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Genetic parameters of Cholistani Cattle in Pakistan

Faisal Ashfaq*[1], Muhammad Iqbal Anjum[1], Shahbaz Javaid[1], Munib Hussain[1], Javed Iqbal[1], Muhammad Asif Yaseen[2], Ahmad Ali Malik[2], Rana Muhammad Bilal[3]

[1]*Animal Sciences Institute, National Agricultural Research Center, Islamabad, Pakistan*

[2]*Livestock Experiment Station, Chak Katora, Hasilpur, Pakistan*

[3]*University College of Veterinary and Animal Sciences, The Islamia University of Bahawalpur, Pakistan*

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Abstract

The cattle population of Pakistan is 47.8 million. The cattle are a major dairy animal contributing more than 35% of the total annual milk production in Paksitan. Predominantly, the cattle are scrub type which doesn't fall in a specific breed and they produce lesser quantities of milk however, Pakistan is home to some famous milk producing breeds. Amongst those, the Cholistani cattle is a unique breed having fair quantity of milk bearing the harsh climatic conditions of the Cholistan desert and adjoining areas of the country. They also bear the challenges posed by hardships of parasitic infestations and diseases of the warm regions while also meeting the production demands and dairying needs of the region. In order to assess the genetic parameters of this important dairy cattle breed, Data on 1473 lactation records of 306 Cholistani cows kept at Government Livestock Farm, Jugait Peer, District Bahawalpur were utilized to estimate the genetic parameters of heritability, repeatability and genetic correlations of different productive and reproductive traits.

* **Corresponding Author:** Faisal Ashfaq ✉ ashfaq.faisal.pk@gmail.com

Introduction

The Cholistani is a dairy cattle breed which serves as a good milk producing animal. It inhabits the Cholistan desert of the Punjab. According to Bhutto *et al.*, (1993), Cholistani cattle can bear severe hot weather in the desert and it has a very good production potential despite bearing the severity posed by desert conditions in the area of its inhabitance. Mason (1996) has described it to be a multipurpose breed, utilized for the beef, dairy and draught. Bhutto *et al.*, (1993) reported that in a 305-day lactation period, It produces about 1800 liters of milk.

The performance of an individual for a particular trait called the phenotypic value besides the environmental factors, is also affected by the genotypic value of the individual. The genotypic value of an animal refers to the combined effect of all the animal's genes at all loci that affect the trait, taking account of the way in which the genes are paired together into a genotype. The genetic sources of variation include all differences that may be attributed to heredity. The proportion of the total phenotypic variance for a trait that is due to the variation in additive gene effects or more simply, the proportion of differences among animals for performance traits that are due to differences in the additive effects of the genes that they possess is referred to as the heritability estimate. High heritability estimates for a trait suggest strong correlation between phenotype and genotype of the individual and selection on the basis of individual's own phenotype should be effective. High estimates of heritability also indicate that additive gene action is important for that trait and the mating of the best to the best should produce more desirable offspring. A low heritability estimate indicates low correlation among genetic makeup and phenotypic expression, therefore more consideration is needed for the performance of collaterally related ones and the offspring (s) in selective breeding procedures for improving the character further.

Repeatability is another parameter of interest in the genetic selection of animals and it refers to the expression of the same trait at different times in the life of the same individual. It is actually the fraction of differences between single records of individuals that are likely to occur in future records of those same individuals. Knowledge of repeatability estimates for various traits may be used in selecting for future performance. When repeatability estimate for a trait is high, culling on the basis of the first record should be effective in improving the overall performance of the herd the next year.

The genetic improvement in performance traits not only depends on the heritability of the traits but also on the genetic correlation between them. The genetic correlation among traits is the measure of the extent to which two traits are determined by the same set of genes. Pleiotrophy is probably the major cause of genetic correlation although it is possible for close linkage to have a similar transitory effect.

A high and positive genetic correlation between two traits suggests that selection for the improvement of one will also result in improvement in the other as a result of correlated response even though direct selection for its improvement has not been practised. Alternatively negative genetic correlation means that selection for the improvement of one, if successful, results in a decline in the other.

Identification of genetic parameters thus provides very important basic information which is used for future selection and identification of genetically elite animals for the animal improvement programs. Therefore, estimation of genetic parameters of livestock is of significant importance. So based on records and available information, it was planned to study them in Cholistani cattle.

Materials and methods

The data consisted of the Pedigree and performance records of three hundred and six Cholistani cows comprising of one thousand four hundred and seventy three lactation records of Government Livestock Farm, Jugait Peer, District Bahawalpur spanning a duration of fourteen years including animal identification numbers, dates of birth, service, calving, drying and disposal along-with lactation milk yield.

The economic traits studied were: productive traits [first lactation milk yield (FLY), lactation milk yield (LY), lactation length (LL) and dry period (DP)], reproductive traits [age at first calving (AFC), service period (SP), calving interval (CI) and breeding efficiency (BE)] and lifetime traits [lifetime milk yield (LMY), productive life (PL), longevity (L) and herd life (HL)]. The animal ID numbers and date records were edited to check for any recording irregularity. Moreover the records containing abortion in cows and missing information for a year because of illness and related causes were excluded. All the performance traits outside plus minus three phenotypic standard deviations from the unadjusted mean were also excluded. The calving age was calculated by finding the duration between the date of birth and date of calving and any outliers with respect to calving ages were excluded. Errors in data recording resulted in heavy editing. For data handling MS Excel computer program was used.

Statistical analyses

Evaluation of genetic parameters

For the evaluation of genetic parameters i.e., heritability, repeatability and genetic correlations, the Restricted Maximum Likelihood procedure (Patterson and Thompson, 1971) was utilized through Animal Model. In this analysis, the complete set of available information on pedigrees was utilized.

The convergence criterion (variance of function values -2 log likelihood) for various genetic parameters was 1 x 10^{-8}.The starting values for the estimation of genetic parameters were given from the average values calculated from the review of literature.

Heritability estimation

For heritability estimation the mathematical model assumed was as follows:

$Y_{ijk} = \mu + A_i + F_j + e_{ijk}$ (Model 1)

Where,
Y_{ijk} = measurement of a particular trait;
μ = population mean;
A_i = random additive genetic effect of ith animal with mean zero and variance σ^2_A;
F_j = fixed effects observed to be significant
E_{ijk} = random error with mean zero and variance σ^2_E

Phenotypic variance (σ^2_P) = Additive genetic variance (σ^2_A) + Residual Variance (σ^2_E)

For the computation of heritability the following formula was used:

Heritability $(h^2) = \sigma^2_A / \sigma^2_P$

Repeatability estimation

The repeatability of lactation milk yield, lactation length, dry period, service period and calving interval were found by the following mathematical model assumption:

$Y_{ijk} = \mu + C_i + F_j + e_{ijk}$ (Model 2)

Where,
Y_{ijk} = measurement of a particular trait
μ = population mean
C_i = the random effect of ith Cow
F_j = fixed effects observed to be significant
E_{ijk} = random error with mean zero and variance σ^2_E

The common environmental parameter estimated (c^2) represented the proportion of phenotypic variance (σ^2_P) attributable to animal's permanent environmental effects and was calculated as follows:

$c^2 = \sigma^2_{PE} / \sigma^2_P$

Repeatability for a particular character was found by:

Repeatability = $\sigma^2_A + \sigma^2_{PE} / \sigma^2_P$

The model included animal's permanent environmental effect in addition to the animal's additive genetic effect and the residual effect assuming that it is uncorrelated to other random effects i.e. additive genetic and residual effects. In this case animal's permanent environmental effect was fitted as an Additional Random effect.

C) Genetic correlation estimation

Statistical analysis of the performance traits was performed for finding out genetic correlations between different performance traits.

For this, the bivariate analysis was conducted using the Individual Animal Model REML (Patterson and Thompson, 1971). The fixed effects for different performance characteristics in this analysis were similar to those used in the univariate analysis.

The bivariate analysis was carried out for the following combinations of performance traits:

First lactation's milk yield & Lifetime milk yield
First lactation's milk yield & Herd Life
First lactation's milk yield & Longevity
First lactation's milk yield & Productive life
First lactation's milk yield & Breeding Efficiency
Age at first calving & First lactation's milk yield
Age at 1st calving & Lifetime milk yield
Age at 1st calving & Herd Life
Age at 1st calving & Longevity
Age at 1st calving & Productive life
Age at first calving & Breeding Efficiency

The Derivative Free Restricted Maximum Likelihood (DFREML) software package (Meyer, 1997) was used for all the analyses work. The standard errors for the genetic correlations were computed as outlined by Falconer and Mackay (1997). The standard errors of heritability estimates obtained from univariate analysis were used for this purpose.

Results and discussion

Genetic Parameters

The genetic composition of Cholistani herd was worked by taking into consideration the relative significance of inheritance with the environment influencing the performance of individual animals with the parameters of heritability, repeatability and genetic correlations.

Heritability and Repeatability Estimates

The heritability estimates for FLY, LY, LL, DP, AFC, SP, CI, BE, LMY, PL, L & HL and repeatability estimates for LY, LL, DP, SP & CI have been shown in Table (1).

The estimated heritability for LL, DP, AFC, CI, BE, L and HL was low. The estimated low heritability found in these characters showed that additive gene action is perhaps not influencing their variation but it is mostly attributable to environmental sources. Maintenance of good recording practices and better feeding and husbandry can bring improvement in these characters. Moderate to high estimates of heritability were found for FLY, LY, SP, LMY and PL which suggest that the additive gene action is imperative for these characters and they can be improved through selection.

Generally, the estimated values for heritability differ in breeds, herds, levels of production, methodology for their computation and duration for a specific characteristic. The genetic variance may be reduced by inbreeding. However, the difference in managemental and environmental factors may increase the phenotypically observable variation in different years, livestock breeds and the animals herds. The estimated low heritabilities might result due to the low productivity, missing identity and the missing information in the pedigrees. The low heritability may also result from a higher value of the phenotypic variance attributable to small herd sizes and masked environmental causes. Due to the weather, illness and other causes due to environment which affect the performance in tropical and sub-tropical areas, the heritability might remain low unsurprisingly. The repeatability estimates for the traits studied varied from moderate to high (Table 1). When repeatability estimate for a trait is high, culling on the basis of the first record should be effective in improving the overall performance of the herd the next year. Knowledge of repeatability estimates of Cholistani cattle for various traits might be used in future selection.

Genetic Correlations

Bivariate Restricted Maximum Likelihood (REML) analytical tool was used for the computation of genetic correlations among different performance traits. It also generated estimates of phenotypic and residual correlations. The criteria used for discussing the magnitude of the genetic correlations (absolute values) was: 0.00-0.25, low; 0.26-0.50, moderate; 0.51-0.75, high and 0.76-1.00, very high. The estimates of genetic, phenotypic and residual correlations between FLY and different performance traits along-with estimates of correlations between AFC and others traits are presented in Table (2).

Table 1. Heritability and repeatability estimates for various performance traits.

HERITABILITY			
Trait	No. of Observations	No. of Cows	Estimate±SE
First lactation's milk yield	131	131	0.658±0.371
Lactation milk yield	949	263	0.323±0.094
Lactation length	1178	283	0.000±0.000
Dry period	1020	246	0.154±0.074
Age at first calving	178	178	0.002±0.001
Service period	453	123	0.333±0.133
Calving interval	1124	260	0.209±0.077
Breeding efficiency	127	127	0.125±0.278
Lifetime milk yield	112	112	0.477±0.477
Productive life	135	135	0.248±0.345
Longevity	21	21	0.009±0.005
Herd life	75	75	0.073±0.040
REPEATABILITY			
Milk yield	949	263	0.334
Lactation length	1178	283	0.171
Dry period	1020	246	0.183
Service period	453	123	0.389
Calving interval	1124	260	0.223

Table 2. Genetic, phenotypic and environmental correlations between different performance traits.

Correlated Traits	Phenotypic	Genetic±SE	Residual
First lactation's milk yield & Age at 1st calving	-0.461	-0.100±0.372	-0.467
First lactation's milk yield & breeding efficiency	0.339	-0.700±0.040	0.339
First lactation's milk yield & lifetime milk yield	0.251	0.292±0.486	0.299
First lactation's milk yield & productive life	0.0259	-0.993±0.009	0.029
First lactation's milk yield & longevity	-0.174	-0.899±0.076	-0.182
First lactation's milk yield & herd life	0.162	-0.874±0.093	0.164
Age at 1st calving & Breeding efficiency	-0.058	-0.997±0.004	-0.045
Age at 1st calving & Lifetime milk yield	-0.255	-0.590±0.326	-0.255
Age at 1st calving & Productive life	-0.686	-0.056±0.588	-0.700
Age at 1st calving & Longevity	-0.269	-0.475±0.288	-0.269
Age at 1st calving & Herd life	-0.076	-0.999±0.001	-0.075

The high estimate of genetic correlation showed a greater degree of genetic association between the two traits meaning that the same genes may be responsible for the change in traits. And selection for one trait will automatically change the other trait. Whereas, the low estimates indicate a lesser degree of genetic association and although the selection for one trait will result in change in the other but to a lesser extent. Whereas zero estimate indicates no genetic association between the traits. A positive estimate indicates that improvement in one will also result in the increase in the other trait whereas, the negative estimate between the two traits suggest that same genes tend to influence the two traits in opposite direction.

Conclusion

The genetic parameters of Cholistani cattle were estimated using the best available analytical procedures which may serve to fill the information gap on this very important dairy cattle breed of Pakistan kept at the Cholistan desert and it is envisaged that it has a good dairy potential despite facing the prevailing harsh climatic conditions of the area. Thereby meeting the production needs of the areas of its destination and information on its genetic parameters might be helpful in future livestock improvement programs.

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