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Balancing production and reproduction traits in frieswal cattle: a multivariate approach

Olympica Sarma*[1], R S Barwal[1] and Mubashir Ali Rather[2]

[1] *Department of Animal Genetics and Breeding, College of Veterinary & Animal Science, G B Pant University of Agriculture & Technology, Pantnagar, Uttarakhand, India*
[2] *Senior Epidemiologist, Diseases Investigation Laboratory, Nowshara, Srinagar, Kashmir, India*

ABSTRACT

This study aimed to estimate breeding values, selection differentials, and response to selection for production and reproduction traits in Frieswal cattle. Data on 1,163 progeny records sired by 69 sires over nine years were collected and analyzed using Average Information Restricted Maximum Likelihood (AI-REML) and principal component analysis (PCA). The traits included age at sexual maturity (ASM), age at first calving (AFC), gestation period (GP), first calving interval (FCI), number of services per conception (NSPC), first dry period (FDP), first service period (FSP), test day peak milk yield (TDPY), first lactation 305-days milk yield (FL305-DMY), fat percentage (FP), and first lactation length (FLL). The response to selection and selection differential for the top 10 individuals showed that FL305-DMY had the highest selection differential (1,726.26 kg) and response to selection (611.10 kg). PCA revealed four principal components that explained 79.90% of the total variance, with PC1 associated with fertility-related traits (FLL, FCI, and FSP), PC2 with sexual maturity (ASM and AFC), PC3 with milk production traits (TDPY and FL305-DMY), and PC4 with milk composition traits (FP and FDP). Although hindered by non-digitized data and complex trait relationships, the study contributes to understanding genetic variability, informs breeding programs, and demonstrates the application of PCA in animal breeding, ultimately enhancing dairy production efficiency. The findings suggest that a multi-trait selection index is essential for achieving sustainable genetic improvement in dairy herds. By considering both production and reproduction traits, breeders can make informed decisions to improve the overall efficiency and sustainability of dairy production.

Keywords: *AI-REML, Breeding values, PCA, age at sexual maturity, age at first calving, gestation period, first calving interval, number of services per conception.*

1. INTRODUCTION

As global demand for cattle production intensifies, breeding strategies must evolve to ensure both high productivity and economic sustainability. Incorporating advanced statistical tools like principal component analysis (PCA) enhances the reliability of genetic evaluations, especially when tackling complex, interrelated traits [1]. Cattle breeding programs traditionally assess milk production and reproductive traits, including lactation yield, peak yield, age at first calving and calving interval which are critical indicators of performance and genetic merit [2]. Estimation of breeding values (BV) plays a central role in quantifying an animal's genetic potential, serving as a cornerstone for selection decisions and long-term herd improvement. PCA supports this process by distilling large datasets into independent principal components that minimize multicollinearity and highlight the traits most predictive of genetic merit [3]. Originally introduced by Pearson and refined by Hotelling in 1933 [4], PCA effectively reduces dimensionality while preserving crucial information [5]. Moreover, multivariate analyses empower breeders to identify genetically superior individuals, fostering progress across generations and amplifying genetic gain [6]. This study leverages PCA to estimate breeding values, selection differentials, and response to selection across production and reproduction traits in Frieswal cattle. The overarching goal is to refine selection models, improve prediction accuracy, and boost the economic potential of dairy herds [7].

2. Materials and Methods

2.1 Management and Feeding: Farmers rearing Frieswal Cattle adopted well-structured husbandry routines to enhance livestock productivity. Pregnant animals nearing parturition were housed separately to ensure comfort and monitoring. Upon calving, the newborn calves are immediately weaned and placed in separate pens. The calves were fed colostrum for the first three days, followed by whole milk for up to three months. From one month of age, their diet was gradually supplemented with green fodder, oil cakes, bran and mineral mixtures. Seasonal feeding patterns were adopted and during the Rabi season (September to March), animals were offered berseem, bran and oil cakes while in the Kharif season (April to August), the diet included sorghum, maize, bajra and berseem hay. Balanced concentrate mixtures and fresh water were provided throughout the year. Pregnancy status was confirmed 60 days post-artificial insemination through rectal palpation by an expert veterinarian, with re-insemination arranged when necessary. Milking was performed twice daily, either manually or using milking machines and the milk was utilized to fulfill either domestic needs or was sold in local markets.

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*Corresponding Author: ***Olympica Sarma***

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Routine health care measures, including deworming and vaccinations to protect livestock against prevalent diseases were followed by farmers.

2.2 Location: The progeny testing program is conducted in Udham Singh Nagar district, located in the Tarai region of Kumaon division, at an altitude of 28.9875º N and longitude of 79.4141º E, with an average elevation of around 830 meters. The region's fertile land supports intensive livestock rearing, with farmers growing fodder year-round.

2.3 Recording of observation: The observations recorded were animal number, date of birth, sire number, dam number, date of successful artificial insemination and dates of first calving, second calving, and drying off.

2.4 Date generated: The above recorded information was used to generate production and reproduction traits, including first lactation 305-days milk yield (FL305-DMY; volume of milk produced in a standard lactation of 305 days.), test day peak yield (TDPY; volume of milk produced by a cow on the test day during the lactation period.), fat percentage (FP; average percent of fat in milk in lactation recorded through automatic measuring devices by taking milk samples at certain defined intervals of lactation), first lactation length (FLL; period from the date of calving to date of drying off) for production, age at sexual maturity (ASM; It is the age when the cow shows sign of the heat for the first time), age at first calving (AFC; It is the age of cow when she gives birth to her first calf), first service period (FSP; period between first calving to subsequent successful service), number of services per conception (NSPC; number of services or inseminations per conception), gestation period (GP), first calving interval (FCI; time period between first and second calving) and first dry period (FDP; period from the date the cow dries off to the next calving) for reproduction.

2.5 Structure of Data: The data used in this study were from Frieswal cattle records. The traits included in the present study were age at sexual maturity (ASM), age at first calving (AFC), gestation period (GP), calving interval (CI), Number of services per conception (NSPC), first dry period (FDP), first service period (FSP), test gay peak milk yield (TDPY), first lactation 305-day milk yield (FL305D-MY), fat % (FP) and first lactation length (FLL). Data on 1163 progeny records sired by 69 sires over a period of nine years were collected from various field units of progeny testing under the All India Coordinated Research Project (AICRP) at Pantnagar, Uttarakhand, for the study.

2.6 Breeding Value estimation

Breeding values for various traits were estimated using the Average Information Restricted Maximum Likelihood (AI-REML) approach under an animal model. The analysis was performed using the WOMBAT, which accounts for fixed and random effects in the model. The statistical model used was as follows:

$y = Xb + Za + e$

Where:

y = vector of observed phenotypic records

b = vector of fixed effects (such as period, season, parity)

a = vector of random animal additive genetic effects

X and Z = incidence matrices relating records to fixed and random effects, respectively

e = vector of random residual effects

2.7 Selection Differential

The selection differential (S) was calculated as the difference between the mean of the trait in the selected individuals and the mean of the same trait in the overall population, as follows:

$S = \bar{X}_s - \bar{X}_0$

Where,

$\bar{X}_s$ = mean performance of selected individuals

$\bar{X}_0$ = mean performance of the overall group

Selection differential was computed separately for each trait of interest to quantify the intensity of selection applied.

2.8 Response to Selection

The expected genetic gain or response to selection (R) was estimated using the formula:

$R = h^2 \times S$

Where,

h^2 = heritability of the trait

S = selection differential

Heritability estimates used in the calculation were derived from the AI-REML analysis. This response indicates the expected improvement in the trait per generation due to selection.

2.9 Principal Component Analysis (PCA): Principal Component Analysis (PCA) was conducted using SPSS software, version 24 [8], on the estimated breeding values (EBVs) of 11 traits, namely age at sexual maturity (ASM), age at first calving (AFC), gestation period (GP), calving interval (CI), number of services per conception (NSPC), first dry period (FDP), first service period (FSP), test day peak milk yield (TDPY), first lactation 305-day milk yield (FL305D-MY), fat percentage (FP), and first lactation length (FLL). To assess the suitability of the data for PCA, the Kaiser-Meyer-Olkin (KMO) measure of sampling adequacy (> 0.5) and Bartlett's test of sphericity were employed ($P < 0.05$) [20, 21]. The KMO measure evaluates the proportion of variance in the data that might be caused by underlying factors, while Bartlett's test assesses the significance of the correlation matrix. Furthermore, only principal components (PCs) with eigenvalues greater than 1 were retained, as these components explain a significant amount of variance in the data. The eigenvalue of a PC represents the total variability of all the EBVs explained by the corresponding eigenvector, which in turn represents the correlation of each trait's variance with the principal component [9].

3. RESULTS AND DISCUSSION

3.1 Response to Selection and Selection Differential: The selection differential and response to selection were estimated for eleven economically important traits in dairy cattle. The analysis was conducted by selecting the top 10 individuals, and the results are summarized in Table 1. Among the studied traits, 305-DMY (FL305-DMY) showed the highest selection differential (1726.26 kg) with a corresponding response to selection of 611.10 kg, indicating substantial potential for genetic improvement in milk yield through selection. The high positive response is attributed to both a large selection differential and moderate heritability (0.354), reflecting effective selection pressure and genetic variability for this trait in the population. Traits related to reproductive performance, such as AFC and ASM, also exhibited high selection differentials (132.71 days and 129.70 days, respectively), with genetic gains of 61.97 days and 60.83 days. These positive responses suggest that selecting animals with superior milk yield may inadvertently result in animals with later sexual maturity and calving, which might not be desirable from a reproductive efficiency perspective. Therefore, these traits should be balanced with production traits during selection to avoid delayed reproduction. Conversely, FCI, NSPC, and FSP recorded negative selection differentials of -15.86 days, -0.28 services, and -18.87 days, respectively, resulting in corresponding negative responses of -6.25 days, -0.02 services, and -8.53 days. These improvements are favorable, as reductions in calving interval, service period, and the number of inseminations per conception enhance reproductive efficiency and reduce overall production costs. FP exhibited a slight negative selection differential (-0.40%) with an expected genetic decline of -0.16%. This suggests that selecting solely on the basis of milk yield may compromise fat content, emphasizing the need for a multi-trait selection index to maintain milk quality alongside yield improvement. Total digestible protein yield (TDPY), a trait indicative of an animal's ability to reach peak milk production early in lactation, showed a positive selection differential of 8.29 kg and an expected genetic gain of 2.06 kg. This indicates that selecting animals based on FL305-DMY also contributes positively to peak yield performance, which is desirable for efficient milk production. First lactation length (FLL) increased by 30.28 days in the selected individuals, with a corresponding response of 11.77 days, which exhibited a longer lactation period and may contribute to increased yield. Therefore, a balanced breeding approach incorporating both production and reproduction traits is essential for achieving sustainable genetic improvement in dairy herds.

Table 1. Predicted response to selection and selection differential

Traits	Population Mean	Selected Mean (Top 10 Individuals)	Selection Differential (S)	Response To Selection (R)
ASM	810.80	940.50	129.70	60.83
AFC	1089.19	1221.90	132.71	61.97
GP	278.39	281.40	3.01	0.78
FCI	373.26	357.40	-15.86	-6.25
NSPC	1.48	1.20	-0.28	-0.02
FSP	94.87	76.00	-18.87	-8.53
FDP	62.54	61.10	-1.44	-0.12
FL305-DMY	3066.20	4792.47	1726.26	611.10
TDPY	12.80	21.09	8.29	2.06
FP	3.48	3.08	-0.4	-0.16
FLL	310.72	341.00	30.28	11.77

1.2 Breding Value: The minimum, maximum, standard errors, accuracy, and range of breeding values for production and reproduction traits of Frieswal cows are presented in Table 2. The observed breeding value range was very high for FL305-DMY, ASM, and AFC, moderate for FLL, FSP, and FCI, whereas low for FP, GP, and NSPC. The substantial genetic variability for FL305-DMY, ASM, and AFC offers an opportunity for enhancement through selective breeding. High genetic variability for FL305-DMY was also reported by previous studies [10, 11, 12]. Furthermore, a high range for FL305-DMY and a low range for NSPC and CI in Holstein Friesian cattle were observed. Additionally, moderate (0.37) to very high (0.86) accuracy was in consonance with the findings of [7].

Table 2. Minimum, maximum, range and accuracy of predicted breeding values for production and reproduction traits in frieswal cows

Traits	Minimum	Standard Error	Accuracy	Maximum	Standard Error	Accuracy	Range
FL305-DMY	-1264.5	32.02	0.69	1094.95	147.91	0.66	2359.45
TDPY	-2.91	0.16	0.86	4.62	0.69	0.81	7.53
FP	-1.03	0.06	0.68	1.14	0.2786	0.66	2.17
FLL	-23.42	7.80	0.85	16.46	10.12	0.81	39.88
ASM	-164.14	11.52	0.75	137.99	50.01	0.71	302.13
AFC	-159.29	19.76	0.75	146.86	58.00	0.72	306.15
FSP	-25.35	1.44	0.69	17.62	4.08	0.66	42.97
NSPC	-0.93	0.02	0.39	1.08	0.1465	0.37	2.01
GP	-11.39	7.24	0.42	7.5	8.74	0.42	18.89
FCI	-22.74	9.68	0.69	17.09	11.90	0.69	39.83
FDP	-5.24	1.52	0.81	4.48	2.844	0.81	9.72

3.3 Principal Component Analysis: Principal Component Analysis (PCA) was conducted on breeding value estimates of 11 performance traits (ASM, AFC, GP, FCI, NSPC, FDP, FSP, TDPY, FL305-DMY, FP, and FLL) of Frieswal cows. The Kaiser-Meyer-Olkin (KMO) measure of sampling adequacy yielded a mean value of 0.610 (Table 3), indicating that the correlations between variables are strong enough to support PCA; therefore, the data are suitable for PCA. However, higher KMO measures of sampling adequacy (0.867, 0.692, and 0.669) were reported by previous studies [13, 14, 15] while conducting PCA with breeding values of production and reproduction traits of different cattle genetic resources, whereas a lower KMO value (0.086) was reported by [7] in Holstein cattle. Furthermore, the overall significance of the correlation matrix was assessed using Bartlett's test of Sphericity, yielding a highly significant chi-square value of 993.598 ($P < 0.01$), which also indicated the suitability of the data for PCA. The highly significant Bartlett's test of Sphericity ($P < 0.01$) in different cattle genetic resources was also observed by other studies [7, 13, 14, 15].

The communality analysis shows that ASM, AFC, TDPY, MY, FLL, FCI, and FSP demonstrate very high communalities (> 0.75), whereas GP, FP, NSPC, and FDP exhibit moderate to high communalities (0.50 to 0.74). The range of high to very high communalities indicates that the traits were strongly represented by the extracted factors, validating the factor solution and demonstrating a robust representation of the data structure. High communalities were also observed by previous studies [7, 3] while performing PCA of breeding values of cattle genetic resources.

The results of the Principal Component Analysis (PCA) for Frieswal cattle are summarized in Table 3, which outlines the total variance explained by each component. The first four principal components (PC1 to PC4) with eigenvalues greater than 1 were extracted, collectively accounting for 79.90% of the total variance. Specifically, PC1, PC2, PC3, and PC4 explained 34.778%, 23.077%, 11.799%, and 10.246% of the variance, with corresponding eigenvalues of 3.826, 2.538, 1.298, and 1.127, respectively.

These findings suggest that the first four components effectively captured the underlying data structure and retained most of the information (Fig. 1). Notably, PC1 and PC2 together explain 57.855% of the total variance, indicating their strong influence and the importance of the traits they represent in understanding genetic diversity in the Frieswal cattle population under study. This substantial contribution of the initial components aligns with findings from other studies [13, 14, 16, 7, 17] on different cattle breeds. Similarly, a study on Can cattle observed that two principal components of breeding values accounted for 73.4% of the total variance [18]. Another study reported that the first and second components accounted for 55.15% and 13.07% (68.22%) of the total variation of breeding values [17].

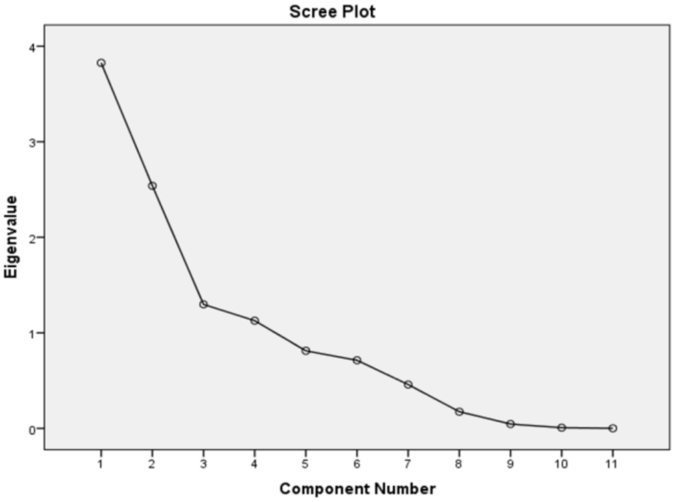

Fig. 1 Scree plot showing component numbers with Eigen values

Table 3. Total variance explained by different components in frieswal cattle

Component	Eigen values	Variance proportion	Cumulative variance proportion
PC1	3.826	34.778	34.778
PC 2	2.538	23.077	57.855
PC 3	1.298	11.799	69.654
PC 4	1.127	10.246	79.900
PC 5	0.812	7.382	87.282
PC 6	0.713	6.481	93.763
PC 7	0.458	4.167	97.930
PC 8	0.174	1.584	99.514
PC 9	0.046	0.415	99.929
PC 10	0.007	0.064	99.993
PC 11	0.001	0.007	100.000
Kaiser-Meyer-Olkin	0.610		
Chi-Square	993.598 with DF 55		
Bartlett's test of Sphericity	0.000		

3.4 The correlation coefficients: The correlation coefficients between the Estimated Breeding Values (EBVs) of the traits under study and the principal components (PCs) in Frieswal cattle reveal distinct patterns of correlation between the traits and the PCs (Table 4). PC1 is strongly positively correlated with first lactation length (0.969), first calving interval (0.963), and first service period (0.939), indicating that these traits are closely related to the first principal component, which may be associated with fertility-related traits. In contrast, PC2 shows strong positive correlations with age at sexual maturity (0.928) and age at first calving (0.933), and a notable correlation with the number of services per conception (0.722), suggesting that PC2 is largely associated with sexual maturity. PC3 demonstrates strong positive correlations with test day peak milk yield (0.822) and milk yield (0.772), indicating that this component is related to milk production traits.

Furthermore, PC4 exhibits strong positive correlations with fat percentage (0.738) and first dry period (0.775), suggesting that this component is associated with milk composition traits. These results indicate that the principal components capture distinct aspects of milk production and reproduction, allowing for a more nuanced understanding of the relationships between these traits in Frieswal cattle.

Moreover, PC1 can be considered a genetic indicator of reproduction, as it can identify animals that are genetically superior for traits such as first calving interval, first lactation length, and first service period. To achieve the goal of increasing first lactation 305-day milk yield, it is necessary to consider positive breeding values for this trait. Simultaneously, decreasing age at sexual maturity, calving interval, and age at first calving is desirable. Therefore, PC3 can be considered a genetic index for production and reproduction because it detects genetically superior animals for traits such as first lactation 305-day milk yield, test day peak milk yield, first calving interval, age at sexual maturity, and age at first calving. Previous studies have reported that PC1 can be a genetic index for reproduction that promotes animals genetically superior for calving interval [7, 18]. The positive correlation between calving interval and the first component is similar to the findings of other studies [17, 19]. The positive correlation between the number of services per conception and PC1 was also observed by [7]. The complex relationship between traits and PCs is in consonance with the findings of [14, 15], reinforcing the utility of PCA in disentangling complex trait relationships and informing genetic improvement programs.

Table 4. Correlation coefficients between ebv of the production and reproduction traits with pc's in frieswal cattle

Trait	PC1 (34.778)	PC2 (23.077)	PC3 (11.799)	PC4 (10.246)	Communalities
ASM	0.063	0.928	-0.080	0.138	0.891
AFC	0.005	0.933	-0.101	0.166	0.908
GP	-0.315	0.334	0.590	0.145	0.580
TDPY	-0.129	-0.226	0.822	-0.199	0.784
FL305-DMY	-0.108	-0.447	0.772	-0.198	0.846
FP	0.090	0.128	-0.168	0.738	0.598
FLL	0.969	0.100	-0.082	0.017	0.955
FCI	0.963	0.072	-0.089	0.198	0.980
FSP	0.939	-0.042	-0.294	0.123	0.984
NSPC	0.061	0.722	-0.135	-0.317	0.643
FDP	0.125	-0.06	-0.027	0.775	0.620

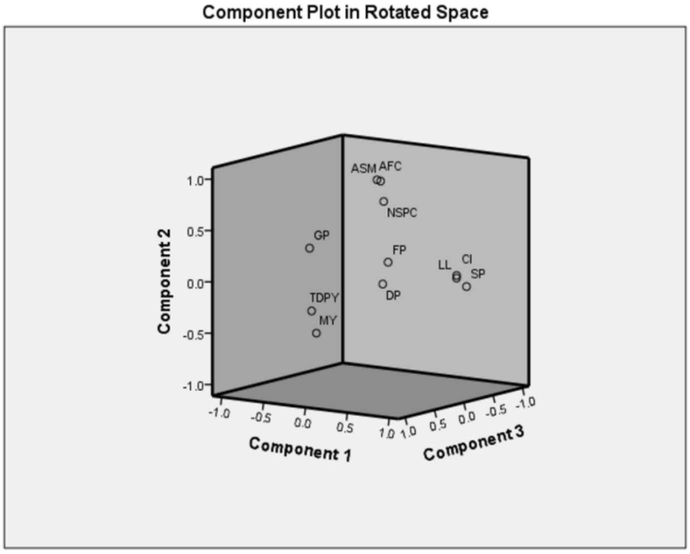

Fig. 2 rotated component plot

4. CONCLUSION

This study highlights the importance of genetic improvement in the cattle population under study through selective breeding, emphasizing the need to balance production and reproduction traits. Furthermore, the principal component analysis revealed distinct patterns of correlation between traits and components, capturing different aspects of milk production, fertility, sexual maturity, and milk composition. Therefore, a multi-trait selection index based on PC3 is recommended to maintain milk quality alongside yield improvement, ensuring efficient and sustainable dairy production.

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6. Conflict of interests: The authors declare that they have no conflict of interest.

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