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Genetic Assessment of Fitness in Beetal Goats

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ABSTRACT

Background: The present study aimed to evaluate the fitness of Beetal goats through a combination of logistic regression and Bayesian statistical approaches using data from the Directorate of Livestock Farms, GADVASU, Ludhiana.

Methods: Fitness classification based on mortality records and non-genetic factors such as sex, season and year of birth from 2015 to 2023 were extracted from records at the Directorate of Livestock Farms, GADVASU. A total of 530 animal records belonging to 230 dam families sired by 52 males were used, out of which 230 death records were reported and 466 animals survived upto one year of age.

Result: Logistic regression analysis revealed that all three variables significantly influenced survival, with female goats and those born in cooler seasons showing higher odds of being classified as high-fitness. Bayesian analysis was subsequently performed on the filtered dataset using the BLUPF90 suite to estimate additive genetic variance and heritability. The estimated heritability of 0.1791 indicated a modest genetic basis for fitness, with environmental factors contributing the majority of variance. These findings underscore the complex, multifactorial nature of fitness in goats, providing insights for sustainable breeding strategies that enhance health resilience without compromising adaptability. The study also identifies specific years and seasons that influence survivability trends, offering practical implications for livestock management and genetic selection programs.

Key words: Bayesian analysis, Beetal goat, Breeding value, Fitness, Heritability.

INTRODUCTION

The goat (*Capra hircus*) is a domesticated goat-antelope species that is commonly raised as livestock. The goats belong to the Bovidae family and the Caprini genus. There are around 300 different goat breeds globally (Hirst, 2019) and 34 registered breeds in India. Throughout the world, goats have been utilised for meat, milk, skin and fur. In 2019, the country's goat population was 148.88 million, accounting for 27.80 per cent of the country's overall livestock population, up 10.1 per cent from the previous census. Punjab has a goat population of 3.47 lakh (Livestock Census, 2019). The Beetal goat is a breed native to India and Pakistan's Punjab area (Bilaspuri and Singh, 1993) and is also known as the Lahori goat utilised in the production of milk and meat. Beetal is a good milker with a large body size, flat, long, curled and drooping ears. Beetal goats have been used extensively over the subcontinent to improve native goats.

Even though goat farming has been practiced for generations, it still poses a number of health problems, as many immunocompromised persons are at danger of having zoonotic diseases from goats. Zoonotic infections are contagious that spread between and affect both human and animals (Rahman *et al*., 2020; Yadav *et al*., 2022; Sharma *et al*., 2025). In goat there are large number of diseases including, bacterial and viral infections which affect the health of animal causing morbidity as well as mortality, the kids are at higher risk than adult animals (Rath *et al*., 2024). This leads to huge economic losses to the farmers (Pal and Chakravarty, 2019). Traditional methods such as vaccination, therapeutic treatments and eradication strategies have long been essential in managing diseases. In animal farming, rather than solely focusing on combating diseases, farmers should select animals based on their genetic resistance to health disorders, a practice considered more sustainable. This approach promotes sustainability by improving the health and resilience of animal populations over generations, which also enhances animal welfare (Do *et al*., 2021).

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The estimates of heritability for survival from birth to 12 months of age ranged from 0.10 to 0.43 (Rout *et al*., 2018). The heritability estimates for survival at 3, 6 and 12 months of age from the Weibull proportional hazard model were 0.10, 0.13 and 0.18, respectively (Tesema *et al*., 2020).

The Fitness is taken as criteria for classification of animals for the current study, which refers to as survival of animals upto 1 year of age. Thus, the breeding value for survival derived from Bayesian analysis, was treated as the breeding value for fitness (BVF).

MATERIALS AND METHODS

Location/place of work

Directorate of Livestock Farms (DLF) and Department of Bioinformatics, College of Animal Biotechnology, GADVASU, Ludhiana.

Source of data

A total of 530 Beetal goats being maintained at DLF were used. The data was collected from birth registers, history sheets and health registers up-to 3 generations for years 2015 to 2023. The following information was collected: animal number, date of birth, dam number, sire number and mortality records.

General information

General information recorded for identification and classification of Beetal goats were as follows:

a. Animal number.
b. Date of birth.
c. Sex.
d. Sire number.
e. Dam number.
f. Mortality (upto 12 months).
g. Date of auction (upto 12 months).

Standardization of data

The records of the beetal goats with known pedigree were used for analysis. Experimental animals were excluded from the study. Animals with any pathological conditions, sale, transfer or auction of animals (Age < 12 months) were not considered under present study. Mortality records of animal which died of natural cause (Age < 12 months) were taken into consideration.

Classification of non-genetic factors

The non-genetic factors (intrinsic and extrinsic) affecting the quantitative traits were studied and the classification was done for Bayesian analysis. The following tentative classification of factors affecting the traits were considered:

a) Year of birth.
b) Season of birth.
c) Gender.

a) Year of birth: The data was divided on yearly basis and the records were taken from 2015 to 2023.

b) Season of birth: Each year was divided into five seasons according to the prevalent geo-climatic conditions *viz*.

c) Gender: Male and Female.

Statistical analysis

Logistic regression analysis

The non-genetic factors *viz*; Gender, Season of birth and Year of birth were analysed by Binary Logistic Regression in SAS Studio.

$$y_{ijkl} = G_i + S_j + Y_k + A_l + e_{ijkl}$$

Where,

y_{ijkl} = Survival of i^{th} animal belonging to i^{th} gender, j^{th} season and k^{th} year.
G_i = Effect of gender of the goat (male or female).
S_j = Effect of season of birth of the goat as classified in Table 1.
Y_k = Effect of year of birth of the goats (ranging between 2015 and 2023).
e_{ijkl} = Random error term.

The backward elimination was practiced for model selection procedure based on the p values of the factors. The Odds Ratio and Maximum Likelihood estimates with Wald's Chi Square taking 95% confidence level were estimated. The significant ($p \leq 0.05$) non-genetic factors were used for further estimation of breeding value for fitness.

Bayesian analysis

After checking the significance of non-genetic factors in Logistic Regression, the data containing significant non-genetic factors *viz*; Year of birth, Season of birth and Gender as fixed effects alongwith the animal as random effects were analysed in animal model using Bayesian Analysis in BLUPF90 suite of software.

$$y_{ijkl} = G_i + S_j + Y_k + A_l + e_{ijkl}$$

Where,

y_{ijkl} = Survival of animal belonging to gender, season and k^{th} year.
G_i = Effect of gender of the goat (male or female).
S_j = Effect of season of birth of the goat as classified in table 2.
Y_k = Effect of year of birth of the goats (ranging between 2015 and 2023).
A_l = Animal effect of l^{th} animal.
e_{ijkl} = Random error term.

Bayesian statistical analysis was carried out using the GIBBSF90 module of the BLUPF90 software suite. Where, the death upto one year was coded as 1 and survival was coded as 2 as per the requirements of the GIBBSF90 and POSTGIBBSF90 software for analysis, since the software treats 0 as missing values.

For the present study, a total of 25,000 Gibbs samples were drawn to ensure sufficient exploration of the posterior distribution. To eliminate the influence of initial values and allow the Markov Chain Monte Carlo (MCMC) to reach a stationary distribution, the first 5,000 samples were discarded as burn-in. Additionally, a thinning interval of 20 was applied to reduce autocorrelation among successive

samples by retaining only every 20th sample after burn-in. As a result, a final set of 1,000 posterior samples was retained for the estimation of parameters.

The survival of animals upto 1 year was taken as the measure of fitness. Thus, the breeding value for survival derived from above Bayesian analysis, was treated as the breeding value for fitness (BVF) and ranking of the Beetal goats was done on the basis of the same. The Beetal goats were then classified as high fitness (mean BVF + 1 Standard Deviation and above), medium fitness (within range of mean BVF ± 1 Standard Deviation) and low fitness (mean BVF - 1 Standard Deviation and below) groups. The existing animals from the high and low fitness group were then examined for their apparent health and hematology. Two existing healthy animals from the most fit and least fit BVF group each were selected for further study.

RESULTS AND DISCUSSION

The logistic regression analysis revealed statistically significant effects of all three explanatory variables. As shown in (Table 3), sex had a significant association with fitness classification (Wald χ^2 = 5.1782; P = 0.0229), suggesting that female goats had higher odds of being ranked in the high-fitness group compared to males. Season of birth also demonstrated a significant association (p = 0.0012), indicating that environmental and management conditions during the early developmental phase influenced long-term fitness outcomes. The year of birth exhibited the most robust statistical response (Wald χ^2 = 70.2874; p<0.0001).

Logistic regression estimates for predictive variables

A detailed analysis of the logistic regression estimates is presented in (Table 4 and Fig 1). Among the categorical contrasts, the female group exhibited 1.493-fold higher odds of being classified as high fitness compared to males (p = 0.0229). Seasonal differences indicated that animals born in the rainy season (R vs. Au) were significantly less likely to fall in the high fitness group (OR = 0.354; p<0.0001), potentially due to postnatal stressors or suboptimal nutrition during that time. Animals born in summer season showed higher odds of survival than all other seasons.

Table 1: Classification of the year of the birth for goats.

Year	No. of observations (n)
2015	43
2016	63
2017	67
2018	30
2019	107
2020	51
2021	95
2022	33
2023	41

Table 2: Classification of the season of the birth for goats.

Month	Season	No. of observations
March-Mid-April	Spring	76
Mid-April- June	Summer	49
July-September	Rainy	163
October-November	Pre-winter	97
December-February	Winter	145

(Government of Punjab, 2025).

Table 3: Logistic regression analysis for non-genetic factors affecting fitness in Beetal goats.

Effect	Degree of freedom	Wald chi-square	Pr > ChiSq
Sex	1	5.1782	0.0229
SoB	4	18.1511	0.0012
YoB	8	70.2874	<.0001

Table 4: Maximum likelihood estimates and odds ratio for non-genetic factors.

Parameter	DF	Maximum likelihood estimates	Wald chi-square	Pr > ChiSq	Odds ratio estimates
Intercept	1	0.750±0.103	52.778	<.0001	
Female vs Male	1	0.201±0.088	5.178	0.0229	1.493
Winter vs Autumn	1	0.095±0.210	0.204	0.6518	0.885
Spring vs Autumn	1	0.081±0.197	0.17	0.68	0.873
Summer vs Autumn	1	0.430±0.253	2.905	0.0883	1.238
Rainy vs Autumn	1	-0.823±0.196	17.693	<.0001	0.354
2015 vs 2023	1	-0.761±0.219	12.061	0.0005	0.055
2016 vs 2023	1	0.201±0.218	0.851	0.3562	0.143
2017 vs 2023	1	0.280±0.283	0.981	0.322	0.155
2018 vs 2023	1	-0.209±0.286	0.532	0.4658	0.095
2019 vs 2023	1	-1.022±0.257	15.849	<.0001	0.042
2020 vs 2023	1	-0.784±0.247	10.043	0.0015	0.053
2021 vs 2023	1	-0.993±0.290	11.695	0.0006	0.043
2022 vs 2023	1	1.141±0.336	11.519	0.0007	0.366

The year-wise contrasts yielded critical insights. Goats born in 2019 and 2021 had notably reduced odds of achieving high-fitness status compared to those born in 2023 (OR = 0.042 and 0.043, respectively; both p<0.001). Conversely, goats born in 2022 showed significantly higher odds (OR = 0.366; p = 0.0007), possibly reflecting improved management or breeding practices in that year.

These findings corroborate earlier reports that shifts in climate, disease prevalence and feed availability can markedly influence phenotypic outcomes (Feng *et al*., 2020 and Do *et al*., 2021).

The ROC curve value 0.73 shows the good performance of logistic regression model in binary classification by plotting true positive rate (sensitivity) vs false positive rate (1-specificity) across various probability thresholds (Fig 2).

Effect of season of birth on fitness classification

The analysis revealed that the season of birth significantly influenced the fitness of goats. As depicted in Fig 7, goats born during the autumn and winter seasons had a higher probability of high fitness compared to those born in summer. The Wald Chi-square test for the season of birth yielded a value of 10.5526 with a p-value of 0.0012, indicating a strong statistical association.

Parameter estimation using bayesian analysis

Bayesian estimation was performed using the 'GIBBSF90+' and 'PostGibbsF90' modules from the 'BLUPF90' software suite (Misztal *et al*., 2014). The model was run for 25,000 Gibbs samples with a burn-in of 5,000 and a thinning interval of 20, retaining 1,000 posterior samples for inference. The aim was to partition the total phenotypic variance of the fitness score into genetic and residual components and estimate the heritability.

The posterior mean for the additive genetic variance (Animal) was estimated at 0.03675±0.00216, with a 95% Highest Posterior Density (HPD) interval ranging from 0.0084 to 0.0734, suggesting a modest yet credible genetic contribution. The residual variance was much larger (0.1665 ±0.00135), indicating a predominant non-genetic contribution to the phenotype. Total phenotypic variance was estimated at 0.20325±0.00062, yielding a heritability estimate of 0.1791±0.01031 (HPD interval: 0.049 to 0.349) as depicted in (Table 5).

Interpretation of bayesian posterior parameters and heritability

The Bayesian analysis provided posterior distributions for four key parameters: additive genetic variance (Animal), residual variance (Residue), phenotypic variance and heritability. These were inferred from the Gibbs sampling process, which after 5,000 burn-in cycles and thinning, yielded 1,000 retained samples shown in (Fig 3, 4 and 5). The Bayesian estimates of effects of sex, season of birth, year wise trend on fitness is shown in (Fig 6, 7 and 8 respectively) and breeding value estimated of fitness of selected Beetal goats is shown in (Fig 9).

Additive genetic variance (Animal effect)

The mean posterior estimate of the additive genetic variance was 0.0367±0.0022, suggesting a relatively modest influence of heritable factors on the immune response phenotype under investigation. The 95% HPD interval (0.0084-0.0734) indicates that while only some variation is due to additive genetic effects, it is never zero. A Geweke diagnostic value of 0.04, combined with low autocorrelation across lags, confirmed chain convergence and parameter stability.

Residual variance

Residual variance was estimated at 0.1665±0.0014, with a narrow HPD interval (0.1368-0.1992), reflecting the dominance of unexplained variability in the model. This is typical of complex threshold traits like fitness where environmental, epigenetic and non-additive genetic factors play substantial roles (Naeem *et al*., 2012 and Lawless *et al*., 2014).

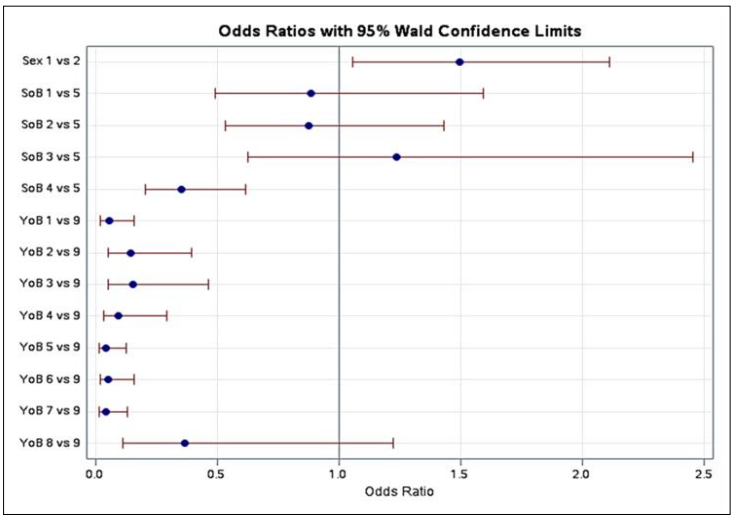


Fig 1: The Odds Ratio from logistics regression model.

Phenotypic variance and heritability

Total phenotypic variance was calculated as 0.2033± 0.0006, encompassing both genetic and residual components. The heritability (h^2) estimates of 0.1791± 0.0103, with a posterior range of 0.049-0.349, suggests that the trait is moderately heritable. This degree of heritability is consistent with findings in goat immune trait studies using similar stimulation models (Khanduri *et al*., 2018 and Wu *et al*., 2019), indicating that while genetic selection may improve immune responsiveness, environmental management remains crucial.

Statistical diagnostics and model strength

- Effective sample sizes were above 60 for most Parameters, with phenotype at 364.4, ensuring precision.
- Low lag autocorrelations (*e.g*., <0.1 for lag-1) and positive convergence diagnostics further validated the quality of MCMC estimation.
- The Geweke diagnostics were <0.05 for all parameters, suggesting that the Markov chains had converged adequately. Autocorrelation values for lags 1, 10 and 50 were all low, supporting the independence of retained samples. Effective sample sizes were above the recommended threshold in most cases (*e.g*., 364.4 for phenotype), reinforcing the robustness of posterior estimates as shown in (Table 6).

Collectively, these results offer compelling evidence that fitness in indigenous goats, though partially heritable, is significantly shaped by environmental exposures and non-additive factors. Such insight informs selective breeding strategies aiming to enhance disease resilience without compromising adaptability.

In this study, data on Beetal goats spanning from 2015 to 2023 were extracted from records at the Directorate of Livestock Farms, GADVASU. A total of 530 animal records belonging to 230 dam families sired by 52 males were

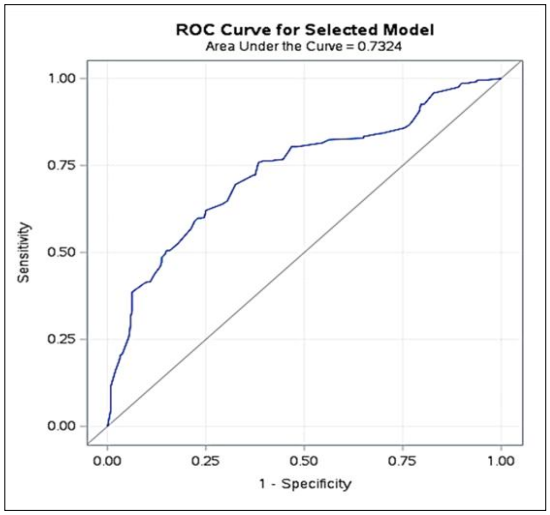


Fig 2: The ROC graph of logistics regression model.

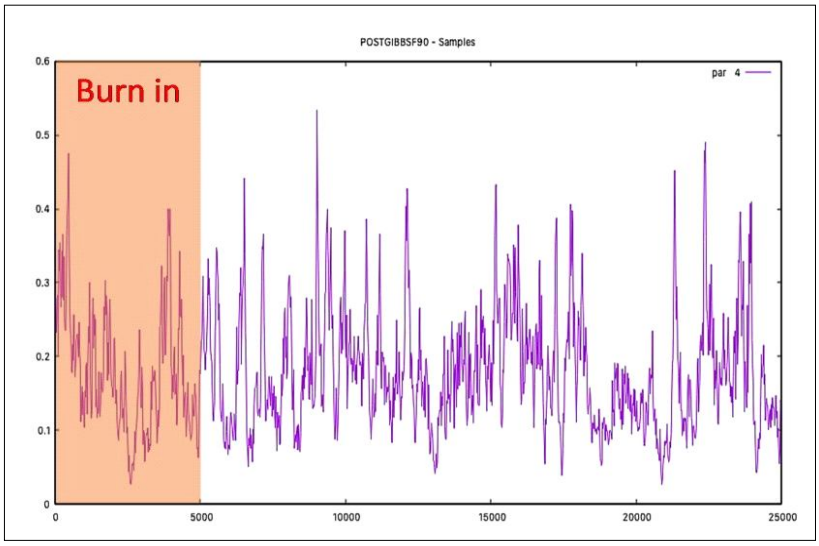


Fig 3: Pre-Burn-in sample distribution of Gibbs samples for animal effect.

Table 5: Bayesian estimates and Monte-carlo errors from post Gibbs samples.

Pos.	Components	Mean±MCE	HPD Interval (95%)	Effective sample size	Independent chain size
1	Animal	0.0367±0.0022	0.0084-0.0734	67.10	82
2	Residue	0.1665±0.0014	0.1368-0.1992	142.30	30
3	Phenotype	0.2033±0.0006	0.1808-0.2274	364.40	14
4	Heritability	0.1791±0.0103	0.04949-0.3490	63.30	82

used, out of which 230 death records were reported and 466 animals survived upto one year of age. Using logistic regression, non-genetic factors such as sex, season of birth and year of birth were evaluated for their influence on survivability upto one year of age. The findings indicated significant effects of these factors, with females and animals born in summer seasons showing a higher likelihood of being categorized into the high fitness group. The breeding values for fitness showed a range of 1.117 with maximum value of 0.303 and minimum value of -0.814 with average value of -0.068. The heritability estimate of 0.1791±0.01031, derived from Bayesian analysis with Gibbs sampling, suggested a moderate genetic influence on the trait under consideration. It suggests that family selection should be practiced for breed improvement programme. These outcomes underscored the complex interplay between environmental exposures and host genetic architecture in shaping immune fitness in goats.

A logistic regression model was employed to assess the influence of sex, season of birth (SoB) and year of birth (YoB) on the classification of goats into high-fitness and low-fitness categories. These fitness categories were foundational for downstream miRNA profiling and differential expression analyses. The observations form logistic regression analysis are in line with previous studies that have identified year-to-year environmental variability and perinatal conditions as critical determinants of phenotypic resilience and immune development in ruminants (Brogaard *et al*., 2016; Bilbao-Arribas *et al*., 2019; Liang *et al*., 2016). Such stratification provides a biologically relevant framework to investigate the endogenous miRNA profiles associated with high and low fitness groups.

The trend of effect of season of birth may be attributed to favorable climatic and nutritional conditions prevailing during the cooler months, which could positively impact neonatal immunity and survivability. Goats born during

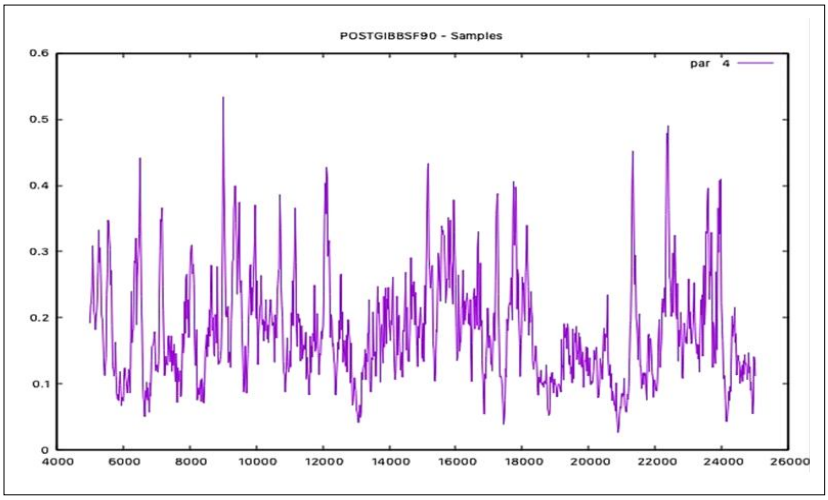


Fig 4: Post-burn-in sample distribution of Gibbs samples for animal effect.

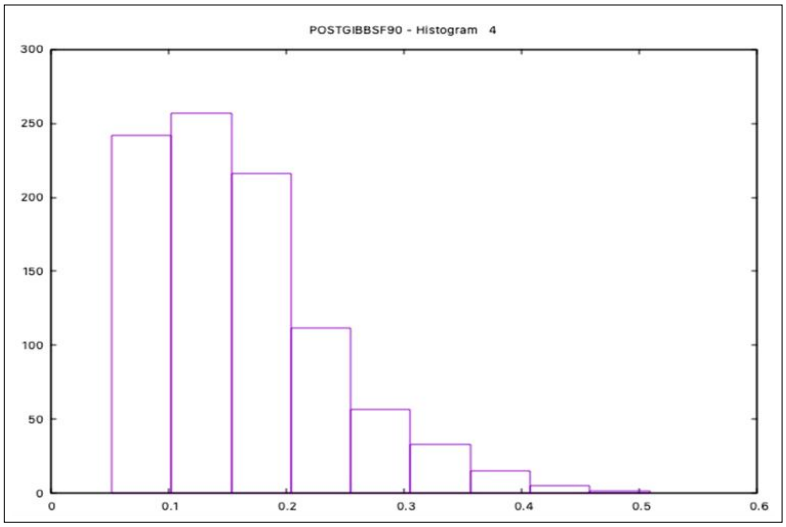


Fig 5: Histogram of posterior distributions of Gibbs samples.

extreme summer are often exposed to higher heat stress and lower feed availability, potentially impairing their early growth and immune programming. These findings underscore the importance of birth season in shaping lifetime health and productivity traits in livestock. The trend of year of birth showed mixed trend but in later years, it showed a positive trend depicting improved management or breeding practices in these years.

The Bayesian estimates and MCE from post-gibbs sample estimates suggest that approximately 17.9% of the variation in the fitness could be attributed to additive genetic effects as heritability, while the remainder arises from environmental and non-additive genetic factors. Such low to moderate heritability is consistent with complex immune traits as documented in livestock studies by Brogaard *et al*. (2018) and Qi *et al*. (2018), where host resistance traits were found to be moderately heritable.

The results of the study indicate that the 95% highest posterior density regions (HPDs) for the major gene parameter, particularly for the major gene variance, indicating the statistical significance of the major gene component by Inan *et al*. (2025).

Practical implications for breeding programs

Moderate heritability (0.1791±0.01031) for fitness suggests family selection using top dam families with high breeding values. Prioritize females and summer-born kids, which show higher survivability per logistic regression. Optimize birth seasons to avoid summer heat stress.

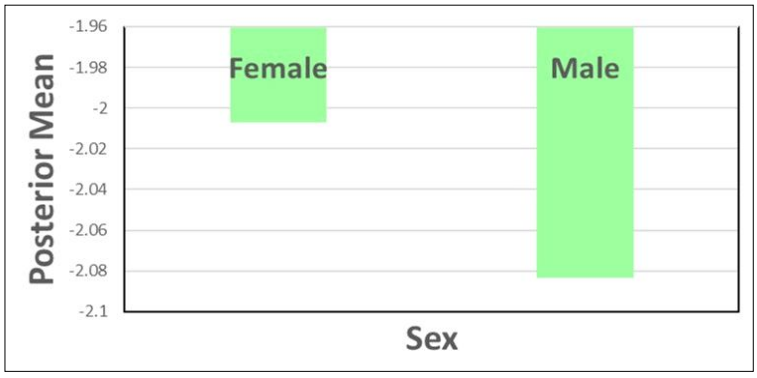


Fig 6: Bayesian estimates of effects of sex on fitness.

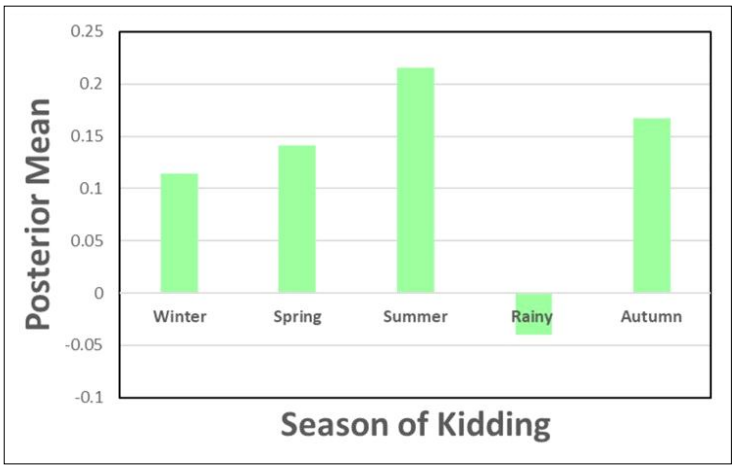


Fig 7: Bayesian estimates of effects of season of birth on fitness.

Table 6: Convergence diagnostics and model strength for bayesian analysis.

Components	Standard deviation	Posterior SD interval (95%)		Geweke diagnostic	Autocorrelations			Independent batches
					lag: 1	10	50	
Animal	0.01777	0.0019214	0.071578	0.04	0.828	0.083	0.034	12
Residue	0.016122	0.13490	0.19810	0	0.512	0.060	0.033	33
Phenotype	0.01188	0.17997	0.22653	0.05	0.147	0.025	-0.051	71
Heritability	0.08067	0.020990	0.33722	0.04	0.830	0.092	0.041	12

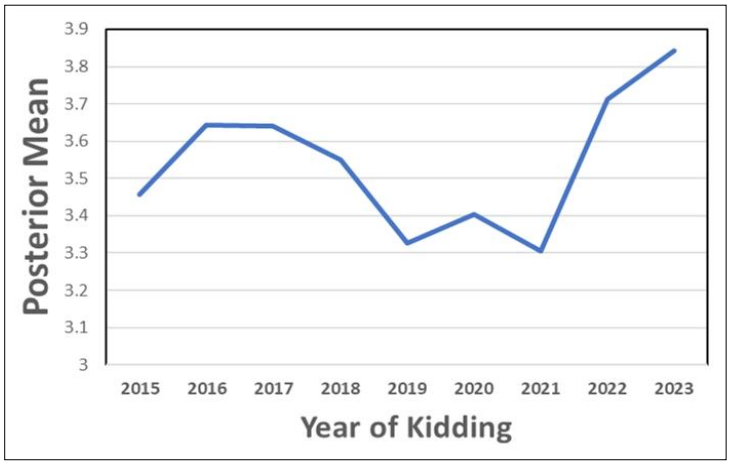


Fig 8: Bayesian estimates of year wise trend of fitness.

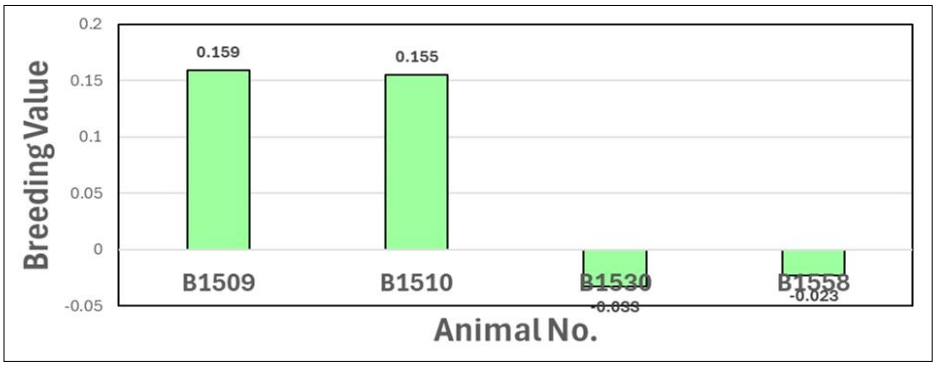


Fig 9: Bayesian estimates of fitness of breeding values of selected beetal goats.

Study limitations

This study was confined to a single farm (DLF, GADVASU, Ludhiana), restricting generalizability to broader Beetal populations or varying management practices across Punjab; the dataset covered a relatively short 9-year period (2015-2023), potentially overlooking long-term environmental trends or rare events; additionally, dependence on farm records risks unmeasured recording inaccuracies and the binary survival metric (up to 12 months) neglects post-yearling fitness or multi-trait dynamics.

Suggestions for future studies

To address the single-farm limitation and enhance generalizability, multi-farm or multi-regional studies across diverse Beetal populations in Punjab and beyond should incorporate longer-term data (*e.g.*, 15+ years) to capture climatic variability and generational trends; expanding the dataset to include post-12-month survival, health metrics and multi-trait analyses (*e.g.*, growth, reproduction alongside fitness) would provide a holistic breeding value framework, while integrating genomic data (*e.g.*, miRNA expression or SNP markers) with these phenotypic records via advanced Bayesian models could validate BVF rankings, identify causal genetic factors and support practical selection programs for improved goat fitness.

CONCLUSION

The breeding values for fitness showed ample variability and significant low to moderate heritability, indicating a scope of genetic improvement in Beetal goats by strategic selection.

Authors contribution

All authors contributed to the study conception and design. Study design and analysis were performed by [Neeraj Kashyap] and data collection and lab experiments were done by [Rana Partap Singh Brar]. Assistance in analysis and interpretation of results was obtained from [Chandra Sekhar Mukhopadhyay] and [Bharti Deshmukh]. The first draft of the manuscript was written by [Rana Partap Singh Brar] and all authors contributed on refinement of the manuscript. All authors read and approved the final manuscript.

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Data availability

The datasets generated during and/or analysed during the current study are not publicly available due to [This research data belongs to the respective institute] but are available from the corresponding author on reasonable request.

Ethics approval

Not applicable.

Conflict of interest

The authors declare no conflict of interest.

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