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Evaluating genetic variability in goats considering von Bertalanffy growth curve parameters

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Abstract

An essential stage of an animal's life, growth affects the various products it produces, including milk, meat, and other foods. It is preferable to investigate animal growth statistically because it is analytically challenging to comprehend a series of weight-age data points. For the purpose of interpreting evolutionary change and developing effective breeding programmes, growth curve inheritance is essential. To investigate the growth metrics' potential utility as selection criterion, the genetic parameters are required. Four models - the Weibull, Von Bertalanffy, Gompertz and logistic models—are fitted to the body weight data of 183 goats in the current study. There were 183 kid's body weight records included, with measurements taken every three months from birth to the 12th month of age. The Von Bertalanffy model had the lowest values of AICc, χ^2 (Chi-square), MAE, and MAPE, according to these results it was best fitted model for this investigation. The growth curve parameters of A (asymptotic weight), B (folding point of growth), and K (maturity rate) had respective least-squares means of 24.44 ± 0.00 (kg), 0.479 ± 0.00 (kg), and 0.37 ± 0.00 (days).

Keywords: Growth, inheritance, selection

Introduction

Growth curve analysis is useful for selecting animals that are highly productive, determining nutritional requirements, determining an animal's weight at an appropriate age, and improving management.

Many investigations in the field of animal research to describe their growth patterns. In addition to fitting standard models like simple linear or exponential growth to size-at-age data, these research also took into account models with sigmoidal (S-shaped) growth curves, the Brody model, and negative exponential growth models. The models of von Bertalanffy, Gompertz, Richards, or Verhulst (logistic growth) are instances of the latter. Google Scholar search yielded about 22,500 and 15,500 papers about the application of the Brody model for sheep and goats, respectively. The Verhulst model came up with roughly 5500 and 3500 hits, the Gompertz model with about 4000 and 2000 hits, and the von Bertalanffy model with about 2500 and 1500 hits (Brunner and Kühleitner, (2020) [4].

Sirohi/Ajmera goats are dual-purpose animals, being reared for both milk and meat. The animals are popular for their weight gain and lactation even under poor quality rearing conditions.

The animals are resistant to major diseases and are easily adaptable to different climatic conditions Specially in hot places. Though the main breeding tracts of Sirohi/Ajmera goats are situated in the Aravalli hills of Rajasthan, they are also widely distributed in several other Indian states.

A variety of non-linear mathematical functions have been used to define the growth curve for evaluating response to a particular treatment at different times, interaction between and within populations for identifying heavier animals at an early age, and Gompertz (Laird, 1965) [7], Bertalanffy (Bertalanffy, 1957) [2], Logistic (Nelder, 1961) [9], and negative exponential (Bathaei and Leroy, 1998) [11] (Magotra *et al.*, 2021) [8].

Materials and Methods

The Sirohi goats were kept on an extensive field grazing system. Every day, the goats spent six to eight hours grazing on the pasture.

The trees, bushes, and grasses that are available for the Sirohi goat in southern Rajasthan are classified as follows: monsoon (Kair, Dhaman, Dudh, Patharchatta, Motha, Akra, and Thur), winter (Neem, Motha, Akra, Keekar, and Beri), and summer (post-harvest leftover residue of Gramme pea (Chickpea), Babul, Kair, and Khejri).

Statistical analysis

Body weights were standardized for 30, 60, 120,150, 210, 240, 300 and 330 days using the following methodology (Warwick and Legates, 1979) [17].

$$P_i = P_{near_i} + ADG (i - \text{age } P_{near_i})$$

Where P_i is the standardized weight at standard age (i),

P_{near} is the weight nearest to standard age (i), ADG is average daily gain considered among the weights after standard age (i) and before standard age (i), (i) is age to which weight is standardized, and age P_{near_i} , age to weight nearest to standard age (i) considering.

Average daily gain in the body weight of individual animal was calculated by using the following formula (Brody, 1964) [3].

$$\text{Average daily gain} = \frac{W_2 - W_1}{t_2 - t_1}$$

Where,

W_2 = Final body weight (kg); W_1 = Initial body weight (kg); t_2 = Age of the animal at the end of the period (days); t_1 = Age of the animal at the beginning of period (days)

Table 1: Different mathematical models were used to estimate growth curve parameters using Systatics 10 software

Non-linear growth curve models	Equations
Von Bertalanffy (Bertalanffy, 1957) [2]	$W_t = A \times (1 - B \times e^{-kt})^3 + \epsilon$

Where: W_t =the expected body weight (Kg) at ‘t’ time; A= is the asymptotic weight; B= the folding point of growth; K= the rate of growth; m= Shape parameter; ϵ = random error; e = the base of natural logarithm; t = time (birth to 12th month of age)

Residuals were plotted graphically which gave an accuracy of the model to fit the growth curves.

$$e = y_i - \hat{y}_i$$

Where: y_i = Observed body weight at time “t”; \hat{y}_i = Predicted body weight by regression model at time “t”.

The Mean Absolute Error (MAE), Mean Absolute Percentage Error (MAPE) was calculated as below (Topal and Balukbasi, 2008) [13].

$$MAE = \frac{\sum_i^n |y_i - \hat{y}_i|}{n}$$

$$MAPE = 1/n \sum_i^n \frac{|y_i - \hat{y}_i|}{y_i}$$

Where: y_i = Observed body weight at time “t”; \hat{y}_i = Predicted body weight by regression model at time “t”; n= Number of observations (data points).

Root of residual mean square error (RMSE) is a type of generalized standard deviation; lowest RMSE value indicates better fit when comparing models and calculated as follows.

$$RMSE = \sqrt{\frac{\sum_{i=1}^n (y_i - \hat{y}_i)^2}{n}}$$

Adjusted coefficient of determination (R_{adj}^2) was calculated using the following formula.

$$R_{adj}^2 = 1 - \left[\frac{(n - 1)}{(n - p)} \right] (1 - R^2)$$

Where: n= Number of observations (data points); p= Number of parameters in the equation; R^2 = Coefficient of determination

Akaike,s Information Criteria (AIC) were calculated as using the equation (Burnham and Anderson 2004) [5].

$$AIC = n * \ln(RSS) + 2p$$

Where: RSS= Residual sum of square

In the case the sample size is smaller than the number of model parameter ($N/K < 40$), the AIC might not be accurate then after use of Akaike, s Information Criteria (AIC_c) was appropriate and calculated as using the equation Motulsky and Christopoulos (2004) [11].

$$AIC_c = AIC + \frac{2p(p + 1)}{n - p - 1}$$

Where: AIC= Akaike’s Information Criteria

Therefore, AIC_c is a good static for comparison of models of different complexity because it adjust the residual sum of squares (RSS) for number of parameters in the model. A smaller numerical value of AIC_c indicates a better fit when comparing models.

The Chi-square (χ^2) values is used to designate the relationship between actual and predicted body weights whether there is a significant difference between the predicted and the observed body weights.

$$\chi^2 = \frac{(y_i - \hat{y}_i)^2}{\hat{y}_i}$$

Where,

y_i = Observed body weight at time “t”; \hat{y}_i = Predicted body weight by regression model at time “t”

Results and Discussion

Growth curve models were used to estimate the growth curve parameters "A," "B," and "K." R^2 , R_{2adj} , MAE, MAPE, MSE, RMSE, AICC, and Chi-square (X^2) values were used to assess the goodness of fit.

In the growth curve model, parameter (A) provided a value of 24.44 kg. This is the greatest number or amount that the system can tolerate over the long term. It can be the maximum population that an environment can support in the context of biological populations.

In the growth curve model, parameter (B) was estimated to be 0.479. The steepness of the curve is influenced by this parameter. The curve is more gradual with a lower b value and steeper with a larger b value. It frequently has to do with how fast the population is getting closer to the carrying capacity.

The growth curve model with a 0.37 value for parameter (K) was provided. This option establishes the population growth rate. Growth is accelerated with a higher k value and slowed with a lower k value.

In practical terms, these parameters are found by using statistical techniques to fit growth model to empirical data. The curve is modified to better fit the system under consideration's observed growth pattern. In ecology, biology, and other disciplines, growth model is extensively employed to simulate population dynamics and growth phenomena.

The adjusted coefficient of determination ($R_{(Adj.)}^2$) for all growth curve models was found to be 98.59 percent, indicating that the models were all fitted to the body weight of Sirohi goats. The growth curve model's modified coefficient of determination ($R_{(Adj.)}^2$) was shown as the best fit.

The best fit growth curve model yielded an estimate of the mean absolute error (MAE). The values of the Bertalanffy 0.53 growth curve model's mean absolute error (MAE).

The growth curve model with a 0.053 error rate yielded the greatest mean absolute percentage error (MAPE) estimates.

The highest values of root mean square errors (RMSE), 0.177, were given to the growth curve model. It's crucial to remember that RMSE and the dependent variable have the same unit, which facilitates interpretation in the context of the current issue. Nevertheless, depending on the particular objectives and features of the modelling assignment, RMSE might not be the only statistic to take into account. It should be used in conjunction with other evaluation metrics.

The growth curve model using 1.17 provided the corrected Akaike information criteria (AICC) values. In non-linear growth curve models, the X^2 (Chi-square) values between the expected and observed body weights were non-significant ($p \geq 0.01$), suggesting that the predicted and observed body weights were not different in Sirohi goats.

In present investigation, the Brody was found to be the best fit for explaining growth pattern followed by von-Bertalanffy, Gompertz and Logistic growth curve models in order of goodness of fit statistics for body weight of Sirohi goat. Similar findings were obtained by Tsukahara *et al.*, (2008)^[14] in Kambing Katjang goat, Tatar *et al.*, (2009)^[13] in Young hair goat, Waheed *et al.*, (2011)^[15] in Beetal goat, Pires *et al.*, (2017)^[10] in Repartida goat,

Conclusion

The study identified several factors that contribute to variation in growth curve model parameters, including but not limited to flock size, species, breed, selection techniques, environmental and managerial conditions, farmer socioeconomic position, differences in growth curve models, and nutritional traits of breeds and species.

Declarations of Competing Interest

The authors declare that they have no conflicts of interest associated with this publication.

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