

# Use of factor scores for determining the relationship between body measurements and semen traits of cocks

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## ABSTRACT

Semen evaluation is required to predict fertility. In most rural African communities, facilities for microscopic evaluation of semen are not available. Therefore, an indirect method of predicting semen traits of cocks is required by poultry farmers. The objective of this study was to use factor scores derived from factor analysis of body measurements to predict some semen traits of cocks. Correlation matrix was obtained by calculating the correlations between body measurements and semen traits of cocks. Kaiser-Meyer-Olkin (KMO) measure of sampling adequacy and Bartlett's test of sphericity were used to test the appropriateness of factor analysis on the data. The extraction of the factors was done by calculating the eigenvalues of the correlation matrix. Variance maximizing rotation of the transformation matrix was done to facilitate the interpretation of the factor loadings. Two factors with eigenvalues greater than 1 were extracted which accounted for 76.96% of the variations present in the original variables. The two factors were used to obtain the factor score coefficients. When utilized as independent variables in multiple regression analysis, the two factors explained 53.20% and 40.80% of the variations in sperm motility and sperm concentration respectively. Factor 1 had more impact on sperm motility than factor 2 as it was significantly related to it. Factor 2 was significantly more related to sperm concentration than factor 1. The relationship between body measurements and semen volume, live sperm and abnormal sperm were weak and mostly negative. Therefore, they were not predicted using factor scores.

**Keywords:** Cocks; Factor Scores; Multiple Regression; Semen Traits

## 1. INTRODUCTION

Poultry production plays an important role as one of the major source of animal protein. Almost every house hold in Nigeria is involved in one form of poultry production activity or the other. Reproduction is a vital aspect of poultry production that ensures the continuity of poultry species. Semen evaluation is required to predict fertility in natural mating and artificial insemination. The fertilizing ability of the breeder cock is dependent upon several semen quality characteristics including sperm concentration, viability and motility [1]. Sperm motility is essential for normal fertilization and it is currently the most common parameter of sperm quality acting as an indirect measure of metabolic activity and sperm viability [2]. Semen can be evaluated microscopically in the laboratory using standard procedures or by measuring the sperm quality index (SQI) using sperm quality analyzer [3]. Computer assisted semen analysis (CASA) provides objective and reproducible data on a number of sperm motion parameters and it should enhance the value of motility assessment to fertility prognosis. In rural African communities where most poultry farmers reside, facilities for microscopic evaluation of semen are not available. Therefore, a simple reliable and indirect method for in vivo estimation of semen quality based on correlation between body parameters and semen traits are needed by poultry farmers. Galal [4] reported that body weight, length of shank, comb, and wattle were good predictors of semen attributes in chicken. Similarly, Udeh *et al.* [5] reported that lengths of beak, comb, shank and wing could be used to predict semen traits of cocks. Although, it is possible to predict semen traits of cocks based on body measurements, the accuracy of the prediction may be bias by multicollinearity among the predictor variables. Multicollinearity refers to the presence of highly inter correlated predictor variables in regression models and its effect is to invalidate some of the basic assumptions underlying their mathematical estimations. One of the approaches to eliminate this problem is factor analysis or principal component analysis [6]. Factor scores

derived from PCA or factor analysis are used as predictors in multiple regression analysis thereby solving the problem of multicollinearity. The objective of this study is to use factor scores derived from factor analysis of body measurements to predict semen traits of cocks.

## 2. MATERIALS AND METHODS

**Study location:** The study was done at the poultry unit of teaching and research farm, Department of Animal Science, Delta State University, Asaba Campus. Asaba is located between 60°12' North and 60°45' East.

**Experimental animals and their management:** Fifty layer type cocks aged 30 weeks were used for the study. The cocks were procured from a reputable farm in Asaba, Delta State at 20 weeks and raised to 30 weeks of age before commencing the study. The birds were provided *ad libitum* broiler finisher diet containing about 20% crude protein. Water was made available all the time.

**Traits measured:** The following measurements were taken at 30 weeks of age: body weight (BWT), shank length (SHL), beak length (BKL), comb length (CBL), thigh length (THL), wing length (WGL) and Wattle length (WTL). The body weights of cocks were recorded in kilogram while the body measurements were recorded in centimeter using a tape.

**Semen collection and evaluation:** Semen was collected from cocks at 30 weeks of age using the massage technique of Burrow and Quinn [7]. Semen was collected into small test tubes and evaluated for volume, motility, concentration, live sperm and abnormal sperm within 10 minutes post collection. Details of semen evaluation had been described by Udeh *et al.* [5].

**Statistical analysis:** Means, standard errors and coefficients of variation of body measurements and semen traits of cocks were calculated. Pearson correlation coefficients between body measurements and semen traits of cocks were calculated and the correlation matrix obtained. Kaiser-Meyer-Olkin (KMO) measure of sampling adequacy was used to test if the sample size was big enough for factor analysis. A KMO of 0.60 is considered adequate [8]. Bartlett's test of sphericity tested the null hypothesis that the original correlation matrix was an identity matrix, that is, no correlation between the variables. If the correlation matrix is an identity matrix, it means that factor analysis is not appropriate. If the data were appropriate, factor analysis was used to extract the factors. The extraction of the factors was done by calculating the eigen values of the correlation matrix. Sharma [6] gave the basic expression for factor analysis as follows:  $Z = \lambda f + e$  where  $Z$  is a  $p \times 1$  vector of variables,  $\lambda$  is a  $p \times m$  matrix of factor loadings,  $f$  is an  $m \times 1$  vector of factors and  $e$  is a  $p \times 1$  vector of error or residual factor. After factor extraction, variance maximizing ortho-

gonal rotation was used to alter the pattern of the factor loadings and hence improve their interpretations. Factor coefficients were used to obtain factor scores for selected factors [9]. Eigenvalues greater than 1 was used in selecting the factors for multiple regression analysis. The selected factor scores were used as independent variables for predicting semen traits of cocks. The multiple regression equation is as follows:  $ST = a + b_1FS_1 + b_2FS_2 + e$ , where  $ST$  is the predicted semen trait of cocks,  $a$  is regression constant,  $b_1$  and  $b_2$  are regression coefficients of factor scores,  $FS$  is factor score,  $e$  is error term of the regression model. The significance of each regression coefficient was tested using a t-test. The  $R^2$  values show how good the factor scores are in predicting semen traits of cocks. All the statistical analysis were done using SPSS 16 [10] statistical package.

## 3. RESULTS AND DISCUSSION

**Table 1** presents the mean, standard deviation and coefficients of variation of body measurements and semen traits of cocks used for the study. The highest variability was recorded by semen volume and the least by body weight. The coefficient of correlations between body measurements and semen traits of cocks are presented in **Table 2**. Positive and highly significant ( $P < 0.01$ ) correlations were obtained for shank length and thigh length ( $r = 0.83$ ), beak length and thigh length ( $r = 0.71$ ) and thigh length and wattle length ( $r = 0.88$ ) indicating very strong association between the variables. The correlation coefficients obtained for shank length and motility ( $r = 0.59$ ), beak length and motility ( $r = 0.70$ ), thigh length and motility ( $r = 0.67$ ) and wattle length and motility ( $r = 0.68$ ) were positive and significant ( $P < 0.05$ ) suggesting high predictability among the variables. Similarly, significant ( $P < 0.05$ ) and positive correlations were obtained for beak length and sperm concentration ( $r = 0.67$ ) and comb

**Table 1.** Descriptive statistics of body measurements and semen traits of cocks.

Traits	Mean	SD	CV
Body weight (kg)	2.93	0.10	3.41
Shank length (cm)	4.08	0.29	7.10
Beak length (cm)	1.79	0.26	14.53
Comb length (cm)	2.13	0.23	10.79
Wing length (cm)	6.08	0.51	8.39
Thigh length (cm)	4.83	0.54	11.18
Wattle length (cm)	2.09	0.45	25.14
Sperm motility (%)	61.67	7.18	11.64
Abnormal sperm (%)	42.50	4.52	10.64
Sperm conc. ( $\times 10^6/ml$ )	6.00	0.83	13.83
Live sperm (%)	50.00	7.17	14.34
Volume (ml)	0.05	0.02	40.00

SD: Standard Deviation. CV: Coefficient of variation (%).

**Table 2.** Coefficient of correlations between body measurements and semen traits of cocks.

Traits	BDW	SHL	BKL	CBL	WGL	THL	WTL	MOT	ABSP	SPC	LSP	VOL
BDW	1.00	-										
SHL	-0.11	1.00	-									
BKL	-0.06	0.56	1.00	-								
CBL	0.41	0.52	0.49	1.00	-							
WGL	0.39	0.41	0.49	0.49	1.00	-						
THL	-0.06	0.83**	0.71**	0.56	0.55	1.00	-					
WTL	-0.14	0.67*	0.57	0.50	0.47	0.88**	1.00	-				
MOT	0.17	0.59*	0.70*	0.42	0.45	0.67*	0.68*	1.00				
ABSP	-0.41	-0.17	0.10	-0.33	-0.29	-0.19	-0.17	-0.14	1.00			
SPC	0.41	0.06	0.67*	0.60*	0.46	0.24	0.26	0.51	0.12	1.00		
LSP	0.47	0.07	-0.21	0.42	0.16	-0.20	-0.26	0.06	-0.42	0.10	1.00	
VOL	-0.50	0.53	0.12	0.00	-0.24	0.12	0.07	0.17	0.41	-0.15	0.09	1.00

\*Correlation is significant at the 0.05 level (2-tailed test); \*\*Correlation is significant at the 0.01 level (2-tailed test); Note: BDW = Body weight, SHL = Shank length, BKL = Beak length, CBL = Comb length, WGL = Wing length, THL = Thigh length, WTL = Wattle length, MOT = Motility, ABSP = Abnormal sperm, SPC = Sperm concentration, LSP = Live sperm, VOL = Volume.

length and sperm concentration ( $r = 0.60$ ). A similar observation was reported by Udeh *et al.* [5]. The correlation coefficients between abnormal sperm, live sperm, and volume and body measurements were mostly negative and non significant ( $P > 0.05$ ). Kaiser-Meyer-Olkin (KMO) measure of sampling adequacy obtained from the correlation matrix was 0.68. According to Eyduran *et al.* [8], KMO measure of 0.60 is acceptable for factor analysis. Results of Bartlett's test of sphericity (chi-square = 40.05, sig = 0.007) indicate that the data set is suitable for this study.

The summary of results of factor analysis is presented in **Table 3**. The communalities are the proportion of variance that each variable has in common with other variables. Thus if the communality of a variable is high, it means the extracted factors explained a big proportion of the variables variance. The communality values ranged from 0.632 - 0.911 indicating that the data are conformable to factor analysis. Two factors with eigenvalues greater than 1 were extracted which accounted for 76.96 % of the variations present in the original variables. The first factor loaded heavily on shank length (0.863), beak length (0.781), thigh length (0.955) and wattle length (0.889) while the second factor loaded heavily on body weight (0.925). Loading is the correlation between the original variables and the factors. The higher the factors loads are the better the variables are characterized by factors [11]. The unique contribution of each variable to the factor scores is presented in the factor score coefficient matrix. The factor score coefficient matrix shows the coefficients or weights by which variables were multiplied to obtain factor scores. The factor scores were used as independent variables to predict semen traits of cocks. According to Yakubu *et al.* [12], the use of factor scores as predictor variables is more reliable than interdependent variables in order to avoid multicollinearity.

**Table 3.** Summary of the results of factor analysis.

Variables	Factor score coefficients		Rotated factor loadings and communalities		Communality
	Factor 1	Factor 2	Factor 1	Factor 2	
BDW	-0.200	0.630	-0.235	0.925	0.911
SHL	0.253	-0.083	0.863	0.057	0.747
BKL	0.216	-0.014	0.781	0.147	0.632
CBL	0.077	0.335	0.548	0.637	0.706
WGL	0.063	0.344	0.504	0.643	0.667
THL	0.270	-0.046	0.955	0.134	0.930
WTL	0.262	-0.093	0.889	0.049	0.793
Eigenvalues			3.947	1.440	
Percentage of total variance			56.392	20.568	

BDW: Body weight; SHL: Shank length; BKL: Beak length; CBL: Comb length; WGL: Wing Length; THL: Thigh length; WTL: Wattle length; Note: Communality is the proportion of variance that each variable has in common with other variables. Factor score coefficient shows the coefficient by which each variable was multiplied to obtain factor scores. Rotated factors means that each factor was linearly transformed until it defined a distinct cluster of interrelated variables.

The results of multiple regression analysis are presented in **Table 4**. The two factors had positive relationship with sperm motility. However, only factor 1 had significant ( $P < 0.05$ ) relationship with sperm motility. The combined effect of the two factors could explain only about 53.20% of the variation in sperm motility. This implies that all those body measurements namely, shank length, beak length, thigh length and wattle length that had contributed significantly to factor 1 could lead to significant increase in sperm motility. In other words, they could be used to predict sperm motility in cocks with reasonable level of accuracy. Similarly, the two factors were positive and explained 40.80% of the variation in sperm concentration. However, only factor 2 was significant implying that body weight which contributed largely to factor 2 could increase sperm concentration in

**Table 4.** Multiple regressions based on factor scores for the prediction of sperm motility and sperm concentration of cocks.

Predictors	Sperm motility				Sperm concentration			
	Coef	S.E Coef	T	P	Coef	S.E Coef	T	P
Factor 1	4.914	1.636	3.003	0.015	0.240	0.215	1.117	0.293
Factor 2	1.807	1.636	1.104	0.298	0.472	0.215	2.192	0.051

Sperm motility: Constant: 61.667,  $R^2 = 53.20\%$ , Adjusted  $R = 42.80\%$ ;  
Sperm concentration: Constant: 6.833,  $R^2 = 40.80\%$ , Adjusted  $R = 26.90\%$ .

cocks.

#### 4. CONCLUSION AND RECOMMENDATION

The relationship between body measurements and semen traits of cocks were examined using multivariate technique in order to eliminate the problem of multicollinearity among predictor variables. It was found that the factor scores derived from factor analysis of body measurements could only explain 53.20% and 40.80% of the variations in sperm motility and sperm concentration of cock's semen. Therefore, all the body measurements which contributed significantly to factor 1 and factor 2 could be used to predict sperm motility and sperm concentration of cock's semen.

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