

## Review Article

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# Association detection and PCA analysis for seed yield and its contributing traits in mung bean (*Vigna radiata* L.) wilczek



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## ABSTRACT

**Background:** The protein in the Mungbean contains a better quantity of essential amino acids, including leucine, phenylalanine, valine, isoleucine, tryptophan, methionine, arginine, and lysine.

**Methods:** A total of 35 Mungbean genotypes, including four standard checks were shown in Randomized Block Design (RBD) with three replications during kharif, 2023.

**Result:** The high heritability accompanied by high genetic advance was recorded for biological yield per plant, plant height, seed yield per plant, days to 50% flowering, and pods per cluster. It indicated that these traits are governed largely by additive gene action and selection. Seed yield per plant had shown a highly significant positive correlation pods per cluster, pods per plant, seed per pod, 100-seed weight, and biological yield per plant. NDM 95-2 was got highest position followed by PMS8 and KM 2328 for profuse podding and seed yield. The PCA results highlight the significant role of a few key components in explaining the variation among traits. F1 and F2 together account for over 54% of the total variance, primarily capturing productivity and yield-related traits. Overall, the results breeders prioritize traits like SYP, PPC, and BYP to enhance crop productivity effectively.

**Keywords:** PCA, Heritability, Correlation, Genetic advance and Path analysis, Mungbean

## INTRODUCTION

Mungbean (*Vignaradiata* L.) Wilczek, is a diploid ( $2n = 2x = 22$ ) legume crops that belongs to species of Fabaceae, subfamily Papilionaceae, and the tribe Viciae with a the genome size of about (497 to 579 Mb). The mature seeds provide an invaluable source of digestible protein for humans in places where meat is lacking or where people are mostly vegetarian (AVRDC, 2012). It has originated from the Indian Subcontinent (Vavilov, 1926 and Zukoveskij, 1962). It contains 25.0 percent proteins with all essential amino acids, which is almost three times more than that of cereals (Saini *et al.*, 2010). The major constraints in achieving higher yields are lack of exploitable genetic variability, absence of suitable ideotype for different cropping system, poor harvest index susceptibility to biotic and abiotic stresses, non-availability of quality seeds of improved varieties and a narrow genetic base due to repeated usage of few parents with high degree of relatedness in crossing programme (Kumar *et al.* 2004). The genetic yield potential of present varieties of mungbean can be enhanced by restructuring of plant type (Nath *et al.* 2018). This can be achieved by using a diverse gene pool in a hybridization programme (Singh and Dikshit 2003).

Contribution of yield contributing characters, it is essential to know the correlation of the various characters along with path coefficients. Multivariate techniques are an efficient tool for interpreting the genetic variation present in the germplasm,

selecting it and develop strategies to incorporate useful diversity in their breeding programmes. (Das *et al.* 2024). principal component analyses are commonly used to estimate quantitative trait variability and identify superior genotypes. (Jeberson *et al.*, 2017). Therefore, the present investigation to assess the genetic diversity using principal component analysis, on the basis of agronomical characters, classify the germplasm in a similar group and identify the superior genotypes for mungbean improvement.

## MATERIALS AND METHODS

### Study area description and Trial management

The study was conducted at the Faculty of Agriculture Experimental Field (Genetics and Plant Breeding), Acharya Narendra Deva University of Agriculture and Technology, Ayodhya (U.P.) India during *kharif*, 2023. Agriculture Experimental Field is located 24.47° to 26.56° N latitude and 82.12° to 83.98° E longitude at an elevation of of 113 m above from sea level in the Gangetic Alluvial Plains of Eastern Uttar Pradesh. The climate of the experimental site is semi-arid with a cold winter and hot summer. Metrological data are also depicted in Fig-1. A total of 35 Mungbean genotypes, including four standard checks namely IPM2-3, MH1142, IPM512-1, and PANTM4 were Randomized Block Design (RBD) with three replications. The gross plot size for the treatment was set at 7.20 m<sup>2</sup> (6 m x 4 m x 0.30 m).

There were six rows on a 4 m by 0.30 m plot, with 30 cm separating rows and 10 cm separating plant to plant.

Data collected: Data were collected for the following key traits, including days to flowering, which was defined as the number of days from planting until 50% of the plants in a given plot had produced flowers.

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Additionally, days to maturity were recorded as the duration from sowing to the point at which 90% of the plants achieved physiological maturity. Observations other than phenological traits, data were recorded on the basis of five plants randomly selected from each entry for plant height (cm),

Number of clusters per plant, number of pods per cluster, number of pods per plant, number of seeds per pod, 100 - seed weight (g), biological yield per plant (g), harvest index (%) and seed yield per plant (g). Statistical analysis: Data were analyzed by one-way ANOVA using the statistical software IBM SPSS. The correlation (Al-ji-bouriet *et al.*, 1958), path coefficient analysis (Dewey and Lu, 1959), heritability (Robinson *et al.*, 1949), genetic advance (Allard, 1960) and analysis of various genotypes was performed with Windostat Version 9.2. Principal Component Analysis (PCA): *Correlation matrix* was used for principal component analysis was performed with XLSTAT 2024.2.2.

$$C1 = b11(X1) + b12 + \dots + b1p(Xp)$$

Here, C1 represents the subject's score on principal component 1, which is the first component extracted;  $b1p$  is the regression coefficient, or weight, for the observed variable  $p$  that was utilized to create principal component 1; and  $Xp$  is the subject's score on the observed variable.

## RESULTS AND DISCUSSION

### Analysis of Variance (ANOVA)

ANOVA results indicated significant genotypic effects on the mean sum of squares for All traits studied (Table-1) indicated the existence of sufficient variability and hence desirable improvement can be brought through selection. Findings agreement with Kumar *et al.* (2020) and Lal *et al.* (2022).

### Genetic components of variation and descriptive statics

Genetic parameters such as genotypic and phenotypic coefficient of variation (GCV and PCV), heritability, genetic advance as percent of the mean, skewness and kurtosis were presented in Table 2. The GCV which shows the extent of genetic variability for the traits studied varied from 8.18% to 18.10% and it was found to be the maximum for biological yield per plant (18.10%) followed by plant height (17.53%), seed yield per plant (17.05%) and pods per plant (12.99%). The values of PCV were ranged from 8.61% to 19.24% with a maximum value of PCV observed for biological yield per plant (19.24%) followed by seed yield per plant (18.74%), plant height (18.25%), and pods per cluster (16.23%). Similar results were reported by Patel *et al.* (2023) and Jain *et al.* (2024). It was observed that PCV was higher than the respective GCV for all the traits exhibiting the role of environment in total variance. The narrow range of difference between PCV and GCV for days to maturity (8.18% and 8.61%), plant height (17.53% and 18.25%), biological yield per plant (18.10% and 19.24%), days to 50% flowering (12.73% and 13.96), harvest index (9.84% and 11.22%), pods per plant (11.08 and 12.68%) and seed yield per plant (17.05% and 18.74%). explained that these traits are governed largely by genetic factors with little role of environmental effects. GCV indicates the extent of degree of genetic variation but the amount of heritable portion of the total variation can only be determined by the heritability and genetic advance estimates. Heritability in a broad sense was estimated to be high for plant height (92.00%), days to maturity (90.00%), biological yield per plant (88.00%), days to 50% flowering (83.00%) and seed yield per plant (82.00%), moderate for pods per plant (76.00%), harvest index (76.00%) and pods per cluster (64.00%), while

cluster per pods (46.00%) recorded low estimate of heritability. High estimates of heritability indicated that improvement through selection for these traits would be rewarding. Similar results were also reported by Joshi *et al.* (2021), Singh *et al.* (2021) and Lal *et al.* (2022).

Heritability suggests the effectiveness of selection on the basis of phenotypic performance only. Heritability estimates in association with the genetic advance were observed to be more useful for effective selection (Johnson *et al.* 1955). The high heritability accompanied with high genetic advance was recorded for biological yield per plant, plant height, seed yield per plant, days to 50% flowering, and pods per cluster.

It indicated that these traits are governed largely by additive gene action and selection based on phenotypic performance would be quite effective. However, days to maturity had high heritability but moderate genetic advance indicating the role of non-additive gene effects and direct selection would not be effective for the trait and for these traits, early generation intermating will be useful. The nature of gene action and the number of genes controlling the traits is revealed through the study of distribution using skewness and kurtosis (Govintharajet *et al.*, 2018). Positive skewness is associated with complementary gene action while negative skewness is associated with duplicate (additive × additive) gene interactions (Venkatesha *et al.*, 2016). Genes controlling the traits with skewed distribution tend to be dominant whether they are exerting an increasing or decreasing effect on the trait. Kurtosis is less than zero or negative (Platykurtic) in the absence of gene interaction and greater than zero or positive (Leptokurtic) in the presence of gene interaction. The traits with leptokurtic and platykurtic distribution are said to be controlled by fewer and many genes, respectively.

Days to 50% flowering, plant height, cluster per pod, pods per plant, 100-seed weight, biological yield per plant, harvest index, and seed yield per plant were found to be positively skewed indicating complementary gene action, while, days to maturity, pods per cluster and seeds per pod were negatively skewed suggesting duplicate gene action. Traits like days to 50% flowering, days to maturity, pods per cluster, pods per plant, seeds per pod, biological yield and harvest index showed platykurtic distribution as the value of kurtosis was less than zero or negative. Whereas plant height, cluster per pod, 100-sees weight and seed yield per plant. showed leptokurtic distribution as the value of kurtosis was greater than zero or positive indicating the presence of gene interaction and the trait was governed by a few number of genes. Overall, plant height, cluster per pod, 100-seed weight and seed yield per plant findings of our study were in agreement with previous studies by Mariyammal *et al.* (2019) and Kaur *et al.* (2023) on skewness and kurtosis distribution.

### Character association

The information regarding interrelationship of different traits with yield is essential before commencing any breeding program for crop improvement. It aids in the selection programme for selecting the individuals based on correlets and assist the breeder for conducting effective selection. In the present study, the genotypic correlation coefficients were shown for all the traits studied (Table 3). Seed yield per plant had shown a highly significant positive correlation between pods per cluster, pods per plant, seed per pod, 100-seed weight, and biological yield per plant. These results were in conformity with those reported by Shakeer *et al.* (2022) and Sofia *et al.* (2023).

It indicated that these traits can be considered for direct selection towards high grain yield. Seeds per pod, biological yield and harvest index were found to be associated significantly and positively with each other. Days to 50% flowering was found to be positively and significantly correlated with days to maturity. Pod per cluster showed a positive and highly significant correlation with pods per plant, seeds per pod and biological yield per plant. Day to 50% flowering had also shown a positive and highly significant correlation with clusters per pod and 100- seed weight. Day to maturity had also exhibited a positive and highly significant correlation with cluster per pod and 100-seed weight. Biological yield per plant had shown a highly significant and positive correlation with pods per plant, seeds per pod, 100- seed weight. On the other hand, seed yield per plant showed a negative association with days to 50% flowering, days to maturity, plant height and cluster per pod. Shakeer *et al.* (2022) and (Srivastava and Singh 2024) were found similar results. Investigation on correlation studies from the present study has revealed that traits like pods per cluster, pods per plant, seed per pod, 100-seed weight, and biological yield per plant were important attributes contributing towards higher grain yield in mungbean. The direct selection for component traits would be effective in achieving these the high grain yield. Knowledge based on the correlation analysis alone may not be always true because two traits might be correlated via another common trait. It describes association in statistical terms and does not provide clear picture about the cause and effect relationship. In order to get a clear picture of the interrelationship among different traits at the genotypic level, the direct and indirect effects of various traits on seed yield were estimated using path analysis. It divides the correlation coefficient into direct and indirect effects and provides the actual information on the contribution of traits.

The genotypic correlation coefficients of different traits partitioned into direct as well as indirect effects using path analysis are summarized in Table 4. 100-seed weight (0.497) had maximum direct effects on seed yield per plant followed by biological yield per plant (0.408), seed per pod (0.328), harvest index (0.283), pods per plant (0.282), pods per cluster (0.202) and cluster per pod (0.132). Days to 50% flowering had negative direct effects on seed yield per plant. The highly significant positive correlation between pods per cluster, pods per plant, seed per pod, 100-seed weight, and biological yield per plant with seed yield per plant were due to its direct effect and indirect effects via biological yield per plant. Khatik *et al.* (2023) and Harsh *et al.* (2024) were similar result reported. The correlation analysis revealed that these are the major yield contributing traits and can be taken as selection criteria for achieving higher yields. Based on the evaluation, few promising genotypes compared to check varieties were identified for different traits (Table-5). These were SVM55 followed by MHBC-70, IPM2K14-9 and MH1772 for days to 50% flowering, VGG18-021, SVM55 and NDM 95-2 for days to maturity. These genotypes are identified as the earlyliness. MH1142 was identified as a dwarf stature followed by KM2417 and IPM2-3. NDM 95-2 was got the highest position followed by PMS8, KM 2328, IPM2-3 and MHBC-70 for profuse podding and seed yield. Dutt *et al.* (2020) and Kumar *et al.* (2020) agreed with same result.

### Principal component analysis (PCA)

The Principal Component Analysis was performed to reduce dimensionality and identify the key components contributing to

variation across traits. The results, including eigenvalues, percentage variability, and cumulative variability, are presented in Table 6. The association between factors and traits is captured through eigenvectors provided in Table 7. Figures 2 and 3 illustrate the loading and scree plots, respectively, aiding in the visual interpretation of the factors.

### Eigenvalues and Explained Variance

The eigenvalues (Table 6) suggest that the first four principal components (F1 to F4) cumulatively explain 76.31% of the total variability among traits. F1 explains 34.34% of the variance. F2 contributes 20.13%, bringing the cumulative variance to 54.47%. F3 and F4 add 12.15% and 9.69%, respectively, resulting in a cumulative variability of 76.31%. The relatively high cumulative variance of the first four components indicates that these factors account for most of the information contained in the original variables. The subsequent components (F5 to F7) explain minor variability with diminishing eigenvalues, suggesting they contribute limited unique information. This is further validated by the scree plot (Fig. 3), where the curve flattens after the fourth factor, indicating the optimal number of components to retain.

### Factor Loadings and Trait Associations

The factor loadings presented in Table 7 provide insights into the relationships between individual traits and the extracted principal components (PCs).

PC1, explaining 34.34% of the variance, is primarily associated with productivity traits. It has strong positive loadings on productive pods per plant (PPC), pods per plant (PPP), and seed yield per plant (SYP). This suggests that higher values for these traits are indicative of increased overall productivity.

PC2, accounting for 20.13% of the variance, is related to yield-related traits and biomass. It has high positive loadings on biological yield per plant (BYP), harvest weight (HSW), and seed yield per plant (SYP). This PC highlights the importance of both biomass production and seed yield in determining overall plant performance. PC3, capturing 12.15% of the variance, is associated with harvest index (HI) and seeds per pod (SPP). The negative loadings on these traits suggest that lower values for HI and SPP are related to this PC. This could indicate a trade-off between seed yield and biomass production.

PC4, explaining 9.69% of the variance, is primarily associated with clusters per plant (CPP). The negative loading on CPP suggests that a lower number of clusters per plant is related to this PC, potentially indicating a different growth strategy or adaptation to specific environmental conditions.

### Trait-Component Interactions

The loading plot (Fig. 2) helps visualize how traits cluster along the first two principal components (F1 and F2). Traits like PPC, PPP, and SYP align positively with F1, indicating their contribution to productivity. On the other hand, traits such as BYP and HSW aligns with F2, emphasizing their importance for biomass accumulation. Interestingly, SPP and HI load negatively on F3, suggesting potential trade-offs between these traits and other productivity-related factors. The PCA results highlight the significant role of a few key components in explaining the variation among traits. F1 and F2 together account for over 54% of the total variance, primarily capturing productivity and yield-related traits. The diminishing eigenvalues for F5 to F7 indicate that these components add minimal new information.

Overall, the results provide useful insights for trait selection, helping breeders prioritize traits like SYP, PPC, and BYP to enhance crop productivity effectively. Similar finding a reported by Jadhav *et al.* (2023) and Das *et al.* (2024).

**CONCLUSION**

On the basis of the result, I concluded that high heritability accompanied by high genetic advance was recorded for biological yield per plant, plant height, seed yield per plant, days to 50% flowering and pods per cluster. It indicated that these traits are governed largely by additive gene action and selection. Seed yield per plant had shown highly significant positive correlation between pods per cluster, pods per plant, seed per pod, 100-seed weight, and biological yield per plant. The PCA results highlight the significant role of a few key components in explaining the variation among traits. F1 and F2 together account for over 54% of the total variance, primarily capturing productivity and yield-related traits. Overall, the results provide useful insights for trait selection, helping breeders prioritize traits like SYP, PPC, and BYP to enhance crop productivity effectively.

**Table 1 Analysis of variance for 11 characters of mungbean germplasms**

Source	DF	Mean Square										
		DM	PH (cm)	CPP	PPC	PPP	SPP	HSW (g)	BYP (g)	HI (%)	SYP (g)	
Replications	2	3.32	33.12**	0.81	0.3	11.61	8.84**	131.59**	0.48	0.01	16.50**	
Treatments	34	81.28**	193.10**	1.41**	2.14**	69.13**	2.79**	149.62**	42.55**	0.68**	17.71**	
Error	68	5.15	5.25	0.39	0.33	6.45	0.75	6.21	3.87	0.12	1.14	
SE		1.31	1.32	0.36	0.33	1.47	0.5	0.21	1.44	0.14	0.62	
CV (%)		2.67	5.08	9.01	9.72	6.16	9.84	9.33	6.53	5.4	7.77	
LSD at 5%		3.70	3.74	1.03	0.95	4.14	1.42	0.58	4.06	3.21	1.74	

\* & \*\* Significant at 5% & 1% Probability level, DFF, Days to 50% flowering, DM, Days to maturity, PH, Plant Height, CPP, Cluster per pod, PPC, Pod per cluster, PPP, Pods per plant

**Table 2 Genetic components of variability, genotypic coefficient of variation (PCV), coefficient of variation (CV), genetic advance mean percent (GAM), and heritability (broad sense) estimate for 11 characters of mungbean germplasms**

Traits	Min	Max	Mean	GCV	PCV	hBS	GAM	Kurtosis	Skewness	Gene action
DFF	31.33	49.66	39.57	12.73	13.96	0.83	23.91	-1.27	0.01	Complementary
DM	56.66	74.00	64.99	8.18	8.61	0.90	16.03	-1.55	-0.24	Duplicate
PH (cm)	35.33	64.13	45.13	17.53	18.25	0.92	34.69	0.83	1.17	Complementary
CPP	6.23	9.46	6.69	8.34	12.28	0.46	11.68	4.44	1.84	Complementary
PPC	4.03	74.00	5.96	12.99	16.23	0.64	21.44	-0.42	-0.12	Duplicate
PPP	34.04	51.90	41.22	11.08	12.68	0.76	19.96	-0.52	0.54	Complementary
SPP	7.88	10.66	8.84	7.33	13.55	0.47	13.18	-1.01	-0.05	Duplicate
HSW (g)	2.94	4.94	3.82	11.32	14.67	0.59	18.01	0.15	0.09	Complementary
BYP (g)	26.83	52.08	38.19	18.10	19.24	0.88	35.07	-0.85	0.33	Complementary
HI (%)	30.11	43.85	36.48	9.84	11.22	0.76	17.77	-1.24	0.08	Complementary
SYP (g)	10.60	20.51	13.78	17.05	18.74	0.82	31.97	0.23	0.75	Complementary

**Table 3 Genotypic Correlation Matrix for 11 characters of mungbean germplasms**

Traits	DFF	DM	PH (cm)	CPP	PPC	PPP	SPP	HSW (g)	BYP (g)	HI (%)	SYP (g)
DFF	1.000	0.975**	-0.273**	0.252**	-0.581**	-0.463**	-0.200*	0.538**	-0.001	-0.159	-0.065
DM		1.000	-0.204*	0.336**	-0.673**	-0.535**	-0.272**	0.506**	-0.069	-0.226*	-0.173
PH (cm)			1.000	-0.057	0.099	0.066	-0.062	-0.220*	-0.093	-0.088	-0.117
CPP				1.000	-0.552**	-0.041	-0.297**	-0.078	-0.133	-0.210*	-0.236*
PPC					1.000	0.849**	0.489**	-0.317**	0.548**	0.075	0.610**
PPP						1.000	0.412**	-0.361**	0.635**	-0.071	0.638**
SPP							1.000	-0.274**	0.278**	0.598**	0.642**
HSW (g)								1.000	0.394**	-0.280**	0.305**
BYP (g)									1.000	-0.424**	0.838**
HI (%)										1.000	0.125

\* & \*\* Significant at 5% & 1% Probability level

**Table 4 Genotypic Path Matrix for 11 characters of mungbean germplasms**

Traits	DFF	DM	PH (cm)	CPP	PPC	PPP	SPP	HSW (g)	BYP (g)	HI (%)	r with SYP (g)
DFF	-0.062	0.067	-0.011	0.033	-0.117	-0.131	-0.066	0.267	-0.001	-0.045	-0.065
DM	-0.061	0.069	-0.008	0.044	-0.136	-0.151	-0.089	0.251	-0.028	-0.064	-0.173
PH (cm)	0.017	-0.014	0.041	-0.008	0.020	0.019	-0.020	-0.109	-0.038	-0.025	-0.117
CPP	-0.016	0.023	-0.002	1.000	-0.111	-0.012	-0.098	-0.039	-0.054	-0.059	-0.236*
PPC	0.036	-0.046	0.004	-0.073	0.202	0.240	0.161	-0.158	0.224	0.021	0.610**
PPP	0.029	-0.037	0.003	-0.005	0.171	0.282	0.135	-0.179	0.259	-0.020	0.638**
SPP	0.013	-0.019	-0.003	-0.039	0.099	0.116	0.328	-0.136	0.113	0.169	0.642**
HSW (g)	-0.034	0.035	-0.009	-0.010	-0.064	-0.102	-0.090	0.497	0.161	-0.079	0.305**
BYP (g)	0.000	-0.005	-0.004	-0.018	0.110	0.179	0.091	0.196	0.408	-0.120	0.838**
HI (%)	0.010	-0.016	-0.004	-0.028	0.015	-0.020	0.196	-0.139	-0.173	0.283	0.125

Diagonal value represent direct and diagonal off show the indirect effects

Table-5: List of promising genotypes for important yield component traits of mungbean

Traits	Genotypes
DFF	SVM55 (31.33),MHBC-70 (32.00),IPM2K14-9(32.00),MH1772( 33.33),KM 2328 (32.00)
DM	VGG18-021(56.67),SVM55 (57.00),NDM 95-2 (57.67),IPM2K14-9(58.00),MH1772 (58.00)
PH (cm)	MH1142 (35.33),KM2417(36.33),IPM2-3(36.33),IPM1205-2 (36.40),IPM512-1 (36.73)
CPP	IPM1704-14(9.47),BCM20-73 (8.57),KM2417 (8.27),SGC25(7.63),MGG5-19 (7.53)
PPC	NDM 95-2 (7.40),MHBC-70 (7.37),MH1142 (check) (7.17),VGG18-021 (7.1),SML1839 (7.10)
PPP	NDM 95-2 (51.91),KM2421 (50.79),SML1839 (49.17),VGG18-021 (49.13),MH1142 (46.38)
SPP	PMS8 (10.67),KM2421 (10.43),SML1839 (10.17),PM1903 (10.13),NDM 95-2 (10.13)
HSW (g)	IPM2-3 (4.95),SVM106 (4.86),PMS8 (4.37),RMG1183 (4.28),AKM12-12 (4.26)
BYP (g)	KM 2328 (52.08),NDM 95-2 (51.40),MH1142 (49.44),IPM2-3 (48.76),PMS8 (47.20)
HI (%)	SKNM2006 (43.85),BCM20-56 (42.70),MH1772 (41.85),PM1903 (40.0), SML1839 (39.94)
SYP (g)	NDM 95-2 (20.51),PMS8 (18.47),KM 2328 (17.68),IPM2-3 (16.61),MHBC-70 (16.29)

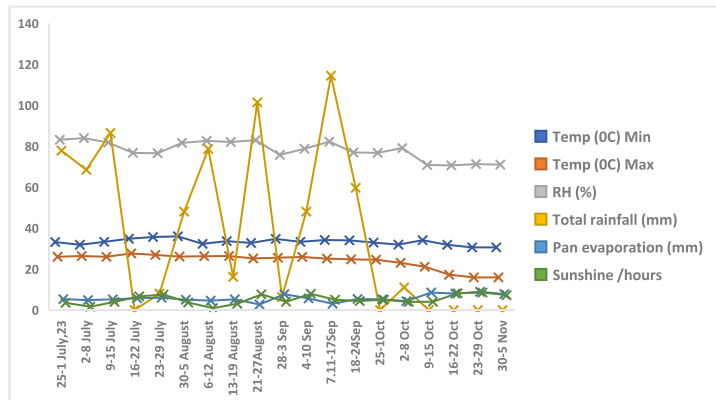


Fig. 1 The average, maximum and minimum temperatures as well as the rainfall data recorded at the research stations for the years 2023-24

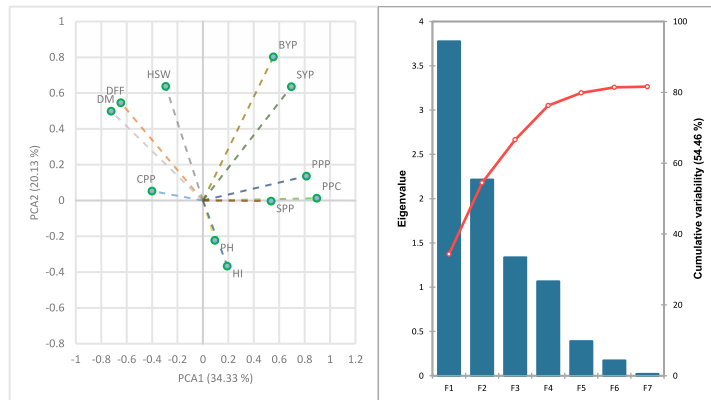


Fig-2 Loding Plot Fig-3 Scree Plot

Table-6 Eigenvectors

Factor	F1	F2	F3	F4	F5	F6	F7
Eigenvalue	3.777	2.215	1.337	1.065	0.390	0.172	0.021
Variability (%)	34.335	20.133	12.152	9.685	3.548	1.566	0.190
Cumulative %	34.335	54.468	66.620	76.305	79.853	81.419	81.609

Table-7 Eigenvectors

Traits/ Factor	F1	F2	F3	F4	F5	F6	F7
DFF	-0.332	0.367	-0.233	-0.034	0.418	-0.157	-0.002
DM	-0.372	0.336	-0.182	-0.075	0.411	-0.056	-0.236
PH	0.049	-0.150	0.148	0.064	0.015	0.304	-0.782
CPP	-0.207	0.036	0.350	-0.797	-0.182	-0.117	0.006
PPC	0.461	0.008	0.048	0.224	0.319	-0.341	0.000
PPP	0.419	0.091	0.270	-0.235	0.313	-0.377	-0.044
SPP	0.276	-0.002	-0.502	-0.328	0.178	0.518	0.072
HSW	-0.150	0.429	-0.053	0.278	-0.490	-0.192	-0.016
BYP	0.287	0.542	0.194	-0.005	-0.048	0.401	0.344
HI	0.098	-0.246	-0.590	-0.193	-0.227	-0.353	0.087
SYP	0.358	0.427	-0.229	-0.164	-0.312	-0.135	-0.447

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