

## GENETIC AND PHENOTYPIC RELATIONSHIP BETWEEN BIRTH WEIGHT AND WEANING WEIGHT IN TEDDY GOAT

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The phenotypic, genotypic and environmental correlations between birth weight and weaning weight were 0.08, 0.212 and 0.49, respectively. The positive and significant phenotypic correlation indicates that higher birth weights are associated with higher weaning weight. The moderate and significant genetic correlation indicates that genes responsible for higher birth weight were also helpful in increasing weaning weight. The low and non-significant environmental correlation suggests that environment affecting birth weight will not affect weaning weight.

### INTRODUCTION

The goat population of world is about 526.40 million (Anonymous, 1990) out of which 36.8 million heads belonging to 29 well-defined breeds are reared in Pakistan. The ruminant has the widest ecological range of all the domestic animals.

There is an acute shortage of animal protein and this gap is increasing day by day due to education and increasing human population. Keeping in view the higher biological value of the food items (meat and milk) and its greater rate of reproduction with better fertility and prolificacy along with smaller generation interval, goat can play very important role in fulfilling the deficiency of animal protein. In spite of its significant role in fulfilling the meat shortage, no systematic work has been undertaken to study the relationship between various traits of economic importance. So, this study was planned to study the genetic and phenotypic relationship between birth weight and weaning weight. This information will be of primary importance in future selection and breeding programs for improvement of this breed.

### MATERIALS AND METHODS

Data consisting of 777 pedigree and performance records of 30 sires of Teddy goat recorded at Livestock Experiment Station, Bahadurnagar, Okara during 1975-90 were used in this study. The feeding and managerial practices during the study period remained in general more or less the same. Breeding of does was practiced throughout the year. The bucks were selected on the bases of their phenotype and pedigree whereas no proper attention was given for the selection of breeding females. After parturition, birth weight of kids was recorded before they were allowed to suckle their dams. All prophylactic measures against contagious, ecto- and endoparasitic diseases were taken. The weaning age varied between 60-152 and the kids having less than 60 days weaning age were not included in this study. The data on the following parameters were recorded:

1. Date of birth
2. Birth weight
3. Birth type
4. Sex of kid
5. Date of weaning
6. Weaning weight

Due to genetic and environmental factors, the early growth rate will be correlated with growth in subsequent period. When the genes responsible for subsequent growth cause most of the hereditary variation, they will contribute to the correlation between birth and weaning weight.

The phenotypic observation  $X_i$  having the following model under assumption that genotype (G) and environment (E) are independent:

$$X_i = G_i + E_i$$

Its variance will be:

$$V(X_i) = V(G) + V(E_i)$$

and covariance between birth weight (X1) and weaning weight (X2) will be:

$$COV(X_1, X_2) = COV(GX_1, GX_2) + COV(E_1, E_2)$$

The first step in the estimation of correlations is to calculate components of variance and covariance, the model adopted is given in Table 1.

Table 1. Model of analysis of variance for working out the components of variance and covariance

Source of variation	df	E.M.S. (XIXI)	Expected mean cross product (XI x X2)	E.M.S. (X2X2)
Between sires progeny	S-1	$a^2w(XI) + Ka^2s(XI)$	$a^2w(XIX2) + Ka^2s(XIX2)$	$a^2w(X2) + Ka^2s(X2)$
Within sires	N-S	$a^2w(XI)$	$a^2s(XIX2)$	$a^2w(X2)$
Total	N-1			

where

- N = Total number of observations
- S = Total number of sires
- K = Average number of progeny per sire

Because of unequal number of progeny per sire, the K was worked out as under:

$$K = \frac{1}{S-1} \left[ N - \frac{1}{N} \right]$$

where

- S = Number of sires
- N = Total number of observations used in the study
- $\Sigma$  = Greek symbol of denoting "sum of"
- n<sub>j</sub> = Number of observations of the i<sup>th</sup> sire

Two causative forces of genetic and environmental origin are responsible for observed relationship among different traits.

The phenotypic, genetic and environmental correlations between birth weight (X1) and weaning weight (X2) were worked out as under:

Phenotypic correlation

$$r_{P_{12}} = \frac{a'w_{P_{12}} + 0.5 a'w_{P_{11}}}{\sqrt{(a'w_{P_{11}} + 0.5 a'w_{P_{12}} + 0.5 a'w_{P_{21}} + a'w_{P_{22}}) (a'w_{P_{11}} + 0.5 a'w_{P_{12}} + 0.5 a'w_{P_{21}} + a'w_{P_{22}})}}$$

Genetic correlation

$$r_{G_{12}} = \frac{a'S_{12}}{\sqrt{(a'S_{11} + 0.5 a'S_{12} + 0.5 a'S_{21} + a'S_{22}) (a'S_{11} + 0.5 a'S_{12} + 0.5 a'S_{21} + a'S_{22})}}$$

Environmental correlation

$$r_{E_{12}} = \frac{c/w_{12}}{\sqrt{(a'w_{11} + 0.5 a'w_{12} + 0.5 a'w_{21} + a'w_{22}) (a'w_{11} + 0.5 a'w_{12} + 0.5 a'w_{21} + a'w_{22})}}$$

### RESULTS AND DISCUSSION

The estimated mean birth weight and weaning weight of 777 kids was  $1.67 \pm 0.31$  lmd  $8.50 \pm 2.18$  kg, respectively. The correlations between the two traits along with variance and covariance components of between and within sires are given in Table 2.

Table 2. Analysis of variance components of variance and covariance for the estimation of phenotypic, genotypic and environmental correlations

Source of variation	Degree of freedom	Mean squares birth weight (X <sub>1</sub> , X <sub>1</sub> )	Mean squares weaning weight (X <sub>2</sub> , X <sub>2</sub> )	Mean cross products (X <sub>1</sub> , X <sub>2</sub> )
Between sires	29	0.2458	5.1360	0.1480
Within sires	747	0.0769	3.5508	0.0384

Phenotypic correlation: The phenotypic correlation between birth weight and weaning weight was 0.08 which was positive and significant. Similar estimation has also been reported by Sireger (1983) and Endang (1988). The positive and significant correlations indicates that higher birth weights were associated with higher weaning weights. Hence, selection for higher birth weight will improve weaning weight of kids.

Genetic correlation: The genetic correlation between the two traits under study was calculated to be 0.212 which was moderate and highly significant. The findings of Maui and

Rodricks (1987) and Endang (1988) are in agreement with this study. The results indicate that probably most of the genes responsible for higher birth weight stimulate growth and are helpful in increasing weaning weight in addition to the environmental factors.

Environmental correlation: The environmental correlation between the two variables was 0.049 which was non-significant. This suggests that environmental situation affecting birth weight will not stimulate growth or will not improve weaning weight. Because environmental effect is always temporary and for better performance suitable environment are to be provided during different parts of life according to the requirements.

### REFERENCES

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