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Nonlinear Models for the Prediction of Yearly Live Weight of Cattle

N. Sultana[1], M.K.I. Khan[2], M.M. Momin[2]

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ABSTRACT

Background: Growth of animals is important for milk and meat production. In developing countries record keeping is difficult and usually complete recording cannot be obtained from the cattle farming. Mathematical models are used to predict values from incomplete or partially recorded data and reduces the confusion for calculating the yield. Therefore, a study was conducted to know the growth of cattle by comparing three non-linear models and predicts the mature live weight.

Methods: The live weight of cattle at 15 day intervals from 15 to 365 days was recorded and calculated the yearly live weight and weight gains of three genotypes (Red Chittagong cattle, Non-descriptive deshi and their cross) of cattle. Three nonlinear model (Brody, Gompertz and von Bertalanffy model) was fitted to weight-age data of 120 female cattle from 15 to 365 days in three locations.

Result: The average live weight and weight gain of three genotype cattle ranging from 198.5 to 207.89 kg and 306 to 361 g/day, respectively. The brody model provides better goodness of fit than other models in all genotypes and Gompertz and the von Bertalanffy model showed better matched between the observed and estimated weights.

Key words: Cattle, Fit statistics, Live weight, Models.

INTRODUCTION

As the non-descriptive (ND) deshi cattle are abundant and distributed throughout the country, however, there are some improved varitey also available in Bangladesh. The available improved variety are Red Chittagong cattle (RCC), Pabna, White Munshigong and North Bengal Gray. Among the indigenous variety, RCC are distinct due to their unique characteristics such as coat colour, body features and regularity of calving and milk yield. The indigenous cattle including the improved varieties have lower mature live weight (187 to 227 kg) compared to existing exotic breeds (for example, Holstein and Sahiwal) and their crosses (350-400 kg) (Bhuiyan *et al.,* 2007; Khan *et al.,* 2012).

Growth is important for livestock production, because growth is the foundation on which the milk, meat and work produces and it assists early selection. The most important tool of management is recording (Silver, 2006). But record keeping is challenging and most of the time complete recording cannot be obtained from the cattle farming in developing countries including Bangladesh. By using mathematical models, it is easy to estimate the productivity of cows on a farm. Using models, one can predict values from the incomplete or partially recorded data. Furthermore, it also reduces the confusion for calculating the yield, by estimating the model parameters. The mathematical models are used to predict growth of cattle of age and weight data by graphical plotting (Bathaei and Leroy, 1996). Alternatively, Souza *et al.* (2010) described the growth curve in cattle and was mainly used non-linear models.

Therefore, the study was conducted with the objectives to (i) study the growth of different cattle genotype and compare the goodness of fit of the weight-age data using the non-linear models (Brody, Gompertz and von Bertalanffy) and (ii) to compare the predicted and estimated live weight of cattle.

MATERIALS AND METHODS

Ethics and experimental period

The study was conducted under the Department of Genetics and Animal Breeding of Chattogram Veterinary and Animal Sciences University (CVASU) from January 2018 to March 2019 following the animal ethics rules and decisions of the ethics committee of CVASU (Memo no. - CVASU/Dir (RandE) EC/2020/165(8), Date 09/03/2020). During this time the field research was done in the Hathazari upazila (sub-district) of the Chattogram district of Bangladesh.

Selection, breeding and management of experimental animals

Cattle genotype (i) Red Chittagong cattle (RCC, red coat colour), (ii) non-descriptive (ND, brown coat colour) and (iii) crossbred (RCC×ND, F_1, reddish-brown) was confirmed from the records as well as with literature (Bhuiyan *et al.*, 2007).

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[1]BRAC Artificial Insemination Enterprize, Mymensingh, Bangladesh.
[2]Department of Genetics and Animal Breeding, Chattogram Veterinary and Animal Sciences University, Khulshi, Chattogram-4225, Bangladesh.

Corresponding Author: M.K.I. Khan, Department of Genetics and Animal Breeding, Chattogram Veterinary and Animal Sciences University, Khulshi, Chattogram-4225, Bangladesh.
Email: kkhan@cvasu.ac.bd

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As per the phenotypic and morphological features, the available cattle were categorized and identified them after birth and ear tagged. The farmers reared their cattle under semi-intensive system of feeding and management. The animals were grazed 4 to 5 hours a day. The pasture value of the grazing land was assumed same in all three locations, as the locations have grasses such as durba (*Cynodon* dactylon), mutha (*Cyperus rotundus*), kurmilata (*Smilax roxburghian*), regrowth paddy and road side grasses. The first basal diet was green grasses and rice straw being the second. Most of the farmers provided rice bran, oil cakes and common salt to their cattle. The experimental animals were vaccinated (against FMD and Anthrax disease) and dewormed at a regular interval.

Growth and growth curve fitting

The live weight of the 120 female cattle (RCC, ND and crossbred) was collected periodically from 15 to 365 days in the three different areas (Location 1, RCC=15, ND=16, crossbred=10), location 2, RCC=12, ND=15, crossbred=11; and location 3, RCC=14, ND=16, crossbred=11) in the farmers' households by the researchers. The similar cattle number was maintained in all age groups during the experimental period and the mortality rate was negligible. From this data, yearly live weight and weight gain of the cattle were calculated. However, the collected data was minimal (due to small number of population) for drawing a conclusion, three non-linear mathematical models were fitted to the curve shape of growth and predicted the yearly live weight of cattle.

Models for the growth curves

The growth curve models (non-linear) were used to study the growth of RCC, ND and their crossbred was as:

Gompertz (1825), $yt = Ae^{-bexp(-kt)} + \in t$

Brody (1945), $yt = A\,(1 - be^{-kt}) + \in t$

Von Bertalanffy (1957), $yt = A\,(1 - be^{-kt})^3 + \in t$

Where,
yt represents the weight of the animal at a given age (t). Parameter A is the asymptotic weight. If $t \rightarrow \infty$, b is a constant without biological interpretation. K is the maturity index. e is the natural base logarithm and εt represents the random errors.

Statistical analysis

The non-linear models (Brody, Gompertz and von Bertalanffy) were fitted to the weight-age data using PROC NLMIXED of SAS (SAS, 2012) and the parameters of the models were estimated. To compare the non-linear models using goodness of fit with actual and predicted live weight the statistical criteria, R^2 (coefficient of determination) and RootMSE (root mean square error) were used. The completely randomized design (CRD) was used to obtain the least square means for each parameter (A, b and K), the predicted 365 days live weight and for each of the fit statistic (R^2 and RootMSE). However, for live weight of different age group cattle in various genotypes in three locations, the randomized block design (RBD) was used. Mean differences were compared using least significant difference (LSD) at the 5% level of significance.

RESULTS AND DISCUSSION

Live weight of different cattle genotype

The live weight (mean±SE) of different genotype in different age under three different locations are presented in Table 1. The growth of cattle of all genotypes showed steady state and linear with the increases of age in all locations. Within the age group 15 to 90 days between the locations, significant differences were found for RCC, but for ND higher live weight was observed in location 2 than the others. From the 90 to 180 days aged cows, the live weight was higher in ND in location 1 compared to other genotypes and locations, but, the values were maximum for the same genotype (ND) from 180 to 270 days on location 2. There were no significant differences observed for the RCC in different locations from 270 to 360 days of age, but the ND showed maximum live weight in location 1 compared to others. At 365 days aged cattle the maximum live weight was obtained in crossbred in location 2 followed by location 3, compare to RCC and ND. The average live weight gain in crossbred was comparatively higher from birth to 360 days of age of RCC and ND in different locations. The average growth rate (kg/day) was comparatively lower in ND than other genotypes (Table 1). The obtained growth rate was 306 to 361 g/day, in the current study in contrary to the other findings (Bahwan *et al.* 2015; Souza *et al.* 2010) wan who obtained a higher weight gain. The fact that difference in nutrition, management practices, levels of genetic and many unknown factors affected growth rate in different cattle genotype.

Non-linear model fittings

The least-squares estimation of parameters A, b and K of three mathematical models (Brody, Gompertz and von Bertalanffy) of different cattle genotypes (RCC, ND and crossbred) with the co-efficient of determination (R^2) and root mean square error (RootMSE) values are presented in Table 2.

Model parameters

In Brody model, the parameter A was maximum in RCC compare to ND and crossbred, but in Gompertz and von Bertalanffy models, this parameter was considerably higher in crossbred than RCC and ND (Table 2). The estimate of b was higher in ND in all models. The crossbred cattle showed the lower estimates of b, in Brody and Gompertz while RCC showed higher b value in von Bertalanffy model. The maturing rate, K was higher in ND in both Brody and Gompertz model and was maximum in crossbred for the von Bertalanffy model than other cattle. For Brody model, the parameter A, asymptotic weight was maximum in RCC than ND and crossbred. In case of Gompertz and von Bertalanffy models, this parameter was higher in crossbred than other genotypes. This result may be obtained due to

Table 1: Mean±SE of live weight of different age group in various cattle genotype under all three locations.

Age group (days)	Genotype	Location			Average
		Location 1 (RCC, N=15; ND, N=16; Cross, N=10)	Location 2 (RCC, N=12; ND, N=15; Cross, N=11)	Location 3 (RCC, N=14; ND, N=16; Cross, N=11)	
15-90	RCC	76.02^{ax}±4.50	73.35^{ay}±2.93	74.53^{a} ±2.25	74.63±3.25
	ND	71.78^{abxy}±2.56	82.79^{bx}±2.56	78.50^{a}±2.12	77.79±2.41
	Cross	63.37^{by}±7.64	81.17^{ax}±3.70	73.55^{b}±3.94	72.70±5.09
90-180	RCC	118.13^{bz}±2.80	115.72^{bz}±2.51	122.80^{bz}±2.49	118.88^{y}±2.60
	ND	171.78^{abx}±2.56	134.25^{ay}±2.22	129.82^{aby}±1.98	145.28^{x}±2.25
	Cross	132.40^{ay}±6.28	141.30^{ax}±5.29	132.29^{ax}±2.22	135.33^{xy}±0.60
180-270	RCC	148.89^{ay} ±7.35	158.53^{by}±6.18	164.39^{aby}±6.64	174.76±6.72
	ND	164.33^{ax}±14.70	188.63^{ax}±7.71	177.59^{ax}±10.35	176.85±10.92
	Cross	163.85^{ax}±3.30	169.22^{by}±1.75	178.33^{bx}±2.06	170.47±2.37
270-360	RCC	186.33^{abx}±7.35	182.20±2.31	189.80^{a}±1.46	186.11±3.70
	ND	190.14^{ax}±6.47	178.22^{b} ±4.52	186.63^{a}±6.96	184.99±5.98
	Cross	172.85^{by}±3.30	180.21^{b}±1.71	193.00^{a}±2.01	182.02±2.34
365	RCC	190.83^{aby}±2.15	204.11^{bx}±5.70	200.56^{b}±4.71	198.50^{xy}±4.19
	ND	196.51^{axy}±6.36	188.73^{ay}±4.37	192.38^{a}±4.18	192.37^{y}±4.97
	Cross	209.29^{ax}±6.47	214.00^{ax}±1.12	200.39^{b}±3.93	207.89^{x}±3.84
Growth rate (kg/day)	RCC	0.306	0.349	0.336	0.330
	ND	0.331	0.283	0.304	0.306
	Cross	0.389	0.354	0.338	0.361

N.B. The mean value with different superscripts are differed at 5% level of significance among location within genotype. RCC = Red Chittagong cattle, ND = Non-descriptive deshi, presented in Table 1. (a and b) and among genotype within location (x and y); N= Number of observation.

the used of younger animals live weight data at the time of study. Similar factors were explained for fluctuation of asymptotic weight of Nelore cows for both Gompertz and von-Bertalanffy models (Forni *et al.,* 2009; Garnero *et al.,* 2005; Banik *et al.,* 2020). Using the estimates of the parameters of the non-linear models, crossbreds can be selected from the maturity rate, because, crossbred with higher maturity rates was earlier than RCC and ND, those showed lower maturity rates in Brody and von Bertalanffy models. The model parameters are very important for selecting the greater growth (Paz *et al.,* 2004). Parameters of b and K were estimated to be 2.11±0.021 and 0.522±0.004 and 0.087±0.001 and 0.127±0.002, for Gompertz and von Bertalanffy models respectively, of the Dafori cattle in Oman (Bahwan *et al.,* 2015), these findings were supported the current results.

The goodness of fit

All competing models in this study had high R^2 value, where RCC had maximum R^2 in Brody and crossbred in both Gompertz and von Bertalanffy models (Table 2). The ND cattle showed the lower RootMSE in all models (Table 2). All models showed overall good fit to the data. If a model achieves R^2 above 90% indicates close agreement with a predicted value (Khan *et al.,* 2012) whereas the lower RootMSE value indicated good fit (Gosh and Khan, 2014).

Actual and predicted weight of growing cattle

Table 2 showed the mean value of actual and predicted live weight (kg) from 15 to 365 days of age of RCC, ND and crossbred. In RCC, the predicted live weight was higher than actual in the Gompertz model than Brody and von Berttalanffy model. Though, the predicted live weight in ND was higher in Brody model, than the Gompertz model, but it was considerably lower in the von Bertalanffy model than the actual value (Table 2). All models in this study showed higher predicted live weight for crossbred. The Gompertz model showed the comparatively more value than other models. The predicted live weight in RCC and crossbred were higher than actual in Gompertz model, which matched with Brody and von Berttalanffy, these results were in harmony with Budimulyati *et al.* (2012). ND showed higher predicted live weight in the Brody model than others, this result was similar with the result of Forni *et al.* (2009).

Curve shape

The growth curves to the weight-age data of RCC, ND and crossbred were fitted using Brody, Gompertz and von Bertalanffy models and plotted in Fig 1.1 to Fig 1.3, respectively. In case of Brody model [Fig 1.1 (a to c)] showed that the live weight with the periodic data from 15 to 375 days for all genotypes was increased by the steady state except crossbred, where it was parallel. A gradual decline was observed for ND from 300 days and onwards for Brody model. These findings agreed with the findings of Garnero *et al.* (2005) and Arango and Van Vleck (2002), they described the Brody model provides the best fit for beef cattle growth curves. The Gompertz model gave a similar growth pattern for all genotypes, where there was an

Table 2: Estimated model parameters (A, b and K), fit statistics (R^2 and RootMSE) and the actual and predicted live weight of different cattle genotypes by fitting three models.

Models	Genotypes		
	RCC	ND	Crossbred
Brody			
A	329.15^{c}±1.63	272.07^{b}±2.23	191.43^{a}±1.82
b	0.71^{b}±0.0005	0.98^{c}±0.0003	0.17^{a}±0.00042
K	0.002^{a}±0.00002	0.003^{b}±0.0002	0.003^{b}±0.00002
R^2	0.99±0.001	0.97±0.001	0.97±0.001
RootMSE	46.06^{b}±1.25	24.79^{a}±2.32	82.90^{c}±2.59
Actual live weight (kg)	198.50±3.25	192.37±5.16	207.89±5.26
Predicted live weight (kg)	199.02^{b}±4.25	207.20^{b}±3.1	212.5^{a}±3.85
Gompertz			
A	159.04^{a}±10.42	139.42^{a}±11.23	190.25^{b}±7.85
b	0.09±1.21	0.29±1.02	0.13±0.92
K	-0.004±0.001	-0.004±0.001	0.003±0.002
R^2	0.97±0.0011	0.96±0.002	0.98±0.001
RootMSE	18.14^{b}±0.75	13.43^{a}±1.02	21.38^{c}±1.74
Actual live weight (kg)	198.50±3.25	192.37±5.16	207.89±5.26
Predicted live weight (kg)	206.12^{a}±6.14	196.01^{a}± 4.18	216.86^{b}±3.87
Von-Bertalanffy			
A	583.65^{b}±6.25	505^{a}±8.21	601.91^{c}±7.26
b	0.59±0.001	0.60±0.002	0.57±0.003
K	0.002±0.00002	0.002±0.00001	0.002±0.00002
R^2	0.97±0.001	0.99±0.0001	0.99±0.0001
RootMSE	16.44^{b}±1.25	6.93^{a}±3.25	16.92^{b}±1.50
Actual live weight (kg)	198.50±4.25	192.37±5.16	207.89±5.26
Predicted live weight (kg)	203.45^{b}±9.70	189.26^{a}±2.42	209.29^{b}±9.72

N.B. A= Asymptotic weight in kg, b= Integration constant, K= Maturity rate in (days)$^{-1}$, Genotype description presented in Table 1. R^2= Coefficient of determination and Root MSE= Root mean square error. The mean value with different superscripts are differed at 5% level of significance among breeds within model.

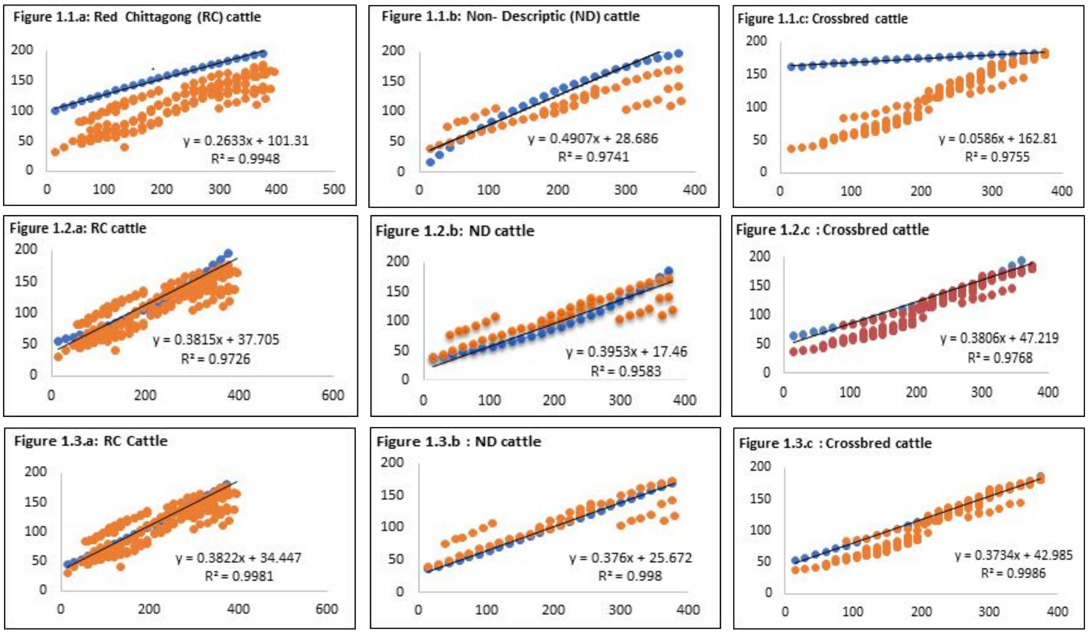

Fig 1: Shape of the growth curves (weight-age data plotted) of different cattle genotype are presented in Fig: 1.1. to 1.3 after fitting Brody, Gompertz, von Bertalanffy model. The age (days) of cattle in x axis and weight of cattle (kg) in y axis.

asymptote growth found from 100 to 300 days (Fig 1.2.a to Fig 1.2.c) and sharp increased was observed after 300 days of age. Similarly, the Gompertz model follows the progressive increases of curve shape for growing Holstein bulls (Tutkun 2019). In von Bertalanffy model, the growth curves for RCC, ND and crossbred was similar and increases steady state (Fig 1.3. a to Fig 1.3. c). The steady and lower growth curves of RCC, ND and crossbred coincide with the findings of Budimulyati *et al.* (2012), who described that von Bertalanffy attained age of puberty lower than the Gompertz and Logistic models. The growth rate of all curves was increased proportionately and the values were positive for all genotypes in all models.

CONCLUSION

In conclusion, it was seen that the live weight and weight gain from 15 to 365 days of age the crossbred showed comparatively higher values than non-descriptive deshi and Red Chittagong cattle. Among the three mathematical models, the Gompertz and von Bertalanffy model indicating a greater relationship between the observed and estimated weights of cattle. Brody model provides better goodness of fit than other models in all genotypes. This study indicated that the mathematical models can be used to predict the growth of cattle from the partially or incompletely collected data for further culling decision.

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Conflict of interest

The authors declare no conflict of interest with funding bodies and others.

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