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Dimensionality reduction of part milk yield in crossbred cattle using Principal Component Analysis

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ABSTRACT: This study employed principal component analysis to examine part milk yield records from first lactation in crossbred cows, aiming to enable early selection decisions while reducing data dimensionality. Monthly milk yield measurements were collected from 529 crossbred cattle (62.5% Holstein-Friesian $\times$ 37.5% Sahiwal) over three decades (1990–2019) at Govind Ballabh Pant University of Agriculture and Technology, Pantnagar. Ten lactation variables representing 30-day intervals up to 300 days were analyzed using varimax rotational principal component analysis with Kaiser normalization. Two principal components emerged with eigenvalues exceeding 1, collectively explaining 77.64% of total variance. Component 1 (43.24% variance) comprised early lactation yields (days 31–120), while Component 2 (34.40% variance) represented late lactation yields (days 211–300). Varimax rotation effectively differentiated component loadings, with phenotypic correlations among traits ranging from 0.41 to 0.87, confirming strong positive associations across lactation periods. Communalities ranged from 0.52 to 0.86 across traits. The findings demonstrate that principal component analysis effectively captures lactation patterns while substantially reducing variable complexity, offering practical applications for genetic evaluation programs in crossbred cattle.

Key words: Crossbred cow, lactation, milk yield, principal component analysis

The intensification of dairy production systems has necessitated the adoption of sophisticated statistical methodologies to interpret the voluminous and complex performance data generated by modern breeding operations. Among these, multivariate analysis techniques offer a distinct advantage over univariate approaches by considering the covariances and correlations inherent among biological traits. Principal component analysis (PCA) serves as a particularly powerful tool in this domain, functioning as a dimensionality reduction technique that transforms a set of correlated response variables into a smaller number of uncorrelated principal components. This transformation preserves the maximum possible proportion of original variation, thereby enabling the visualization of relationships between observations and variables while facilitating the identification of latent, biologically meaningful patterns within high-dimensional datasets (Vargas *et al.*, 2018; Kramarenko *et al.*, 2022). India maintains its position as the preeminent global producer of milk, with

annual output reaching 247.87 million tonnes during 2024–25, reflecting a consistent growth trajectory from the 239.30 million tonnes recorded in the previous fiscal year (BAHS, 2025). This sustained increase in production has been accompanied by a notable shift in the composition of the milch herd. Crossbred cattle, which combine the genetic potential of temperate dairy breeds with the adaptive hardiness of indigenous stock, now contribute disproportionately to national output. Comparative productivity estimates indicate that crossbred cows produce an average of 8.12 kg/day, substantially exceeding the 4.01 kg/day observed in indigenous nondescript cattle (Singh, 2016). This productivity differential underscores the strategic importance of crossbreeding as an intervention to enhance dairy sector efficiency, improve household incomes, and ensure nutritional security in rural economies. Despite the recognized productive advantages of crossbred cattle, a significant gap persists in the scientific literature regarding the detailed characterization of their first lactation performance

using part lactation records. Conventional selection and evaluation protocols typically rely on complete 305-day milk yields. However, the extended duration required to obtain such records delays genetic progress and prolongs the generation interval. Monthly or fortnightly milk yields offer a pragmatic alternative, potentially enabling earlier selection decisions and more timely culling of inferior animals. Researchers have demonstrated the utility of part lactation yields for predicting total lactation output and for sire evaluation in dairy cattle (Mundhe *et al.*, 2018; Girimal *et al.*, 2023), yet comprehensive multivariate analyses focusing specifically on first lactation performance in crossbred populations remain sparse. The application of PCA to delineate lactation performance is not merely a statistical exercise but is biologically justified by the inherent correlation structure among production traits. For instance, peak yield, persistency of lactation, and monthly production intervals are often genetically and phenotypically intercorrelated, creating redundancy in selection indices. Studies in related species have successfully employed PCA to reduce this redundancy, identify independent biological biotypes, and link early growth traits to subsequent productive life (Dadoudis, 2012). Furthermore, principal component regression techniques have been utilized to predict lifetime performance based on initial part-lactation records (Khan *et al.*, 2013). The present investigation addresses the identified research gap by applying PCA to first lactation part milk yields in crossbred cattle. The specific objectives are: to delineate the principal components that account for the majority of variance in monthly yield records, to facilitate early selection decisions by identifying the most informative periods of the lactation curve and to characterize distinct lactation patterns and potential biotypes within the crossbred population through effective data reduction and visualization.

MATERIALS AND METHODS

Research design

The investigation utilized historical performance records from 529 crossbred cows (62.5% Holstein-Friesian, 37.5% Sahiwal) maintained at the dairy

cattle farm of Govind Ballabh Pant University of Agriculture and Technology, Pantnagar, over a 30-year period (1990–2019). First lactation milk yields were recorded at monthly intervals across 300 days, generating ten distinct variables: yields for days 1-30, 31-60, 61-90, 91-120, 121-150, 151-180, 181-210, 211-240, 241-270 and 271-300.

Statistical methods

Phenotypic correlations among production traits were computed following established methods (Snedecor and Cochran, 1967). Principal component analysis was implemented as the primary analytical technique, aiming to construct composite variables that capture maximum variation from the original dataset. The analytical sequence incorporated validity assessments through Kaiser-Meyer-Olkin (KMO) measure of sampling adequacy and Bartlett's test of sphericity at 1% significance threshold. Component retention followed Kaiser's criterion, retaining components with eigenvalues exceeding unity (Johnson and Wichern, 1982). Sampling adequacy was evaluated using Kaiser's Measure of Sampling Adequacy (MSA), with values below 0.5 considered unacceptable. The mathematical formulation transformed original multivariate observations ($X_1, X_2, \dots, X_n$) into uncorrelated component scores ($Y_1, Y_2, \dots, Y_n$):

$$Y_1 = a_{11}X_1 + a_{12}X_2 + \dots + a_{1n}X_n$$

$$Y_2 = a_{21}X_1 + a_{22}X_2 + \dots + a_{2n}X_n$$

$$Y_n = a_{n1}X_1 + a_{n2}X_2 + \dots + a_{nn}X_n$$

Varimax orthogonal rotation was applied to maximize variance distribution across the factor pattern matrix, enhancing interpretability of extracted components. All computations were executed using SPSS Version 24 factor analysis module.

RESULTS AND DISCUSSION

Principal Component Analysis

The Kaiser-Meyer-Olkin (KMO) measure of sampling adequacy was 0.89, indicating that the sample was suitable for factor analysis. The Bartlett's test of sphericity yielded a chi-square value

of 5233.11 with 45 degrees of freedom (df), and the significance level (p-value) was 0.00. This result was highly significant ($p < 0.05$), confirming that the correlation matrix was not an identity matrix and that factor analysis could proceed. Application of the Kaiser Rule Criterion (Johnson and Wichern, 1982) resulted in the selection of two components with eigenvalues greater than 1 (Table 1). The first two components collectively explained 77.64% of the total variance. The first principal component (PC1) exhibited an eigenvalue of 6.60, accounting for 66.02% of the total variance (Table 1). PC1 primarily described milk yield for 30 days, milk yield from 31 to 60 days, milk yield from 61 to 90 days, and milk yield from 91 to 120 days. The second component (PC2) had an eigenvalue of 1.16, contributing 11.61% of the variance and described milk yield from 181 to 210 days, 211 to 240 days, 241 to 270 days, and 271 to 300 days. Remaining components with eigenvalues below 1 contributed progressively less to the variance, with the third component having an eigenvalue of 0.70 (7.01%), the fourth contributing 0.44 (4.42%), and so on. The scree plot (Figure 1) depicted the total number of components and confirmed that retaining two components was appropriate, as the third and subsequent components contributed minimally to explaining the total variance. These findings aligned with the initial eigenvalues and cumulative variance explained.

Factor Analysis

Table 3 presents the principal component estimates

for different traits following varimax rotation. After rotation, the variance was more evenly distributed, with 43.23% attributed to component 1 and 34.40% to component 2. Component 1 demonstrated high loadings for MY 30 days (0.78), MY 31 to 60 days (0.87), MY 61 to 90 days (0.87), and MY 91 to 120 days (0.85), indicating its association with early lactation stages. Component 2 showed strong associations with later lactation stages, reflected by high loadings for MY 181 to 210 days (0.73), MY 211 to 240 days (0.84), MY 241 to 270 days (0.88), and MY 271 to 300 days (0.82). The rotated component matrix (Figure 2) illustrated the pattern of associations among variables and the two components. Communality estimates (Table 2) ranged from 0.52 (MY 151 to 180 Days) to 0.86 (MY 241 to 270 Days). Variables with high communalities (0.80 to 0.86) were well-explained by the extracted components. MY 151 to 180 days exhibited the lowest communality (0.52), suggesting that this variable may possess unique characteristics not fully captured by the factor model. After varimax rotation, communality estimates for component 1 ranged from 0.23 (MY 271 to 300 Days) to 0.87 (MY 31 to 60 Days) (Table 3).

Phenotypic Correlations

The estimated phenotypic correlations between milk production traits were positive, ranging from 0.41 (MY 151 to 180 Days to MY 271 to 300 Days) to 0.87 (MY 91 to 120 Days and MY 121 to 150 Days) (Table 4), indicating that changes in one trait would alter the expression of other traits.

Table 1: Total variance explained by different components in crossbred cattle

S.no.	Initial Eigenvalues			Extraction Sums of Squared Loadings			Rotation Sums of Squared Loadings		
	Total	% of Variance	Cumulative %	Total	% of Variance	Cumulative %	Total	% of Variance	Cumulative %
1	6.60	66.02	66.02	6.60	66.02	66.02	4.32	43.23	43.23
2	1.16	11.61	77.64	1.16	11.61	77.64	3.44	34.40	77.64
3	0.70	7.01	84.65						
4	0.44	4.42	89.07						
5	0.36	3.61	92.68						
6	0.20	2.02	94.71						
7	0.19	1.90	96.61						
8	0.12	1.26	97.88						
9	0.12	1.22	99.10						
10	6.60	66.02	66.02						

Principal component analysis

The KMO value of 0.89 obtained in this investigation was substantially higher than the minimum required threshold of 0.5 (Vohra *et al.*, 2015; Sinha *et al.*, 2023), confirming that the data were adequate for factor analysis. This value was comparable to the findings of Ratwan *et al.* (2017), who reported a KMO value of 0.82 for lifetime performance traits in Jersey crossbred cattle. However, the present KMO value was higher than those reported by Vohra *et al.* (2015), Sarma *et al.* (2024), and Kaur *et al.* (2025), who documented KMO values of 0.74, 0.69, and 0.58, respectively, for production and reproduction traits in crossbred cattle populations. The significant Bartlett's test result further confirmed the suitability of the correlation matrix for factor analysis, consistent with the requirement that a p-value less than 0.05 indicates the correlation matrix is not an identity matrix. The selection of two principal components with eigenvalues exceeding 1 followed the Kaiser

Table 2: Communalities for different traits in crossbred cattle

Traits	Extraction
MY 30 Days	0.66
MY 31 to 60 Days	0.83
MY 61 to 90 Days	0.85
MY 91 to 120 Days	0.84
MY 121 to 150 Days	0.80
MY 151 to 180 Days	0.52
MY 181 to 210 Days	0.79
MY 211 to 240 Days	0.84
MY 241 to 270 Days	0.86
MY 271 to 300 Days	0.73

MY= Milk yield

Table 3: Estimates of principal components for different traits using varimax rotation

Traits	Component 1	Component 2
MY 30 Days	0.78	0.23
MY 31 to 60 Days	0.87	0.26
MY 61 to 90 Days	0.87	0.30
MY 91 to 120 Days	0.85	0.34
MY 121 to 150 Days	0.78	0.42
MY 151 to 180 Days	0.56	0.45
MY 181 to 210 Days	0.50	0.73
MY 211 to 240 Days	0.36	0.84
MY 241 to 270 Days	0.27	0.88
MY 271 to 300 Days	0.23	0.82

Table 4: Phenotypic correlation between traits

Traits	MY 30 Days	MY 31 to 60 Days	MY 61 to 90 Days	MY 91 to 120 Days	MY 121 to 150 Days	MY 151 to 180 Days	MY 181 to 210 Days	MY 211 to 240 Days	MY 241 to 270 Days	MY 271 to 300 Days
MY 30 Days	1	0.82**	0.67**	0.62**	0.58**	0.45**	0.52**	0.48**	0.47**	0.43**
MY 31 to 60 Days	0.82**	1	0.83**	0.76**	0.71**	0.51**	0.58**	0.55**	0.51**	0.48**
MY 61 to 90 Days	0.67**	0.83**	1	0.86**	0.78**	0.56**	0.63**	0.56**	0.52**	0.50**
MY 91 to 120 Days	0.62**	0.76**	0.86**	1	0.87**	0.59**	0.68**	0.60**	0.53**	0.47**
MY 121 to 150 Days	0.58**	0.71**	0.78**	0.87**	1	0.67**	0.73**	0.63**	0.57**	0.48**
MY 151 to 180 Days	0.45**	0.51**	0.56**	0.59**	0.67**	1	0.66**	0.54**	0.47**	0.41**
MY 181 to 210 Days	0.52**	0.58**	0.63**	0.68**	0.73**	0.66**	1	0.81**	0.70**	0.61**
MY 211 to 240 Days	0.48**	0.55**	0.56**	0.60**	0.63**	0.54**	0.81**	1	0.81**	0.66**
MY 241 to 270 Days	0.47**	0.51**	0.52**	0.53**	0.57**	0.47**	0.70**	0.81**	1	0.77**
MY 271 to 300 Days	0.43**	0.48**	0.50**	0.47**	0.48**	0.41**	0.61**	0.66**	0.77**	1

Correlation coefficient (below diagonal) with their standard error (above diagonal)

**Correlation is significant at the 0.01 level, *Correlation is significant at 0.05 level

Rule Criterion (Johnson and Wichern, 1982). The cumulative variance explained by the first two components (77.64%) was within the range observed in previous studies. Fraga *et al.* (2016) reported that the first two PCs accounted for 89.40% of total variation in crossbred Holstein $\times$ Zebu cows. Similarly, Ratwan *et al.* (2017) found that the first two components yielded 97.24% variance in Jersey crossbred cattle, with PC1 accounting for 90.49% of the variance. Mello *et al.* (2020) observed that the first three principal components explained more than 90% of total variation for functional traits in Red Sindhi cattle. Sanad *et al.* (2021) extracted four PCs in Holstein cattle, with percent variance explained as 44.0%, 38.30%, 17.60%, and 0.20%,

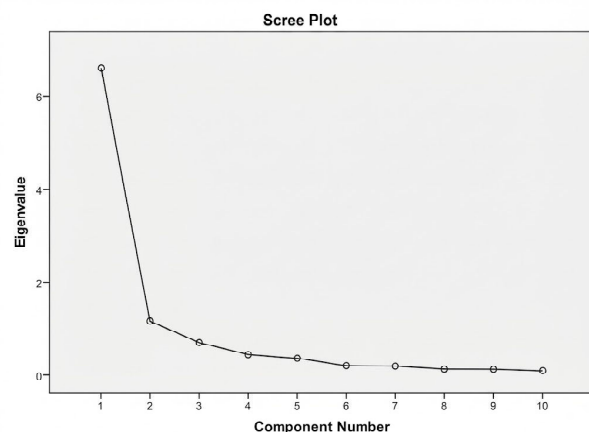


Fig. 1: Scree plot depicting component number with eigen value

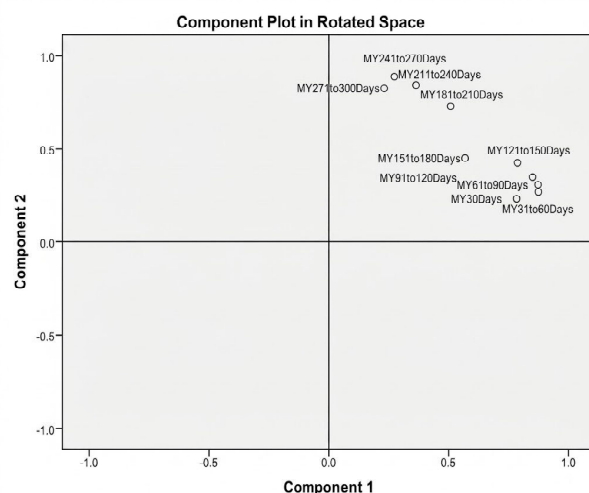


Fig. 2: Component plot in rotated space depicting different traits in crossbred cattle

respectively. Sarma *et al.* (2024) reported that the first three PCs accounted for 35.54%, 23.37%, and 15.38% of variance, with a cumulative variance of 74.30% in Frieswal cattle. Kaur *et al.* (2025) reported that four components explained 77.49% of total variance in crossbred cattle.

Factor analysis

The varimax rotation facilitated interpretation by differentiating high from low loadings across factors. After rotation, the variance distribution became more balanced between components, with 43.23% for component 1 and 34.40% for component 2. These findings were consistent with Dominguez-Castaño *et al.* (2020), who reported that the first factor had high positive loadings correlated with all production traits, indicating that the factor expressed the amount of milk produced. Kaur *et al.* (2024) similarly reported that component 1 captured overall milk production, with highest loadings for MY305D (0.95), MY300D (0.95), FLMY (0.85), and PY (0.78). Sarma *et al.* (2024) reported that PC2 had high loads on test day peak yield and 305 days milk yield. The communality estimates indicated that most variables were well-represented by the extracted components. The high communalities (0.80 to 0.86) suggested that the factors explained substantial portions of variance in corresponding variables, while lower values indicated areas requiring further exploration. Ratwan *et al.* (2017) reported communalities ranging between 0.95 and 0.99 for first principal component. Moawad and Osman (2018) reported communalities ranging from 0.32 to 0.89 in Holstein Friesian cattle. Dominguez-Castaño *et al.* (2020) reported communalities from 0.01 to 0.97. Sarma *et al.* (2024) documented communalities from 0.24 to 0.93, while Kaur *et al.* (2025) reported values from 0.53 to 0.99 in Frieswal cattle. The varimax rotated coefficients in this study showed that component 1 coefficients ranged from 0.23 to 0.87, while component 2 coefficients were comparatively lower. Ratwan *et al.* (2017) found rotated coefficients for first principal component ranging from 0.90 to 0.43. Sanad *et al.* (2021) described first principal component coefficients ranging from -0.43 to 0.92 and second component coefficients from -0.07 to 0.8. Kaur *et al.* (2024)

reported coefficients for components 1, 2, 3, and 4 ranging from -0.18 to 0.95, -0.01 to 0.96, -0.08 to 0.69, and -0.009 to 0.25, respectively.

Phenotypic correlation between traits

The positive phenotypic correlations ranging from 0.41 to 0.87 indicated strong positive associations among milk production traits. These findings contrasted with Moawad and Osman (2018), who found correlation coefficients ranging from -0.02 to 0.90, with negative correlations indicating that increased calving interval would decrease days in milk. Dominguez-Castaño *et al.* (2020) estimated phenotypic correlations for production traits ranging from 0.67 to 0.90 in Holstein cattle.

CONCLUSION

Principal component analysis successfully reduced the dimensionality of first lactation part milk yield records in crossbred cattle, identifying two distinct components that explained 77.64% of total variation. The strong communality estimates (0.52–0.86) confirmed adequate representation of most lactation intervals, with the mid-lactation period (days 151–180) showing the lowest common variance, suggesting unique physiological regulation during this transitional phase. These findings have significant practical implications for dairy genetic improvement programs. The component structure enables breeders to focus on early lactation records as reliable predictors of overall productive capacity, potentially reducing the recording period from 300 to 120 days and accelerating selection decisions. This dimensional reduction facilitates streamlined data collection protocols without substantial loss of information, lowering operational costs in large-scale breeding operations. Furthermore, the identified components can serve as composite selection criteria in multi-trait evaluation models, enabling simultaneous improvement of both peak production and lactation persistency, two economically critical traits with distinct genetic architectures. The methodological framework demonstrated here provides a template applicable to other livestock species and production systems, supporting evidence-based breeding decisions in

resource-constrained environments where complete lactation records are often unavailable. Future research should validate these component structures across different genetic groups and environmental conditions, and explore their utility in genomic prediction models for enhanced accuracy of early selection.

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