Prediction of carcass weight using multiple regression, Bayesian networks and artificial neural networks in Nigerian indigenous chickens based on earlier expressed phenotypic traits

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ABSTRACT

The prediction potential of carcass weight (CW) in chicken is an important undertaking that can help commercial enterprises make better management decisions. The goal of this study was to examine alternative modeling approaches for predicting CW in meat-type Nigerian indigenous chickens using 19 biometric variables, as well as to discover early expressed traits that may be employed in CW breeding selection. Using multiple linear regression (MLR) and stepwise regression (SWREG), artificial neural networks (ANNs), and Bayesian networks (BN), the biometric traits of 320 chickens were modeled to predict CW. The accuracy of the models was evaluated based on their values of root mean square error (RMSE), mean square error (MSE), mean absolute error (MAE), mean absolute percentage error (MAPE), coefficient of determination (R^2), and correlation coefficient (r) between the predicted and the observed values of CW. The results showed that the MLR model was the least capable of predicting CW (MAE = 0.608, RMSE = 2.020, and MAPE = 93.244), followed by SWREG (MAE = 0.426, RMSE = 0.855, and MAPE = 77.168) compared to the ANNs and BN models. The estimated values of MAE, RMSE, and MAPE for the ANN1 model were 0.091, 0.201, and 52.891 respectively while that of ANN3 were 0.081, 0.101, and 36.765 respectively. The estimated values of MAE, RMSE, and MAPE for the MMHC model were 0.095, 0.129, and 63.551 respectively while that of RSMAX2 were 0.099, 0.132, and 66.193 respectively. Although it is possible to achieve a higher-performing SWREG model, in this study the SWREG (R^2 = 57.84%) cannot be considered an optimum model for predicting CW. Based on statistical parameters (i.e., R^2, MAE, r, and MAPE), the result of the study showed that the BN models provided a more powerful tool than the regression models and ANNs for predicting CW. The findings of this study showed that day-old chick weight, hatched weight, live weight, and body weight at 8 weeks are good predictors of CW. This could be used for management decisions in the chicken industry in the determination of CW at an earlier age of chickens.

Keywords: Body weight, stepwise, Markov blanket, selection

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INTRODUCTION

Carcass weight (CW), which is closely related to live weight, is a significant trait in meat-type poultry breeding programs. Live weight is accumulated from 6 to 10 weeks of age in broiler chickens; early management decisions such as selection cannot be based on it. As a result, predicting CW using early expressed traits as explanatory variables could be valuable in production and breeding systems to aid decision-making. If a broiler's anticipated CW potential is poor, it may be culled sooner. Selective breeding for CW in poultry broilers based on qualities expressed in the early weeks of life can result in increased live body weight, improved carcass composition, shorter production times, and significantly increased carcass dressing percentage.

Regression analysis, Bayesian networks (Bishop, 2006), and artificial neural networks (Hastie *et al*., 2009) are some of the methods that can be used to predict phenotypes. Frequentist regression approaches have been widely used in scientific studies involving a variety of livestock species and attributes for a variety of objectives, including phenotypic forecasting. Multiple regression analysis is a well-known technique for predicting a target variable conditionally on a group of covariates (explanatory variables) using least squares regression modeling (Hastie *et al*., 2009). Various subsets of the available observable covariates, as well as interaction terms between them, could be used to fit a variety of models. However, one of the difficulties with regression is determining the optimal collection of covariates, because including correlated predictors will increase the standard errors of the regression coefficients, making predictions more sensitive to model modifications (Burnham and Anderson, 2002; Adenaike *et al*., 2015). Artificial neural networks (ANNs) are nonlinear statistical modeling methods that offer a fresh option for multiple regressions. The ability to implicitly detect complicated nonlinear correlations between dependent and independent variables, the ability to detect all conceivable interactions between predictor variables, and the availability of different training procedures are all requirements for neural networks. The ANNs are based on the biological nervous system of humans and are made up of layers of interconnected neurons (linear or nonlinear computing elements; Bishop, 2006). The neural network's first layer gathers raw data, processes it, and sends the processed data to the hidden layers. The information is transferred from the concealed layer to the final layer, which generates the output. Aside from ANNs, Bayesian networks (BNs) learning methods can be utilized to study relationships between traits. The BNs are conditional independencies models that depict the joint distribution of random variables. Constraint-based and score-based algorithms are the two basic types of BNs learning algorithms. The former uses a series of conditional independence tests to discover the network of variables, whereas the later employs a score to compare the fit of many (preferably all) feasible networks to the empirical data. Hybrid learning algorithms combine constraint-based and score-based algorithms to compensate for each other's flaws and build dependable network architectures in a range of settings. The Max-Min Hill-Climbing method (MMHC) by Tsamardinos *et al*. (2006) and the Hybrid HPC (RSMAX2) by Gasse *et al*. (2014) are the two most well-known hybrid learning algorithms, both of which improve on the sparse candidate algorithm originally proposed by Friedman *et al*. (1999). Correa *et al*. (2009) provide more information on BNs, whereas Heald *et al*. (2000) work provides more information on ANNs.

The ANNs and BNs have been used for many purposes in quantitative genetics, for example, total egg production of European quails using earlier expressed phenotypic traits (Felipe *et al*., 2015) and linkage disequilibrium using single nucleotide polymorphism markers (Morota *et al*., 2012). Furthermore, many studies have investigated connections among several traits via a BN analysis incorporating quantitative trait loci and phenotypic data (Neto *et al*., 2010; Hageman *et al*., 2011; Wang and van Eeuwijk, 2014; Peñagaricano *et al*., 2015). In addition, ANNs have been applied to the prediction of egg production (Ghazanfari *et al*., 2011; Wang *et al*., 2012; Yakubu *et al*., 2018), hatchability (Bolzan *et al*., 2008), weight and number of eggs (Semsarian *et al*., 2013), growth curves (Ahmad, 2009) and nutritional requirement estimation (Mehri, 2012) in poultry.

The objective of the present study was to compare the efficiency of multiple regressions, BN, and ANNs to predict CW of Nigerian indigenous chickens using earlier measured biometric traits. As a result, we constructed ANNs and compared them with multiple regressions and BNs as well as demonstrated the superiority of BNs. As far as we know, there have been no comparisons of how well these techniques performed in the prediction of CW in chickens.

MATERIALS AND METHODS

Experimental Site and Birds

The experiment was carried out at the Poultry Breeding Unit of the Directorate of University Farm (DUFARM) of the Federal University of Agriculture Abeokuta, Ogun State, Nigeria. The University is located within latitude 7°10'N and longitude 3°2'E and lies in the south-western part of Nigeria.

The experimental birds consist of 320 Nigerian indigenous chickens generated from mating of parent stocks through artificial insemination. The chicks were brooded in deep litter in an animal farmhouse. All the chicks were wing-tagged for proper identification and subjected to the same management practices throughout the experimental period of 8 weeks. Individual hatched weight of chicks was measured immediately after the chicks were received from the hatchery while the weight of day-old chick was measured 24 hours after. Body weight, shank length, keel length, and breast girth were measured at 2 weeks intervals. At 8 weeks old, the chickens were starved overnight before slaughtering. The birds were weighed before slaughtering by severing the carotid artery and jugular vein and de-feathered before evisceration according to the method described by Hahn and Spindler (2002). All weights were measured using an electronic scale, while breast girth, shank, and keel lengths were measured using the tape rule. All the measured traits were hatched weight (HW), day-old chick weight (DOCW), body weight at 2 (BW2), 4 (BW4), 6 (BW6), and 8 (BW8) weeks old, breast girth at 2 (BG2), 4 (BG4), 6 (BG6), and 8 (BG8) weeks old, shank length at 2 (SL2), 4 (SL4), 6 (SL6), and 8 (SL8) weeks old, keel length at 2 (KL2), 4 (KL4), 6 (KL6), and 8 (KL8) weeks old, live weight before slaughtering (LW), and carcass weight (CW).

Statistical Analysis

The input data were normalized to correct variations due to differences in scales of measurements before analyses. The entire dataset was randomly divided into two subsets viz, the training set (consisting of 70% of the entire dataset) and the testing set (consisting of 30% of the entire dataset). Each statistical method used to analyze the data is explained further below:

Regression method

Standard multivariate linear regression and stepwise regression models were used to evaluate the data using R software (R Core Team, 2021).

$$y_i = \beta_0 + \beta_1X_{i1} + \beta_2X_{i2\,+}\,\beta_3X_{i3} + \ldots.. + \beta_pX_{ip} + \varepsilon_i$$

where i is the number of observations, y_i is the carcass weight, β_0 is the intercept, β_p is the slope coefficients for each dependent trait, and ε_i is the residual error term

Bayesian networks method

A Bayesian network (BN) is a graphic representation of a joint probability distribution (or joint density) which can be described by the structure of a directed acyclic graph. Factorization of the BN is a chain of products of conditional probabilities, as one node, given its parents, is conditionally independent of its non-descendants (Scutari and Denis, 2015). This is a convenient representation of the joint probability distribution, allowing for inference on the desired traits. The joint probability distribution is defined as:

$$P\,(X_1,X_2\ldots..X_p) = \prod_{i=1}^{n} (X_1\ |Pa_i)$$

where p is the number of variables, i is the counter of samples, n is the number of observations, and Pa_i is the parent of X_i

The initial step for BN was carried out to have an algorithm to learn the basic graph structure (Scutari, 2010) which followed the learning of the implicit local distributions for this given structure (Scutari *et al*., 2014).

The joint distribution can be represented as Pr (CW, HW, DOCW, LW, BW2, SL2, KL2, BG2, BW4, SL4, KL4, BG4, BW6, SL6, KL6, BG6, BW8, SL8, KL8, BG8) = Pr (HW) Pr (DOCW) Pr (BW2)

Pr (BG8) Pr (BW4|BW2) Pr (BG4|BW4) Pr (BW6|BW4) Pr (BW8|BW6) Pr (CW|BW2:BW8) Pr (KL4|CW) Pr (KL6|HW:BW4:KL4:BW8) Pr(LW|CW:KL6) Pr (KL2|BW2:KL4:KL6) Pr (SL2|HW:BW2:KL2) Pr (BG6|BW2:SL2:BW4) Pr (KL8|SL2) Pr (SL6|LW:KL6:KL8:BG8) Pr (BG2|BW2:SL6) Pr (SL8|BW2:BW6:SL6) Pr (SL4|KL2:BW4:SL8)

where Pr is the probability of the traits.

Two BNs models (MMHC and RSMAX2) were used. The choice of algorithms was based on their computational efficiency. Also, the constraint-based methods do not always provide a structure with directed edges because of the statistical equivalence of structures. The models were fitted using the package “bnlearn” (Scutari, 2010) in R software (R Core Team, 2021).

Artificial neural networks method

For ANN, backpropagation with backtracking algorithm containing one input layer with 19 nodes, with varying number of hidden layers, and one output layer with one node were fitted using “neuralnet” package in R software (R Core Team, 2021). Two neural networks were selected from the ANNs based on good generalization capacity. These were single hidden-layered artificial neural networks (ANN1); three hidden-layered artificial neural networks (ANN3). The backpropagation learning algorithm can be divided into 2 phases: propagation and weight update. Each propagation involves forward propagation of a training pattern input through the neural network to generate the output activation of the propagation, along with backpropagation of this output activation through the neural network, using the training pattern target to generate the deltas for all the output and hidden neurons. In the weight update phase, the output delta of each synaptic weight is multiplied by the input activation to obtain the gradient of the weight and bring the weight in the opposite direction to the gradient by subtracting a ratio of the gradient of the weight from the weight (Pal and Mitra, 1992).

The net input function of ANN to the jth hidden neuron is given as:

$$Y_j(x) = \sum_{i=1}^{n} w1_{ji} w_i + b1_j$$

where $w1_{ji}$ is the weight between the ith node of the input layer and the jth node of the hidden layer and $b1_j$ is the bias at the jth node of the hidden layer. The output of the jth hidden node is given as:

$$Z_j(x) = (1 + \exp^{(-y_j(x))})^{-1}$$

For an input vector x, the output, value $O_k(x)$ of the Kth node of the output layer is equal to the sum of the bias of the Kth node of the output layer and weighted outputs of the hidden nodes and is given as:

$$O_k(x) = \sum w2_{kj}\, z_j + b2_k$$

where $w2_{kj}$ is the weight between the jth node of the hidden layer and the kth node of the output layer and $b2_k$ is biasing term at the kth node of the output layer. The nodes represent the measured traits.

Predictive ability of models

The results from the BNs and ANNs were compared with that of the fitted regression models. Carcass weight estimated by the models was compared based on performance measurements. The measurement used to validate the estimation methods were: i) correlation between the predicted value and the actual value estimated, which indicates the degree in which the estimated outputs are close to the actual outputs. The predictive ability of the different models was assessed by computing the correlation (r) between the observed and the predicted CW, ii) root mean square error (RMSE), iii) mean absolute error (MAE), iv) mean absolute percentage error (MAPE), v) mean percentage error (MPE), vi) mean error (ME), vii) mean square error (MSE), and viii) coefficient of determination (R^2).

RESULTS AND DISCUSSION

The descriptive statistics of carcass weight, live weight, body weight, breast girth, keel length, and shank length of chickens in the training and testing datasets are reported in Table 1. The statistical characteristics of the training and testing datasets were highly similar. The skewness coefficients for the dependent variables of carcass weight were low. In general, Table 1 shows satisfactory statistical characteristics for the training and testing datasets in terms of mean, standard deviation, coefficient of variation, and skewness. The observed similarity in statistical characteristics of the training and testing datasets led to better performance of the models. This similarity showed that there is no change in the data distribution which is known as a data shift between the training and the testing datasets. Also, the low values of the skewness coefficient in the traits improved the performance of the models. In general, the satisfactory statistical characteristics for the training and testing datasets in terms of mean, skewness, and coefficient of variation increased the performance of the prediction models.

Table 1 Descriptive statistics of measured traits in Nigerian indigenous chickens

Traits	Training set				Testing set			
	Mean	**SD**	**CV**	**Skewness**	**Mean**	**SD**	**CV**	**Skewness**
HW (g)	35.60	3.88	10.90	10.91	35.33	3.08	8.72	8.72
DOCW (g)	34.43	3.28	9.53	8.34	34.67	3.71	10.70	10.70
BW2 (g)	235.87	17.64	7.48	10.91	242.68	13.12	5.41	5.41
BW4 (g)	524.90	49.21	9.38	11.33	516.85	55.99	10.83	10.83
BW6 (g)	838.83	62.45	7.44	28.86	823.37	67.31	8.17	8.17
BW8 (g)	1,220.06	79.36	6.50	9.62	1,208.14	88.66	7.34	7.34
BG2 (cm)	14.84	1.60	10.78	15.58	15.10	2.19	14.50	14.50
BG4 (cm)	19.95	2.17	10.88	11.77	19.02	3.40	17.88	17.88
BG6 (cm)	22.79	2.58	11.32	20.20	21.93	2.15	9.80	9.80
BG8 (cm)	24.39	2.03	8.32	12.71	25.43	2.28	8.97	8.97
SL2 (cm)	3.69	0.35	9.49	20.55	4.15	0.42	10.12	10.12
SL4 (cm)	5.04	0.41	8.13	14.70	5.25	0.57	10.86	10.86
SL6 (cm)	6.32	0.77	12.18	9.55	6.55	0.46	7.02	7.02
SL8 (cm)	8.07	1.53	18.96	20.85	8.30	1.18	14.22	14.22
KL2 (cm)	6.07	1.26	20.76	12.31	7.05	0.97	13.76	13.77
KL4 (cm)	7.80	1.31	16.79	19.04	8.27	1.51	18.26	18.26
KL6 (cm)	10.46	1.63	15.58	14.06	10.17	2.12	20.85	20.85
KL8 (cm)	14.30	1.68	11.75	10.81	15.36	1.85	12.04	12.04
LW (g)	1,190.60	167.44	14.06	16.83	1,150.16	133.45	11.60	11.60
CW (g)	1,133.22	163.53	14.43	14.43	1,050.41	176.41	16.79	16.79

Note: SD = standard deviation, CV = coefficient of variation, HW = hatched weight, DOCW = day-old chick weight, BW2 = body weight at 2 weeks old, BW4 = body weight at 4 weeks old, BW6 = body weight at 6 weeks old, BW8 = body weight at 8 weeks old, BG2 = breast girth at 2 weeks old, BG4 = breast girth at 4 weeks old, BG6 = breast girth at 6 weeks old, BG8 = breast girth at 8 weeks old, SL2 = shank length at 2 weeks old, SL4 = shank length at 4 weeks old, SL6 = shank length at 6 weeks old, SL8 = shank length at 8 weeks old, KL2 = keel length at 2 weeks old, KL4 = keel length at 4 weeks old, KL6 = keel length at 6 weeks old, KL8 = keel length at 8 weeks old, LW = live weight before slaughtering, CW = carcass weight

The evaluation criteria used to determine the quality of the carcass weight estimation methodologies used in MLR, ANN and BN models are shown in Table 2. The MLR had the highest values for ME (0.425), RMSE (2.020), MAE (0.608), MPE (55.824), MAPE (93.244), and MSE (4.082). Correlation coefficient (r) between the observed and the predicted CW values was highest in the two models of BN (0.989 in MMHC and 0.988 in RSMAX2) while the estimated r in MLR was lowest (0.157). Estimated coefficients of determination (R^2) by models from ANN and BN were above 95%. The prediction efficiency of regression-based models depends on the existence of linear relationships between input and output variables. Due to their simplicity, MLR models have been used in many studies compared to any other modeling techniques in agricultural sectors (Golkar *et al*., 2011; Ghoreishi *et al*., 2012; Huang *et al*., 2013; Abdipour *et al*., 2016; Adenaike *et al*., 2018; Basak *et al*., 2020). However, the drawbacks of SWREG, such as bias in parameter estimation and inconsistencies among model selection algorithms, are well known (Burnham and Anderson, 2002; Whittingham *et al*., 2006).

Table 2 The predictive abilities of each models used to train and test the measured traits

Parameters	MLR	SWREG	ANN1	ANN3	MMHC	RSMAX2
ME	0.425	0.178	0.074	0.014	6.87×10^{-17}	1.60×10^{-17}
RMSE	2.020	0.855	0.201	0.101	0.129	0.132
MAE	0.608	0.426	0.091	0.081	0.095	0.099
MPE	55.824	34.543	30.696	23.408	23.323	21.353
MAPE	93.244	77.168	52.891	36.765	63.551	66.193
MSE	4.082	0.731	0.040	0.010	0.017	0.017
R^2	0.355	0.578	0.945	0.986	0.977	0.976
r	0.157	0.645	0.957	0.987	0.989	0.988

Note: MLR = multiple linear regression, SWREG = stepwise regression, ANN1 = single hidden-layered artificial neural network, ANN3 = three hidden-layered artificial neural networks, MMHC = Bayesian network using Max-Min Hill-Climbing algorithm, RSMAX2 = Bayesian network using Hybrid HPC, ME = mean error, RMSE = root mean square error, MAE = mean absolute error, MPE = mean percentage error, MAPE = mean absolute percentage error, MSE = mean square error, R^2 = coefficient of determination, r = correlation coefficient

In this study, using a linear model with the stepwise procedure to predict CW did not find an optimal set of predictors. Compared to the regression procedures (MLR and SWREG), MMHC was approximately 58.1% and 34.4% respectively more accurate in prediction while RSMAX2 was approximately 58.0% and 34.3% more accurate in prediction than MLR and SWREG respectively. ANN performed better than regression models for CW prediction, probably due to the existence of nonlinear relationships among traits. This result is expected given that non-linear components and potential interactions among predictors were not considered in the linear model. The result is similar to the report of Yakubu *et al*. (2018) who worked on modeling egg production in Sasso chickens and observed higher predictive performance of ANN models over both linear and quadratic regression. The authors attributed better performance of ANN to the degree of robustness and the ability to tolerant fault compared to regression models. The predictive abilities of ANN and BN were closed. However, BNs can be used either as a pre-selection algorithm of input variables or a selection algorithm for CW prediction, unlike ANN which can only be used as a selection algorithm. The regression models were significant and specifically described the influence of the input variables on the CW. The regression models are shown below:

Equation 1 (MLR): $$CW = 0.0219 - 0.0126HW - 0.0061DOCW + 0.7473LW - 0.0673BW2 + 0.0186SL2 + 1.4027KL2 + 0.0201BG2 + 0.0346BW4 + 0.0286SL4 - 0.6236KL4 + 0.0013BG4 - 0.0215BW6 - 0.0084SL6 - 1.3275KL6 - 0.0015BG6 + 0.0352BW8 - 0.0594SL8 - 0.0019KL8 + 0.0059BG8$$

Equation 2 (SWREG): $$CW = -0.0040 - 0.0359DOCW + 0.7327LW - 0.1210BW2 + 2.7781KL2 + 0.1557SL4 - 3.7065KL6 + 0.1582SL2$$

The predicted CW value in equations 1 and 2 is a linear combination of the input variables, such that the sum of the squared deviations of the measured and predicted CW values is minimal. A formula model in equations (1 and 2) is useful in understanding how CW changes with input variables and what values of these variables are required to achieve the optimal value of CW. The SWREG algorithm retained 7 predictor variables for the CW, each of which was significant at the 5% level. In this study, ANN models were performed to identify the relationship between input and output variables aided by hidden layer nodes, which the nodes clarify the conformation of the data measured from the experiment. Figures 1 and 2 show neural networks using a single hidden layer and four hidden layers. Although different numbers of hidden layers were used in ANNs only single and four hidden layers showed better results. Each input was synaptically connected to the output node which comprises bias and the response variable (CW). The relative error (0.004) for training the network was nearly the same with that of testing (0.006). The network structures obtained, comprising 20 phenotypic traits (CW and 19 covariates) for MMHC and RSMAX2 algorithms are presented in Figures 3 and 4, respectively. For the MMHC (Figure 3), results indicate that CW is directly connected to LW, HW, and DOCW. The remaining observed traits are not expected to contribute to predicting the CW in the presence of (i.e., conditionally on) LW, HW, and DOCW. In further analysis (graphic not shown), in which LW was removed from the dataset, BW8, HW and DOCW became only traits that are directly connected to CW.

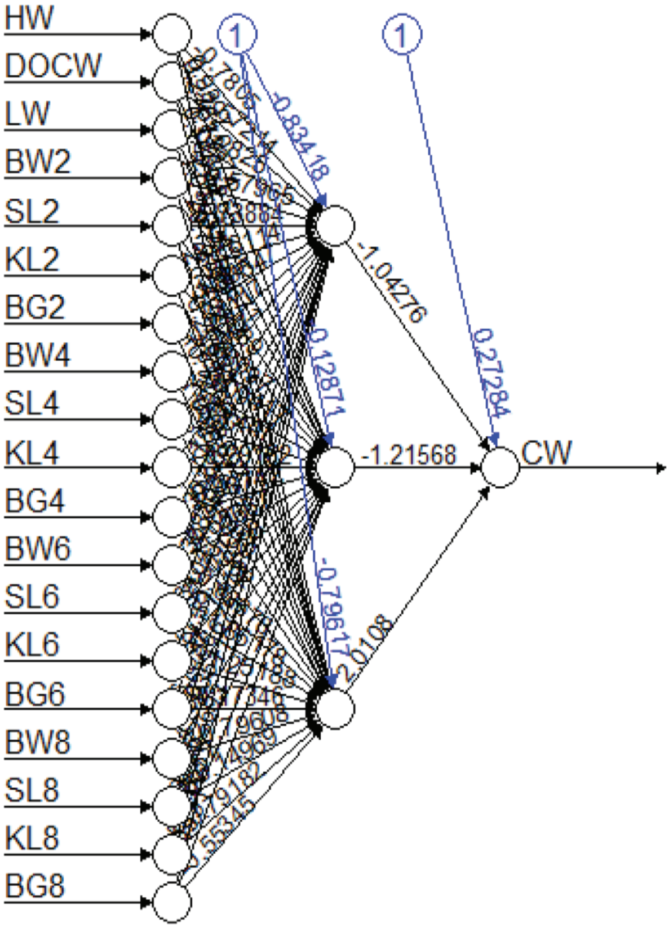

Figure 1 Schematic representation of the three hidden-layered artificial neural networks. Weighted sum of the inputs (phenotypic traits) and bias term were passed to the activation level through the transfer function to produce the output (carcass weight). CW = carcass weight, HW = hatched weight, DOCW = day-old chick weight, LW = live weight before slaughtering, BW2 = body weight at 2 weeks old, SL2 = shank length at 2 weeks old, KL2 = keel length at 2 weeks old, BG2 = breast girth at 2 weeks old, BW4 = body weight at 4 weeks old, SL4 = shank length at 4 weeks old, KL4 = keel length at 4 weeks old, BG4 = breast girth at 4 weeks old, BW6 = body weight at 6 weeks old, SL6 = shank length at 6 weeks old, KL6 = keel length at 6 weeks old, BG6 = breast girth at 6 weeks old, BW8 = body weight at 8 weeks old, SL8 = shank length at 8 weeks old, KL8 = keel length at 8 weeks old, BG8 = breast girth at 8 weeks old.

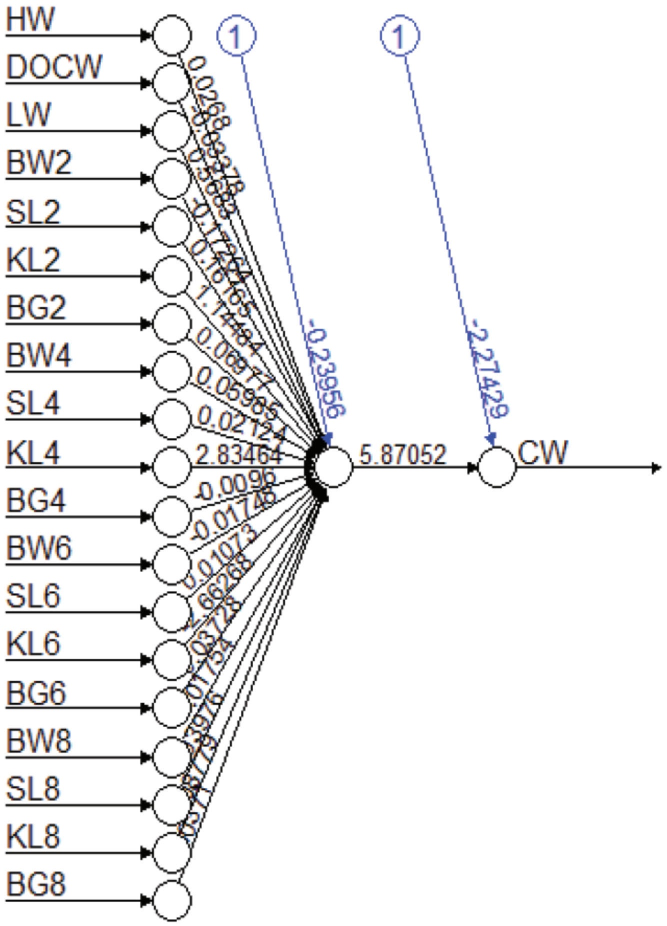

Figure 2 Schematic representation of the single hidden-layered artificial neural network. Weighted sum of the inputs (phenotypic traits) and bias term were passed to the activation level through the transfer function to produce the output (carcass weight). CW = carcass weight, HW = hatched weight, DOCW = day-old chick weight, LW = live weight before slaughtering, BW2 = body weight at 2 weeks old, SL2 = shank length at 2 weeks old, KL2 = keel length at 2 weeks old, BG2 = breast girth at 2 weeks old, BW4 = body weight at 4 weeks old, SL4 = shank length at 4 weeks old, KL4 = keel length at 4 weeks old, BG4 = breast girth at 4 weeks old, BW6 = body weight at 6 weeks old, SL6 = shank length at 6 weeks old, KL6 = keel length at 6 weeks old, BG6 = breast girth at 6 weeks old, BW8 = body weight at 8 weeks old, SL8 = shank length at 8 weeks old, KL8 = keel length at 8 weeks old, BG8 = breast girth at 8 weeks old.

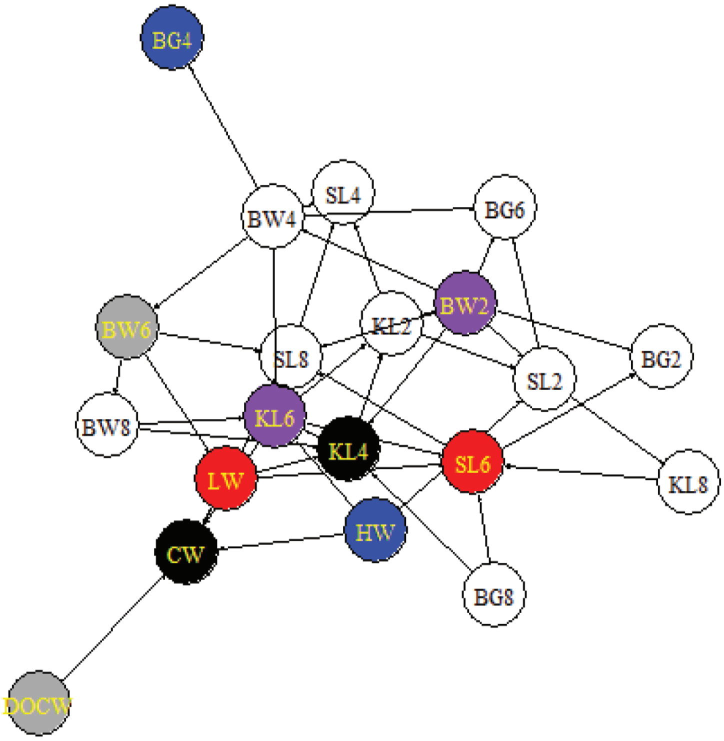

Figure 3 Schematic representation of the Bayesian network using MMHC algorithm. CW = carcass weight, HW = hatched weight, DOCW = day-old chick weight, LW = live weight before slaughtering, BW2 = body weight at 2 weeks old, SL2 = shank length at 2 weeks old, KL2 = keel length at 2 weeks old, BG2 = breast girth at 2 weeks old, BW4 = body weight at 4 weeks old, SL4 = shank length at 4 weeks old, KL4 = keel length at 4 weeks old, BG4 = breast girth at 4 weeks old, BW6 = body weight at 6 weeks old, SL6 = shank length at 6 weeks old, KL6 = keel length at 6 weeks old, BG6 = breast girth at 6 weeks old, BW8 = body weight at 8 weeks old, SL8 = shank length at 8 weeks old, KL8 = keel length at 8 weeks old, BG8 = breast girth at 8 weeks old.

For RSMAX2 (Figure 4), the directed acyclic graph (DAG) shows that CW is directly dependent on LW, BW8, HW, and DOCW. The structures learned for MMHC and RSMAX2 present a different number of directed edges, 40 edges in MMHC and 13 edges in RSMAX2. Comparison of different approaches for prediction of CW in Nigerian indigenous chickens using phenotypes expressed early in life as predictor variables was the objective of this study. BN analysis was performed to obtain a phenotypic network that was compatible with the joint distribution of the traits, and therefore make explicit the conditional independencies for this distribution. This information described which nodes (traits) comprise the Markov Blanket (a set of nodes including its parent(s), child(ren), and spouse(s)) of CW. This is important information for the prediction of CW given that the remaining nodes do not contribute to the prediction conditionally on the MB set. Also, such data-driven analysis is interesting to verify that the statistical consequences of the generated DAG were consistent with prior beliefs about the observed biological system. In both methods used under BNs, CW was independent of all other observed traits given DOCW, HW, LW, and BW8, indicating that using these traits alone to construct regression models for prediction of CW would be sufficient in Nigerian indigenous chickens. This dependence between CW and those traits (DOCW, HW, LW, and BW8) that had a direct effect on CW was expected given that the traits shared the same unit (g) with CW. This implies that if any DOCW, HW, LW, and BW8 has high heritability when estimated, it may be used to accurately predict whether a chicken has the genetic potential for carcass weight (Chomchuen *et al*., 2022). So, DOCW and HW are early good indicators of CW in Nigerian indigenous chickens. The modtableel generated from RSMAX2 is given as CW = 0.0188 – 0.0003HW – 0.0545DOCW + 0.4001LW + 0.6705BW8. A comparison of observed CW values with predicted CW values from all models is shown in Table 3. The values of CW from RSMAX2 prediction indicate the promising use of RSMAX2 in bringing these values closer to the observed CW values. Therefore, the proposed RSMAX2 equation indicates good accuracy for prediction of CW at early age of chicken.

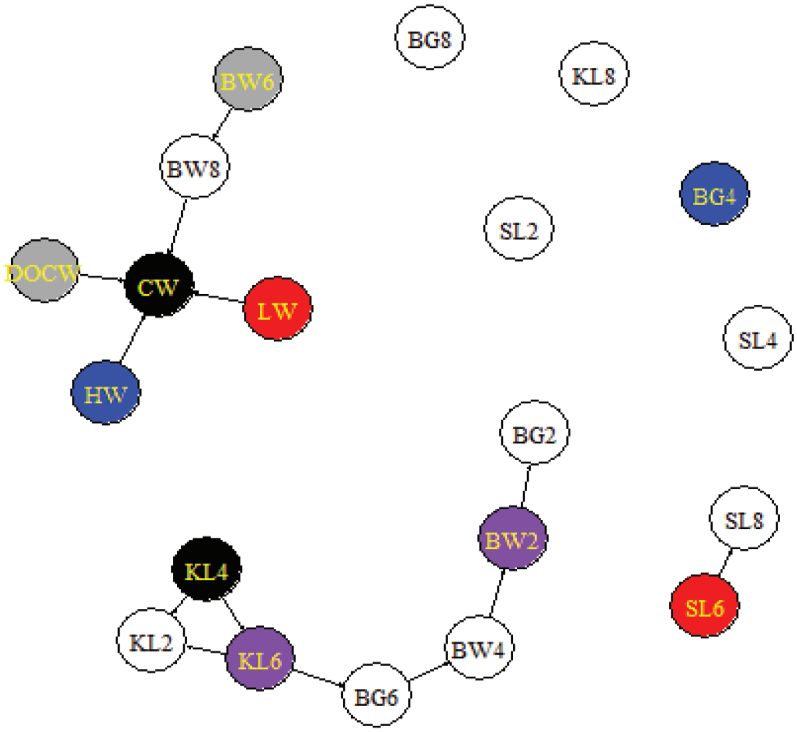

Figure 4 Schematic representation of the Bayesian network using RSMAX2 algorithm. CW = carcass weight, HW = hatched weight, DOCW = day-old chick weight, LW = live weight before slaughtering, BW2 = body weight at 2 weeks old, SL2 = shank length at 2 weeks old, KL2 = keel length at 2 weeks old, BG2 = breast girth at 2 weeks old, BW4 = body weight at 4 weeks old, SL4 = shank length at 4 weeks old, KL4 = keel length at 4 weeks old, BG4 = breast girth at 4 weeks old, BW6 = body weight at 6 weeks old, SL6 = shank length at 6 weeks old, KL6 = keel length at 6 weeks old, BG6 = breast girth at 6 weeks old, BW8 = body weight at 8 weeks old, SL8 = shank length at 8 weeks old, KL8 = keel length at 8 weeks old, BG8 = breast girth at 8 weeks old.

Table 3 Carcass weight (g) predicted from regression, artificial neural and Bayesian networks methods

Obs. CW	MLR	SWREG	ANN1	ANN3	MMHC	RSMAX2
1,102.50	1,007.54	1,060.63	1,005.56	1,044.23	1,054.54	1,060.63
1,059.90	864.82	988.28	940.53	985.95	1,009.15	1,012.85
1,214.60	1,179.03	1,171.18	1,159.24	1,209.96	1,177.01	1,180.57
1,228.80	1,213.96	1,212.26	1,296.41	1,227.36	1,219.69	1,223.41
1,106.80	948.60	1,023.49	1,022.81	1,047.71	1,052.23	1,056.11
981.10	865.71	882.49	811.86	874.27	889.87	897.40
1,183.10	1,111.83	1,162.73	1,199.48	1,156.48	1,165.52	1,170.21
1,070.60	902.05	991.65	1,013.84	1,000.40	1,030.85	1,034.99
1,288.20	1,406.71	1,279.81	1,363.55	1,306.65	1,239.01	1,242.34
1,078.40	1,116.37	1,058.66	1,081.20	1,033.20	1,077.21	1,090.78
1,131.40	1,061.66	1,083.12	1,089.45	1,088.62	1,091.51	1,096.93

Note: Obs. CW = observed carcass weight, MLR = multiple linear regression, SWREG = stepwise regression, ANN1 = single hidden-layered artificial neural network, ANN3 = three hidden-layered artificial neural networks, MMHC = Bayesian network using Max-Min Hill-Climbing algorithm, RSMAX2 = Bayesian network using Hybrid HPC

Hence, in the absence of genetic marker information for prediction of CW, management decisions should be based only on traits relative to CW because only DOCW, HW, LW, and BW8 satisfactorily predict CW. Despite the cost of generating genetic marker information is becoming cheaper, it still remains a challenge in Nigeria because of technicality and other factors (Okpeku *et al*., 2019). We were surprised that BW2, BW4, and BW6 were not part of the predictors of CW being weight traits. The higher correlation value between observed and predicted CW in BN indicates that DOCW, HW, LW, and BW8 are good predictors of CW. Such predicted CW could be used for management decisions in production systems of Nigerian indigenous chickens as broiler type of chickens for the populist.

CONCLUSION

Bayesian networks had best performance in predicting the carcass weight of Nigerian indigenous chickens, followed by artificial neural networks. Among the earlier expressed traits in the chickens, DOCW, HW, LW, and BW8 were good predictors for CW. Our results indicate that to achieve reasonable predictive ability for CW, the measurements of DOCW and HW are necessary selections to be made earlier in Nigerian indigenous chickens. We recommend BN as a good variable selection tool to describe distributions in a more parsimonious way for improving generalization being the most efficiency.

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