



Genetic Variability of Growth Curve Parameters in Goats: Application of Bootstrap Techniques

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SUMMARY

Growth is an important phase in the life of animals which influences the different forms of production such as milk, meat etc. Since a series of weight-age data points are analytically difficult to interpret, it is desirable to study the growth of animals statistically. Inheritance of growth curves is critical for understanding evolutionary change and formulating efficient breeding plans. The genetic parameters are necessary to examine the potential usefulness of the growth parameters as selection criteria. In the present study, four models namely Logistic, Von bertallanffy, Gompertz and Weibull models are fitted to the body weight data of the goats of 142 animals. The Von bertalanffy model comes out to be the best model for the data under consideration. To this end, the statistical properties of the growth curve parameters are discussed by using bootstrap techniques and the distributions of these genetic parameters are found to be non-normal. The genetic correlation between the mature weight and maturity rate is found to be moderately negative correlated which indicates the selection of animals having higher maturity rate could lead to lighter mature weight. The heritability of mature weight is found to be highly heritable indicating the mature weight can be used for selection purposes.

Keywords: Growth curve parameters, Heritability, Genetic correlation, Bootstrap techniques.

1. INTRODUCTION

Growth is defined as the increase in body size per unit time and is the combination of hereditary and environmental effects. The relationship between body weight and age is important particularly in meat producing animal such as beef, cattle, goat, pig, sheep etc. Growth studies are generally done by fitting growth models which summarize information needed to understand the biological phenomenon of growth. Since a series of weight-age data points are analytically difficult to interpret, it is, therefore, desirable to study statistically the growth of animals. Statistical analysis of data on growth of animals involves choosing a suitable growth curve/model and proper method of pooling the results over the group of experiments. The improvement in most of the characters of economic importance in both plant and animals can be achieved by formulating efficient selection strategies. The formulation of sound selection program is only possible when

complete information about the genetic properties of the population as well as character is known. The response to selection and the consequent genetic advance depends on the intensity of selection, magnitude of genetic variability among the individuals in the initial populations and accuracy of the selection. A quantitative measure of genetic variability is provided by the genetic parameter 'heritability'. Heritability expresses the reliability of the phenotypic values as guide to the breeding value. Further heritability is not only the property of the character but also of the population. The improvement of a character in any population cannot be done in isolation because it also changes other correlated traits of the population following selection in the main traits. It is, therefore very important to have the knowledge of genetic correlation among traits. It is also useful in obtaining simultaneous improvement in two or more than two characters at a time by constructing a suitable selection index.

Brown *et al.* (1976) fitted some non-linear growth models to female cattle. There was consistent negative genetic correlation between mature weight and maturity rate. DeNise (1982) has observed negative genetic correlation as -0.57 between maturing size and maturing rate. Kachman *et al.* (1988), in their study, found that age at point of inflection was moderately correlated with the body weight at second and third weeks of age and not correlated with mature body weight. Gwaze *et al.* (2002) estimated the genetic parameters of the growth curve parameters for *Pinus taeda*. They found negative correlation between the asymptote and the rate parameter which shows that trees with the smaller asymptotes reach maximum height earlier. Wahi *et al.* (2004) studied the growth pattern in crosses and pure Indian breeds of goats. Gompertz model was found to be best model to describe the growth pattern in goat. Logistic non-linear growth model was fitted to estimate the genetic parameters of the growth curve variables Lambe *et al.* (2006) compared the use various models to describe the growth in lambs of 2 contrasting breeds from birth to slaughter and also found out the genetic parameters of the growth curve parameters. Kor *et al.* (2006) aimed to determine the growth of 26 Akkeci (white goat) female kids by using different nonlinear growth models.

In the recent past more robust methods based on resampling techniques have emerged. The most common of these methods are the Jackknife (Efron 1979) and Bootstrap method (Efron 1982). Aastveit (1990) has also applied the Bootstrap technique to obtain the confidence intervals of genetic components of variance and covariance in plant breeding data. Jayasankar (1992, 1996) used the Bootstrap technique for estimation of heritability and for studying the distributional properties of heritability. Singh and Wahi (2003) obtained the optimum family size and structure for estimating the standard error of heritability in half-sib model. Singh *et al.* (2006) studied the robustness of bootstrap estimates of variance of heritability to master samples by drawing independent master samples in half-sib model. Singh *et al.* (2015) investigated the growth pattern of cattle under different error structures. However, a series of body weight–age data points is analytically

difficult to interpret. So it is necessary to condense the information contained in such a data series into a few biologically interpretable parameters of non-linear growth models. Moreover, if any evidence is found regarding the association of parameters of non-linear growth models with the economically important trait like milk yield, body weight at slaughtering age, nutrition status in the milk or meat in either direction, we can employ this knowledge in indirect selection for improving the economically important trait through directly selecting the animals on the basis of that associated parameters. So, in our present study the emphasis is given on the study of the genetic parameters of the growth curve parameters through Bootstrap technique.

2. MATERIALS AND METHOD

In this section, a brief description of data used, description of models, criteria of model selection for the present study has been illustrated. Followed by, the methodology to study the properties of genetic parameters using Bootstrap technique is given.

2.1 Data Description

The body weight data of 142 goats from goat farm of C.I.R.G., Makhdoom, Uttar Pradesh for the year 2005 has been considered for the study. The body weight data (in Kilogram) is available at 12 different point of time i.e. for 12 months. Here, in our study, four nonlinear growth models were considered. They are as follows:

i. **Logistic model:**

$$W(t) = \frac{a}{1 + be^{-ct}} + e$$

ii. **Gompertz model:**

$$W(t) = a \exp(-b \exp(-ct))$$

iii. **Von-Bertalanffy model:**

$$W(t) = a[1 - b \exp(-ct)]^3$$

iv. **Weibull model:**

$$W(t) = a - (a - b) \exp[-(ct)^d]$$

where, $W(t)$ = Body weight at age t , b = constant coefficient, c = maturity rate, a = mature weight, d = additional parameter.

The estimation of parameters was carried out using SAS 9.1 package.

2.3 Criteria of Model Selection

Following criteria have been used for selecting the best model.

- (i) The lowest RMSE (Root Mean Squared Error)
- (ii) The highest determination coefficient R^2 (%)
- (iii) Absolute Reduction Ratio (ARR %) (Eyduran 2008)

2.4 Estimation of Genetic Parameters

2.4.1 Half Sib Model

Let each of a set of s sires is mated to several dams, selected at random and each mating produces a single progeny.

Then the half sib model will be

$$Y_{ij} = \mu + s_i + e_{ij}$$

where μ is the common mean, s_i is the effect of the i^{th} sire and e_{ij} is the uncontrolled environmental and genetic deviations attributable to individuals within sire groups. All effects are assumed random and independent with expectations equal to zero and variances

$$E(s_i^2) = \sigma_s^2 \text{ and } E(e_{ij}^2) = \sigma_e^2$$

2.4.2 Heritability

In narrow sense, it expresses the proportion of total phenotypic variance which can be attributed to the average genic affect (Average effect of gene) controlling the character (Jain 1992).

$$\text{Mathematically, } h^2 = \frac{\sigma_A^2}{\sigma_P^2}$$

where, σ_A^2 = Additive genotypic variance, σ_P^2 = Phenotypic variance.

An analysis of variance is then made by which the phenotypic variance is partitioned into

observational components i.e. the between-sire and within-sire components.

The next step is to estimate σ_s^2 (sire variance component) and σ_e^2 (error variance component) by equating expected mean squares with corresponding observational components. Therefore, the estimate of heritability can be obtained as

$$\hat{h}^2 = \frac{4\hat{\sigma}_s^2}{\hat{\sigma}_s^2 + \hat{\sigma}_e^2}$$

Approximate sampling variance of the heritability estimate (as given by Falconer 1996)

$$\text{is } \hat{\sigma}_{h^2}^2 = 32 \frac{\hat{h}^2}{T} \text{ (Half sib).}$$

where, $T = nN$, n and N being the number of individuals per family and number of families respectively.

3. GENETIC CORRELATION

It is the correlation between the additive genetic factors of two characters. The estimate of Genetic correlation between two characters X and Y is

$$\hat{r}_A = \frac{\hat{\sigma}_{sxy}}{\sqrt{\hat{\sigma}_{sx}^2 \hat{\sigma}_{sy}^2}}$$

In the present study the Bootstrap technique (Efron 1979) has been used to estimate standard errors of genetic parameters (heritability and genetic correlation) of the growth curve parameters.

3.1 Estimation of Variance and Covariance Components

Estimates of variance and covariance components were obtained using maximum likelihood estimation method and restricted maximum likelihood method as the data considered under study was unbalanced. The estimation procedures are not discussed here because statistical packages like SAS, SPSS provide the facility of computing variance components using all the four methods. For estimating covariance component, we employ the method given by Kempthorne (1982). Suppose we have two observations, y and

z , on each individual instead of only one. We can obviously consider the compound observation $y + z$ for each individual and make the same analysis of variance for this compound observation as for each basic observation y and z . Exactly the same formulae will hold for the expectations of mean squares, the components of variance being those for $y + z$ rather than for y and z . Also we know that

$$V(y + z) = V(y) + V(z) + 2 \text{Cov}(y, z)$$

So we can write

$$\sigma_{h(y+z)}^2 = \sigma_{hy}^2 + \sigma_{hz}^2 + 2\sigma_{hyz}$$

where

$\sigma_{h(y+z)}^2$ is the component of variance for $y + z$ attributable to the source of variation h .

σ_{hy}^2 is the component of variance for y attributable to the source of variation h .

σ_{hz}^2 is the component of variance for z attributable to the source of variation h .

σ_{hyz} is the component of variance for y and z attributable to the source of variation h .

Now, the estimate of σ_{hyz} will be obtained as

$$\sigma_{hyz} = \frac{1}{2} \left(\sigma_{h(y+z)}^2 - \sigma_{hy}^2 - \sigma_{hz}^2 \right)$$

3.2 Monte Carlo Algorithm to Obtain the Bootstrap Estimates of Genetic Parameters

There are number of ways in which the bootstrap samples can be obtained in order to obtain the bootstrap estimates of the parameters, variance, standard error and confidence intervals. In the present investigation, sampling procedure

is based on the resampling from levels of the sires family directly from the data. In case of half sib family model, sires were resampled based on the resampling directly from the master sample. The bootstrap algorithm used can be described as follow:

Divide the whole data material into K classes corresponding to the sire families. Let \hat{F} 's stand for multivariate empirical distribution where each family has mass $1/K$

Draw a random sample with replacement of K classes from \hat{F} 's

Then select all the progenies in the sire family or choose the progenies randomly with replacement from the progenies in that family fixed size p .

Analyze the data according to the model under study.

Estimate the parameters r_g and h^2 as desired.

Go back to 2 and draw a fresh sample from the data and the same procedure is repeated N times such that we get N estimates of r_g and h^2 .

4. RESULTS AND DISCUSSION

4.1 Model Selection

The four models namely Logistic, Von bertallanffy, Gompertz and Weibull models are fitted to the body weight data of the goats of 142 animals. Weibull model does not fit the data well. So this model is not considered for this study. The other models like Gompertz, Logistic and Von bertalanffy models have no much problem in fitting the given set of data. The parameter estimates of the fitted models along with their standard errors are reported in Table 1. To study the statistical properties of the criteria of goodness of fit like R^2 , RMSE and absolute reduction ratio (ARR) empirically, bootstrap technique is used.

Table 1. Parameter estimates of the fitted models

Parameter	Logistic		Gompertz		Von Bertallanffy	
	Estimate	Std Error	Estimate	Std Error	Estimate	Std Error
Alpha	32.5393	6.3961	42.9655	14.1101	37.622	6.1991
Beta	3.7563	0.7149	1.8836	0.2706	2.0996	0.2572
Gamma	0.1716	0.0320	0.0862	0.0274	0.1258	0.0457

For this, 1000 Bootstrap samples are created from the master sample (110 animals i.e. no. of animals that fit data well in three models) by using sampling with replacement where selection is done on the progenies level. All the three models viz Gompertz, Logistic and Von Bertalanffy are fitted to the body weight data of all animals of each bootstrap samples. For each animal, its growth parameters along with criteria of model selection viz R^2 , RMSE and absolute reduction ratio (ARR) are estimated. Then, for a Bootstrap sample of size 110, R^2 , RMSE and ARR have been obtained. The overall mean of these respective criteria i.e. average of all 1000 average values of each criteria and their standard deviations have been found out for each models mentioned above. The bootstrapped samples results as well as the results of master sample are tabulated in Table 2. From Table 2, it is noticed that the bootstrap estimate

values have less standard error as compared to master sample.

According to value of R^2 , all the models fit the data well i.e. the value of R^2 exceeds 99% but standard deviation of Von- bertalanffy model has lower than the other models. Von-bertalanffy model has also smaller estimates values of ARR and RMSE than other models and it has also lower standard deviations of ARR and RMSE than that of others model. So Von bertalanffy model has been found to be the best fitted model to the goat growth data.

Again in changing the Bootstrap samples size to 200, 500, still Von-bertalanffy model has lower values RMSE, ARR and higher value of R^2 and it has also lower standard deviations (Table 3-4). So it has been concluded that size of the Bootstrap samples doesn't affect the criteria of model selection to describe the growth pattern.

Table 2. Goodness of fit criteria along with their standard deviation based on 1000 bootstrap samples and estimate of master sample with S.D.

	R²(m)	RMSE(m)	ARR(m)	R² (SD)	RMSE(SD)	ARR(SD)
Master Sample						
Logistic	0.9866	0.832	45.515	0.000159	0.036	3.456
Von bertalanffy	0.9897	0.776	31.14	0.000155	0.027	3.296
Gompertz	0.9896	0.793	35.987	0.000212	0.036	3.367
Bootstrap Samples						
Logistic	0.9976	0.853	47.502	0.00013	0.026	3.298
Von bertalanffy	0.9979	0.785	32.234	0.00012	0.025	3.258
Gompertz	0.9979	0.801	36.977	0.00012	0.025	3.280

Table 3. Goodness of fit criteria along with their standard deviation based on the 200 bootstrap samples

	R²(m)	RMSE(m)	ARR(m)	R²(SD)	RMSE (SD)	ARR (SD)
Logistic	0.9976	0.854	47.067	0.0001	0.027	3.091
Von bertalanffy	0.9979	0.787	31.846	0.0001	0.026	2.996
Gompertz	0.9979	0.802	36.541	0.0001	0.026	3.041

Table 4. Goodness of fit criteria along with their standard deviation based on the 500 bootstrap samples and estimate of master sample with S.D

	R²(m)	RMSE(m)	ARR(m)	R²(SD)	RMSE(SD)	ARR (SD)
Master Sample						
Logistic	0.986	0.832	45.515	0.00015	0.036	3.456
Von bertalanffy	0.989	0.776	31.14	0.00015	0.027	3.296
Gompertz	0.989	0.793	35.987	0.00021	0.036	3.367
Bootstrap Sample						
Logistic	0.997	0.855	47.515	0.00013	0.026	3.258
Von bertalanffy	0.997	0.787	32.206	0.00013	0.026	3.183
Gompertz	0.997	0.803	36.932	0.00013	0.026	3.257

4.1.1 Estimation of genetic parameters of the growth curve parameters and their standard errors

As per the methodology described in the above, data was generated using Bootstrap sampling method to study the statistical properties of heritability and genetic correlation of the growth curve parameters by half sib method.

5. ESTIMATION OF HERITABILITY

To find the bootstrap estimates of the heritability of the growth curve parameters, first selection of samples are done on the sire level in 21 sires with replacement from the master sample considering all the progenies of each sire for inclusion in the selected sample. The total number of half sib animals is 82. The body weights of all the progenies of the selected sires of each bootstrap samples are, then, fitted to the Von bertalanffy model as this model comes out to be the best model to describe the growth pattern. The estimation of heritability of the growth curve parameters is done by ANOVA method. The master sample is also analyzed to obtain the estimates of the heritability of the growth parameters along with their standard errors (Table 5). The distribution of the bootstrap estimates of the heritability based on the 200 sample size is tested by obtaining the value of coefficient of skewness and kurtosis. It was found that the distribution of heritability estimates of three growth curve parameters was not normal. The distributions of the heritability of three growth parameters are also found to be skewed. The bias in the bootstrap estimates varied for the three parameters and bias was positive, that

means the bootstrap estimates of the parameters have higher value than that of the estimates of the master sample. It can be seen from the result that the usual estimates of the standard error of the heritability was lower than the corresponding bootstrap estimates except parameter *b* which has lower standard error of heritability estimate in bootstrapping than usual estimate of standard error. The reason for higher standard error of bootstrap estimate may be due to sampling fluctuation i.e. small number of animals.

The heritability estimates of the three growth parameters *a* (asymptotic body weight), *b* (constant) which is related to the initial body weight and *c* (maturity rate) are high to moderate (Table 5). High heritability value of asymptotic body weight has been found. Same result is also found in the literature (Northcutt and Wilson 1993). So the selection based on this characteristic should be effective and this parameter asymptotic body weight can be genetically altered through selection. The parameter *b* has also high heritability, so it can be used in the selection purpose to change the initial body weight because this parameter is related to initial body weight of the animal.

5.1 Estimation of Genetic Correlations

The estimates of genetic correlations among the growth curve parameters found from the fitting of the Von bertalanffy model based on the 200 bootstrap samples are given in the Table 6. The master sample from which the bootstrap samples are selected with replacement

Table 5. Heritability estimates of growth curve parameters and their statistical measures based on master sample as well as on 200 bootstrap samples

	Heritability (<i>a</i>)	Heritability (<i>b</i>)	Heritability (<i>c</i>)
Master Sample			
Estimate	0.957	0.774	0.429
Standard error	0.491	0.481	0.450
Bootstrap Sample			
Mean	0.977	0.834	0.636
Std error	0.526	0.315	0.561
Median	1.090	0.968	0.705
Skewness	0.709	0.633	1.108
Variance	0.277	0.099	0.315
Kurtosis	-0.070	0.396	2.128

Table 6. Estimates of genetic correlations among growth curve parameters and their statistical measures based on master sample as well as on 200 bootstrap samples

	Genetic Corr(<i>ab</i>)	Genetic Corr(<i>ac</i>)	Genetic Corr(<i>bc</i>)
Master Sample			
Estimate	0.921	-0.318	-0.154
Standard error	0.059	0.461	0.557
Bootstrap Sample			
Mean	0.888	-0.313	-0.065
Standard error	0.095	0.546	0.491
Median	0.901	-0.444	-0.084
Skewness	-2.008	1.861	0.530
Variance	0.009	0.298	0.241
Kurtosis	7.192	5.333	1.773

is also analyzed to obtain the estimates of the genetic correlations among the growth curve parameters and reported in Table 6. This gave the information about the deviation of bootstrap estimates of the genetic correlations between the parameters from the estimates obtained from the master sample. The mean bootstrap estimate of the correlation between the parameters *a* and *b* are almost equal to its median. The coefficient of the skewness is -2.0085, which shows the curve is negatively skewed and its coefficient of kurtosis is 7.1926 i.e. curve is leptokurtic. So it was found that the distribution of this genetic correlation was non-normal. The bootstrap estimate value is lower than that of the master sample showing that the negative bias and it has higher value of bootstrap standard error than usual estimate of the standard error. This is perhaps due to the approximations involved in the derivation of formula for the standard error and due to small sample size.

The bootstrap estimate of genetic correlation between parameter *a* and *c* is found to be nearer to the median value. The values of coefficient of skewness and kurtosis indicate the non-normal distribution. The bootstrap estimate has lower value than that of master sample i.e. negative bias. Similarly the genetic correlation between *b* and *c* has bootstrap estimate almost equal to its median value. The value of coefficient of skewness and kurtosis shows the non-normal nature of the distribution. The genetic correlation between the asymptotic body weight and maturity rate has moderately negative correlation as -0.3185. This indicates that the selection of faster or higher maturity rate could lead to the lighter mature weight. Negative genetic

correlation coefficients between maturity rate and mature weight were also found in the literature (Brown *et al.* 1972). The genetic correlation between the parameter *a* and *b* has high value 0.9212. The negative correlation between the parameter *b* (related to initial weight) and *c* (mature weight) indicates that selection of higher maturity rate could result the lower birth weight.

6. CONCLUSION

Knowledge of the heritability of growth curve parameters and genetic correlation between growth curve parameters helps in selecting best individual at early stage. It will also save time as well as money by discarding the non-performing animals. It will help the breeder to select the best individual at early stage for breeding purpose. In general, the master sample provides better results. Whereas, in case of small sample size, one can go for bootstrap method for precise estimation of heritability and genetic correlation and their standard errors. Biased nature of the bootstrapped samples is clearly visualized from the above tables. It can be concluded that as sample size increases, the parameter estimates of the bootstrapped samples are closed to that of the master sample i.e. reducing the bias.

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