.323 ^{ns}	0.028 ^{ns}		0.179 ^{ns}
Breast width	0.863 ^{****}	-0.010 ^{ns}	0.117 ^{ns}	

N = 28.

**** = Significant at $P \leq 0.0001$; ns = not significant ($P \leq 0.05$).

These conclusions proposed that in Mehallah 85 turkeys BW and BRW would respond better to selection for correlated traits than among the rest. It is worthy to state that, Spearman correlation coefficients gave values similar, to great extent, to those of the product moment correlation coefficient in case of the data under study, while Kendall and Hoeffding correlation statistics gave a smaller figures compared with those reported here. These results make known that, in the light of these data, Spearman and product moment correlation coefficients may be more sensitive in studying correlations between SBV of different traits. However, the later conclusion disagreed with those reported by Sadek *et al.* 1993 meanwhile it coincides with those reported by Abdel-Ghany *et al.* 1998.

REFERENCES

- Abd El-Gawad, E. M.; H. A. Gad; M. M. Balat; N. M. El-Naggar and M. Y. Mostafa (1993). Mehallah85 a new strain of turkey. *Egypt. Poult. Sci.*, 13: 225-251.
- Abdel-Ghany, A. M. (1995). The effectiveness of polyallel crossing of some exotic breeds of chickens with some local breeds. Ph. D. Thesis, Faculty of Agriculture, Suez Canal University, Ismailia, Egypt.
- Abdel-Ghany, A. M; E. G. Ahmed; N. S. Hassan and A. A. Amin (1998). Sire best linear unbiased prediction of litter gain traits pertaining two standard breeds of rabbits raised under semi-arid environmental conditions. *J. Union Arab Biol. Cairo*, Vol. 9 (A), Zoology (Suppl. Issue): 429-439 (1998). Proceeding of the 5th International Conference, Ismailia, Egypt. 8-11 Nov., 1998.
- Aggrey, S. E. and K. M. Cheng (1994). Animal model analysis of genetic (co) variance for growth traits in Japanese Quail. *Poult. Sci.*, 73 (12): 1822-1828.
- Balat, M. M; N. A. El-Sayed; H. A. Gad; N. M. El-Naggar and E. M. Abd El-Gawad (1993). Heritability estimates and genetic relationships among some economic traits in the new turkey strain Mehallah 85. *Egypt. Poult. Sci.*, 13:175-198.

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- Bulmer, M. G. (1980). *The Mathematical Theory of Quantitative Genetics*. Clarendon Press, Oxford.
- Calo, L. L.; McDowell, R. E. Van Vleck, L. D. and P. D. Miller (1973). Genetic aspects of beef production among Holstein-Friesian pedigree selected for milk production. *J. Anim. Sc.*, 37:676-682
- Chapman, A. B. (1985). *General and quantitative genetics*. Elsevier Science Publishers B. V., New York.
- Chyr, S.; A. E. Freeman and J. Berger (1979). Estimation of milk production ability of Holstein cows. *J. Dairy Sci.*, 62(11): 1774-1783.
- Ferraz, J. B. S. and R. K. Johnson (1993). Animal model estimation of genetic parameters and response to selection for litter size and weight, growth and backfat in closed seedstock populations of Large White and Landrac Swine. *J. Anim. Sci.*, 71:850-858.
- Harvey, W. R. (1990). *User's Guide for LSMLMW. Mixed model least squares and maximum likelihood computer program. PC-Version 2*. Ohio State University, Columbus, USA (Mimeograph).
- Henderson, C. R. (1973). Sire evaluation and genetic trends. *Proceedings of the Animal breeding and Genetics Symposium in honour of Dr. J. L. Lush in Blacksburg, Virginia. ASAS and ADSA*, pp. 10-41.
- Khalil, M. H.; I. H. Hermes and A. H. Al-homidan (1999). Estimation of Heterotic components for growth and livability traits in a crossbreeding experiment of Saudi chickens with White Leghorn. *Egypt. Poult. Sci.*, 19 (III): 491-507.
- Krueger, W. F.; R. L. Atkinson; J. H. Quisenberry and J. W. Bradley (1972). Heritability of body weight and conformation traits and their genetic association in turkeys. *Poult. Sci.*, 51: 1276-1282.
- Lukefahr, S.D. (1992). Animal models for quantitative genetic analysis in rabbit breeding programs. *J. Appl. Rabbit Res.*, 15: 104-130.
- Mostafa, M. Y. (1997). *Genetical studies on turkey " Selection for specific gravity of live bird in turkey"*. Ph. D. Thesis, Faculty of Agriculture, Tanta University, Kafr-El-Sheikh, Egypt.
- Mostafa, M. Y. and R. Y. Nofal (2000). Effects of crossing two breeds of turkey on live body measurements, growth performance and liveability. *Egypt. Poult. Sci.*, 20 (2): 239-252.
- Mrode, R. A. (1996). *Linear Models for the Prediction of Animal Breeding Values*. Center for Agriculture and Bioscience (CAB) international. Wallingford, UK.
- Nestor, K. E. (1977). Genetics of growth and reproduction in the turkey. 5- Selection for increased body weight alone and in combination with increased egg production. *Poult. Sci.*, 56: 337-347.
- Nestor, K. E. (1984). Genetics of growth and reproduction in the turkey. 6- Long-term selection for increased 16- week body weight. *Poult. Sci.*, 63: 2114-2122.
- Nestor, K. E. (1985). Genetics of growth and reproduction in the turkey. 10- Tandem selection for increased body weight and egg production. *Poult. Sci.*, 64: 2221-2222.

- Nestor, K. E.; W. L. Bacon; Y. M. Saif and P. A. Renner (1985). The influence of genetic increase in shank on body weight, walking ability and reproduction of turkey. *Poult. Sci.*, 64: 2248-2255.
- Nestor, K. E.; D. O. Noble and D. A. Emmerson (1997). Genetics of growth and reproduction in the turkey. 13- Effects of repeated backcrossing of an egg line to two sire lines. *Poult. Sci.*, 76: 227-235.
- Nofal, R. Y.; A. M. Abdel-Ghany and M. Y. Mostafa (2001). Best Linear Unbiased Prediction of Broad Breasted Bronze Turkey Toms for Body Weight and Conformation Measures at 16 Wk. of Age. 2nd International Conference on Animal Production and Health in Semi-Arid Areas (in Press).
- Sabra, Z. A. M. (1990). Estimation of Heterosis and combining abilities for some economic traits in chickens. M. Sci. Thesis, Faculty of Agriculture at Moshtohor, Zagazig University, Banha Branch, Moshtohor, Egypt.
- Sadek, M. H.; A. A. Halawa and A. A. Ashmawy (1993). Effect of using the additive genetic relationship matrix on sires' proofs. *Egypt. J. Anim. Prod.*, 30 (2): 189-200.
- SAS Institute, (1988). SAS/STAT User's Guide. 6.03 Edition. SAS Institute Inc., Cary, NC.
- Van der Werf, J. H. J.; T. H. E. Meuwissen; G. De Jong (1994). Effects of correction for heterogeneity of variance on bias and accuracy of breeding value estimation for Dutch dairy cattle. *J Dairy Sci.*, 77 (10): 3174-3184.
- Youssef, M. K. (1998). Genetic analysis for productive life of doe rabbits. Ph. D. Thesis, Faculty of Agriculture, Moshtohor, Zagazig University, Banha Branch, Egypt.

دراسات قيم وترتيبات الارتباط لأفضل تنبؤات خطية غير متحيزة لصفات وزن ومقاييس الجسم عند عمر ١٦ أسبوع لأبء الرومي من سلالة المحللة ٨٥
محيى الدين يوسف مصطفى
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حلت بيانات وزن و مقاييس (أطوال القص و الساق و عرض الصدر) الجسم لعدد ١١٠٣ من نسل الرومي لسلالة المحللة ٨٥ (Mehallah 85) والناتجة من ٢٨ ذكر (أباء) وذلك باستخدام طريقة معظمة الاحتمال المقيدة (REML) لحل معادلات النموذج المختلط. شملت التقديرات الخطية المثلى الغير متحيزة (BLUE) تأثيرات الفقس، الجنس و التداخل بين تاريخ الفقس و الجنس وذلك بالإضافة للتأثير العشوائى (BLUP) لعدد ٢٨ ذكر (أب). وقد كانت قيم التقديرات الخطية المثلى الغير متحيزة (BLUE) لصفات وزن و مقاييس (أطوال القص و الساق و عرض الصدر) الجسم عند عمر ١٦ أسبوع لسلالة المحللة ٨٥ هي على الترتيب ٦٠٩٥,٥٠ جرام و ١٣١,٩٢ ملم، ١٥٦,٩٢ ملم، ٢٠٧,٦٥ ملم. إحتوى نموذج التحليل الإحصائى على التأثيرات الثابتة لكل من الفقس و الجنس وكذلك التداخل بينهما ولقد كانت كلها عالية المعنوية (باحتمال أقل من أو يساوى ٠,٠٠٠١) وذلك لكل الصفات المدروسة. وقد تراوحت تقديرات القيم التمريرية لسلالة المحللة ٨٥ عند عمر ١٦ أسبوع بين - ٥٦١,٢٦ : ٣٨٩,٢٨ (المدى ٩٥٠,٥٤ جراماً ١٤,٧٣ ملم) لطول عظمة الساق، - ٨,٢٠ : ٦,٧٠ (١٤,٩١ ملم) لعرض الصدر. وقد تراوحت هذه التقديرات بالنسبة لأعلى ٣٠% من الأباء فى ترتيبها التنازلى بالنسبة للقيم التمريرية ٢٧٠,٤٥ جرام ٣,٥٤ ملم، ٥,٧٢ ملم و ٥,٣١ ملم على الترتيب. هذا و قد كانت أعداد الذكور ذات القيم التمريرية الموجبة حوالى ٥٠% فى أغلب الصفات المدروسة.

و قد كانت تقديرات معامل بيرسون للارتباط بين القيم التمريرية، معامل سبيرمان للارتباط بين الترتيب التنازلى للصفات المدروسة ضعيفاً و غير معنوي لكل الصفات ما عدا وزن الجسم و عرض الصدر حيث كانت عالية المعنوية (باحتمال أقل من أو يساوى ٠,٠٠٠١) وكانا ٠,٨٧٨، ٠,٨٦٣ على التوالي .
وقد كانت تقديرات المكافئ الوراثى للصفات محل الدراسة متوسطة نسبياً و تراوحت بين ٠,٢٦٥ - ٠,٣٧٥، كما تراوحت تقديرات النسبة المئوية لمكون التباين الأبوى بين ١٣,٢٧ : ١٨,٧٦ فى قطيع الرومي محل الدراسة.