Himachal Journal of Agricultural Research
Volume 52, Issue 1, June 2026; pp. 57–66; DOI: 10.18311/HJAR/2026/53116

INFORMATICS JOURNALS
Crop improvement

Estimation of Variability Parameters, Association and Principal Component Analysis for Yield and related Traits in Red and White Rice Genotypes

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Abstract

An experiment was conducted during the 2024 *kharif* season at RWRC Malan, CSK HPAU, Palampur, comprising 9 white rice lines and 5 red rice lines. The experiment was conducted to investigate genetic variability, correlation, path coefficient analysis, and principal component analysis for yield and its contributing traits. Analysis of variance revealed significant genotype effects across all examined traits. Genetic variability measures demonstrated high phenotypic and genotypic coefficients for key traits like flag leaf width and grains per panicle, with most traits showing high heritability and genetic advance. Correlation and path-coefficient analyses identified total and productive tillers, thousand grain weight, harvest index, and panicle length as critical direct contributors to yield. Principal component analysis revealed that the first two components explained over 53% of the variance, indicating contrasting patterns between maturity- and yield-related traits. These findings underscore the potential of exploiting genetic diversity and trait interrelationships to guide effective breeding strategies.

Keywords: Contributing Traits, Correlation and Path Coefficient Analysis, Genetic Variability, Principal Component Analysis, Rice Yield

Rice (*Oryza sativa* L.), a monocotyledonous angiosperm belonging to the Poaceae family, has three subspecies: *Indica*, *Japonica* and *Javanica*. The genus *Oryza* consists of 24 known species, including 22 wild and two domesticated ones: *Oryza sativa* and *Oryza glaberrima*. More than half of the global population relies on rice as a primary food source, with 90% of its production and consumption concentrated in Asia. Currently, rice is cultivated on approximately 167.6 million hectares worldwide, yielding 517.3 million metric tons with an average productivity of 4.17 tons per hectare, as forecasted for 2024–2025[1]. India is the second largest rice producer, generating 137.8 million metric tons with an average yield of 2.8 tons per hectare across 47.8 million hectares[1]. As a vital staple crop, rice plays a crucial role in delivering essential nutrients through the food chain. To sustain a projected global population of nine billion by 2050, rice production must increase by at least 50%[2].

Assessment of genetic variability is essential in plant breeding as it provides the basis for effective selection and crop improvement[3]. It helps in identifying superior genotypes with desirable traits such as higher yield, quality and stress tolerance. Estimation of variability also aids in understanding the extent of genetic diversity present in a population and in selecting suitable breeding

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Manuscript Received: 17.11.2025; Accepted: 28.11.2025

strategies[4]. To effectively accumulate multiple yield-contributing traits within a single genotype, it's crucial to know their interrelationships. Correlation analysis determines the degree and direction of association between yield and its component traits[5]. Strategic breeding should therefore consider these relationships when selecting for yield improvements. However, correlation alone may not reveal the true contribution of each trait to yield. Path coefficient analysis, originally introduced by Dewey and Lu[6] in 1959 for use in plant breeding, enables more informed selection decisions. The estimation of Principal Component Analysis helps in reducing the dimensionality of complex datasets by transforming correlated variables into a smaller number of uncorrelated principal components[7]. It enables the identification of major sources of variation among traits and helps in selecting important characters contributing to overall variability. Thus, PCA facilitates efficient interpretation of multivariate data in breeding and genetic studies.

The present investigation was undertaken to estimate the genetic variability, correlation and path analysis in red and white rice genotypes for various agro-morphological traits in order to facilitate the efficient selection process for a productive breeding program. The findings of this study will aid in identifying highly suitable genetic material and assist in designing subsequent breeding programs to promote varietal improvement initiatives.

MATERIALS AND METHODS

The experiment was conducted at the Rice and Wheat Research Centre (RWRC), Malan, Chaudhary Sarwan Kumar Himachal Pradesh Agriculture University, Palampur, Himachal Pradesh, India 176047, during the Kharif 2024 season. The climate in RWRC Malan during May to November is characterised by a shift from the hot and dry summer season to the monsoon. A total of 14 rice genotypes that include 9 white rice lines viz., HPR 2865 (Palampur Purple/ Kasturi), HPR 2143 (Phulptas/ HPV7413), HPR 2880 (HPU 2216/ Tetep), HPR 2929 (Kalizhini/ HPR2143// HPR2143), HPR 3203 (HPR 2143/ Balwam), HPR 3202 (T23/ IR 67011// Hasan Sarai), HPR 3201 (HPR 2143/ AC 19146), HPR 3212 (HPR 2686 × HPR 2216), HPR 3216 (HPU 741/ HPR 2512/ HPR 1149) and five red rice lines, *i.e.*, Karad (Landrace from Chamba), Chohartu (Landrace from Shimla), Sukara (Landrace from Chamba), Gocha (Landrace from Kangra) and HPR 2720 (Improved begmi, as Check variety) were used to study the genetic variability, correlation, path coefficient analysis and principal component analysis for yield and its contributing traits. The material was raised in a randomised complete block design with three replications with a spacing of 20 × 15 cm.

The observations were recorded on important agronomic and yield-related traits viz; days to 50% flowering, days to maturity, plant height, flag leaf length, flag leaf width, flag leaf area, total tillers per plant, productive tillers per plant, panicle length, number of spikelets per panicle, number of grains per panicle, spikelet fertility, harvest index, grain length, grain breadth, grain L: B, and grain yield per plant. The data were recorded on ten randomly selected plants from each genotype, except for days to 50% flowering and days to 75% maturity, and the mean values were used for statistical analysis.

Analysis of Variance (ANOVA) was done to determine the significance of differences among the genotypes for various agro-morphological traits following standard procedures described by Panse and Sukhatme[8]. Genetic variability parameters, including Genotypic Coefficient of Variation (GCV), Phenotypic Coefficient of Variation (PCV), broad-sense heritability and genetic advance as a percent of the mean were calculated as per Burton and De Van[9] and Johnson *et al.*[10]. Correlation coefficients were estimated following the method of Al-Jibouri *et al.*[11] whereas Path coefficient analysis was carried out according to the procedure described by Dewey and Lu[6] to partition correlation coefficients into direct and indirect effects and to identify the most important traits contributing to grain yield. All statistical analyses were performed using OPSTAT statistical software developed by CCS Haryana Agricultural University, Hisar, India (Sheoran *et al.*[24]).

RESULTS AND DISCUSSION

The analysis of variance showed significant differences among the rice genotypes for all the traits studied (Table 1). This pronounced variability likely stems from the diverse geographic origins of the genotypes and environmental effects on phenotype expression. These findings also imply that this population is highly responsive to selection. Earlier scientific studies by Nagaraju *et al.*[12] in 2023 have reported varied responses of rice genotypes for grain yield and component traits.

Table 1. Estimates of parameters of variability for various traits

Traits df	Analysis of variance			Mean+ SE	Range	PCV (%)	GCV (%)	Heritability (%) (h^2 bs)	Genetic advance (%)
	Replication	Treatment	Error						
	2	13	26						
DFF	46.56	67.59*	2.25	89.88+1.22	83.93-97.41	5.45	5.19	80.61	10.18
DM	46.82	152.45*	2.94	118.60+1.40	107.63-125.53	6.12	5.95	84.41	11.91
PH	18.67	645.95*	0.59	118.97+0.62	96.9- 150.73	12.34	12.32	89.72	25.35
FLL	0.21	66.59*	0.05	34.14+0.19	29.60-44.47	13.79	13.77	89.74	28.33
FLW	0.01	0.45*	0.01	1.84+0.01	1.5-2.51	21.14	21.13	89.98	43.54
FLA	1.64	255.62*	0.12	46.86+0.29	32.70-60.27	19.70	19.69	89.85	40.53
TTP	1.45	7.07*	0.27	10.95+0.43	8.07-12.80	14.55	13.73	79.10	26.71
PTP	0.11	8.27*	0.20	8.67+0.36	5.45-11.06	19.59	18.90	83.04	37.56
PL	1.56	21.96*	1.34	27.53+0.94	23.50-33.03	10.41	9.52	73.68	17.94
SPP	293.34	1742.57*	267.64	137.72+13.35	108.96-201.62	20.00	16.16	54.75	26.68
GPP	199.12	1457.80*	68.94	98.17+6.78	80.93-158.53	23.49	21.91	77.03	42.12
SF	9.40	292.64*	28.73	71.66+4.37	58.44-91.61	15.07	13.08	65.37	23.40
HI	5.70	83.12*	4.68	40.13+1.76	30.51-45.51	13.83	12.74	74.79	24.16
TGW	15.64	50.71*	8.58	25.69+2.39	15.60-29.77	18.51	14.58	52.07	23.66
GL	0.01	0.45*	0.01	6.57+0.01	5.86-7.17	5.91	5.91	89.87	12.16
GB	0.01	0.07*	0.01	2.40+0.01	2.20-2.68	6.63	6.62	89.64	13.62
GLB	0.01	0.24*	0.01	2.74+0.01	2.36-3.22	10.43	10.42	89.71	21.44
YPP	3.69	47.16*	2.65	20.86+1.33	14.22-26.33	20.04	18.46	74.83	35.02

*Significant at 5 per cent level; where, DFF: Days to 50% flowering, DM: Days to 75 % maturity; PH: Plant height; FLL: Flag leaf length; FLW: Flag leaf width; FLA: Flag leaf area; TTP: Total tillers per plant; PTP: Productive tillers per plant; PL: Panicle length; SPP: Spikelets per panicle; GPP: Grains per panicle; SF: Spikelet fertility; HI: Harvest index; TGW: Thousand grain weight; GL: Grain length; GB: Grain breadth; GLB: Grain length width ratio; YPP: Yield per plant

Understanding the extent of genetic variation in a plant population is essential for any plant breeder aiming to initiate a successful breeding program. To assess this variation, breeders examine key metrics such as mean, range, phenotypic and genotypic coefficients of variation (PCV and GCV), broad-sense heritability (h^2), and the expected Genetic Advance as a percentage of the Mean (GAM). Genotypic and phenotypic variability play a crucial role in choosing superior cultivars and initiating an effective breeding program[13]. In the present study, the phenotypic coefficients of variation were higher than the genotypic ones across all the traits evaluated. High PCV and GCV were observed for flag leaf width, grains per panicle and yield per plant. Similar findings were observed by Babu *et al.*[14]. Medium PCV and GCV were observed for plant height, flag leaf length, flag leaf area, total tillers per panicle, productive tillers per panicle, panicle length, spikelets per panicle, spikelet fertility, harvest index, thousand-grain weight and grain length breadth ratio. Other traits like days to 50% flowering, days to maturity, grain length and grain breadth recorded low PCV and GCV. These findings are supported by the study done by Kumar *et al.*[15].

Heritability is a valuable quantitative metric that gauges how much a trait's expression is shaped by genetic inheritance versus environmental influences[16]. Effective selection largely depends on substantial additive genetic effects and minimal environmental interference. Broad-sense heritability (h^2bs) reflects this balance. According to Robinson[17], heritability estimates in the broad sense are categorised as high (above 75%), medium (50-75%), or low (below 50%). All the traits recorded high heritability except spikelets per panicle, spikelet fertility and thousand-grain weight, which recorded a medium heritability percentage (Table 1). These findings are supported by the work done by Kesh *et al.*[18] in rice. The findings of the present study on heritability estimates suggest that genetic inheritance plays a dominant role in the variation of traits, influencing how these traits are selected and expressed. The medium broad-sense heritability values for spikelets per panicle and thousand-grain weight imply that environmental factors may have an impact on their expression. Consequently, traits exhibiting low heritability are generally not amenable to direct selection.

It is important to note, however, that high heritability alone does not guarantee substantial genetic improvement; hence, evaluating both heritability and expected genetic advance together provides a more accurate prediction of breeding success[19]. High heritability coupled with high genetic advance was observed for flag leaf width, flag leaf area, productive tillers per plant, grains per panicle and grain yield per plant. Similar observations were also reported by Hani *et al.*[14].

For breeders aiming to enhance grain yield, it's vital to grasp how the various traits underlying this complex characteristic interconnect and contribute. Grain yield does not function in isolation, but it emerges from the combined influence of multiple component traits. The genetic architecture of yield is shaped by how these components interact, whether directly or indirectly, ultimately defining the overall effect on yield across all crops[20]. Among all the traits studied, total tillers per plant, productive tillers per plant, panicle length and harvest index showed a significantly positive correlation with grain yield per plant (Table 2). Similar results were found by Madishetty *et al.*[21]. On the other hand, days to 50% flowering exhibited a significant negative correlation with grain yield per plant. This negative correlation suggests that earlier flowering may increase yield, whereas late flowering tends to be associated with lower yield.

Path coefficient analysis separates the correlation between traits into two parts: direct effects, which measure how much a specific trait directly impacts the target traits, such as yield, and indirect effects, which show how a trait affects yield through its connection with other traits. This method assists plant breeders in pinpointing the traits that genuinely enhance yield, rather than those that are only correlated with it[22]. Days to maturity, flag leaf length, flag leaf width, total tillers per plant, grains per panicle, harvest index and grain length exhibited positive direct effects, indicating the direct contribution of these traits towards grain yield (Table 3). These results aligned with findings from Saran *et al.*[23], where biological yield and harvest

Table 2. Estimates of phenotypic correlation coefficients among yield and contributing traits

Trait	DM	PH	FLL	FLW	FLA	TTP	PTP	PL	SPP	GPP	SF	HI	TGW	GL	GW	GLB	YPP
DF	0.66*	-0.25	-0.11	0.13	0.06	-0.66	-0.67*	-0.44	0.03	-0.07	-0.18	-0.60*	0.08	0.16	-0.13	0.16	-0.63*
DM		-0.45	-0.37	0.46	0.22	-0.63*	-0.54	-0.21	0.11	-0.03	0.12	-0.56*	-0.05	0.39	-0.36	0.44	-0.52
PH			0.66*	-0.55*	-0.13	0.33	0.34	-0.17	0.23	0.37	0.21	0.33	-0.27	-0.39	0.39	-0.47	0.34
FLL				-0.38	0.29	0.36	0.37	0.01	0.11	0.32	0.33	0.30	-0.31	-0.22	0.05	-0.18	0.39
FLW					0.76*	-0.26	-0.25	0.02	-0.04	0.13	0.31	-0.25	-0.19	0.17	-0.22	0.24	-0.01
FLA						-0.02	0.01	0.01	-0.01	0.32	0.56*	-0.49	-0.38	0.03	-0.22	0.14	0.07
TTP							0.96*	0.53	-0.12	-0.07	0.07	0.90*	0.08	-0.23	-0.17	-0.03	0.94*
PTP								0.50	-0.19	-0.10	0.12	0.90*	0.07	-0.20	-0.22	0.01	0.95*
PL									-0.16	-0.08	0.11	0.49	0.11	0.37	-0.41	0.48	0.59*
SPP										0.79*	-0.18	-0.17	-0.73	-0.12	0.25	-0.23	-0.19
GPP											0.44	-0.11	-0.93*	-0.08	0.29	-0.23	-0.06
SF												0.05	-0.46	0.02	0.07	-0.03	0.18
HI													0.19	-0.18	-0.22	0.02	0.94*
TGW														0.04	-0.19	0.15	0.11
GL															-0.38	0.83*	-0.16
GW																-0.83	-0.23
GLB																	0.04
YPP																	

*Significant at 5 per cent level

Table 3. Path coefficient analysis among various yield and morphological traits in rice

Traits	DF	DM	PH	FLL	FLW	FLA	TTP	PTP	PL	SPP	GPP	SF	HI	TGW	GL	GB	GLB	r
DF	**-0.57**	0.71	0.09	-0.15	0.17	0.08	-0.08	0.16	0.16	-0.79	-0.28	0.19	-0.51	-0.02	0.34	0.12	-0.25	-0.63*
DM	-1.13	**0.99**	0.15	-0.5	0.54	-0.26	-1.78	1.67	0.06	1.36	-0.41	0.2	-0.41	-0.04	0.06	0.95	-0.93	-0.52
PH	0.46	-0.49	**-0.32**	0.5	-0.62	0.15	0.76	0.5	0.05	-0.35	0.3	-0.33	0.24	0.42	-0.95	-0.05	0.07	0.34
FLL	0.19	-0.39	-0.21	**0.78**	-0.43	0.33	0.31	-0.69	-0.03	-0.14	0.87	-0.18	0.29	0.48	-0.67	-0.38	0.26	0.39
FLW	-0.7	0.48	0.17	-0.49	**0.62**	-0.88	-0.07	0.02	0.01	0.45	0.15	-0.9	-0.17	0.29	0.32	0.75	-0.06	-0.01
FLA	-0.1	0.23	0.04	0.37	0.86	-0.65	-0.04	-0.03	-0.03	0.17	0.81	-1.76	-0.03	0.59	0.25	0.19	-0.8	0.07
TTP	0.27	-0..19	-0.11	0.49	-0.31	0.02	**0.57**	-0.75	-0.15	0.97	-0.14	-0.28	0.67	-0.09	-0.56	0.39	0.52	0.94*
PTP	0.23	-0.1	-0.11	0.52	-0.29	-0.01	0.46	**-0.76**	-0.15	0.75	-0.07	-0.2	0.67	-0.12	-0.6	0.88	-0.15	0.95*
PL	0.21	-0.24	0.06	0.15	0.23	-0.16	0.43	-0.57	**-0.28**	0.94	-0.42	-0.11	0.32	0.06	0.11	0.55	-0.69	0.59*
SPP	-0.16	-0.17	-0.09	0.18	-0.06	0.02	-0.32	0.12	0.01	**-0.74**	0.83	-0.04	-0.02	0.79	-0.64	-0.53	0.63	-0.19
GPP	0.05	-0.05	-0.12	0.24	0.15	-0.39	-0.2	0.32	0.01	-0.45	**0.52**	-0.21	-0.07	0.2	-0.28	-0.38	0.6	-0.06
SF	0.32	0.17	-0.07	0.48	0.41	-0.75	0.12	-0.34	-0.01	-0.05	0.38	**-0.8**	-0.02	0.29	0.3	-0.6	0.35	0.18
HI	0.61	-0.62	-0..61	0.42	-0.3	0.06	0.64	-0.77	-0.13	0.33	-0.51	0.58	**0.67**	-0.01	-0.48	0.86	-0.41	0.94*
TGW	-0.03	-0.04	0.11	-0.51	-0.28	0.57	0.19	-0.28	0.01	0.18	-0.29	0.59	0.01	**-0.68**	0.47	0.87	-0.78	0.11
GL	-0.28	0.41	0.12	-0.28	0.2	-0.53	-0.15	0.59	-0.11	0.19	-0.75	-0.52	-0.25	-0.57	0.93	0.97	-0.13	-0.16
GB	0.43	-0.38	-0.12	0.56	-0.25	0.75	-0.46	0.64	0.1	-0.95	0.71	-0.21	-0.26	0.29	-0.87	-0.69	0.48	-0.23
GLB	-0.28	0.46	0.15	-0.22	0.27	-0.16	-0.1	-0.03	-0.14	0.23	-0.01	0.16	0.02	-0.23	0.19	0.36	-0.63	0.04

Residual effect: 0.187

*Significant at 5 per cent level; where, r- correlation with yield per plant; DFF: Days to 50% flowering, DM: Days to maturity; PH: Plant height; FLL: Flag leaf length; FLW: Flag leaf width; FLA: Flag leaf area; TTP: Total tillers per plant; PTP: Productive tillers per plant; PL: Panicle length; SPP: Spikelets per panicle; GPP: Grains per panicle; SF: Spikelet fertility; HI: Harvest index; TGW: Thousand grain weight; GL: Grain length; GB: Grain breadth ; GLB: Grain length width ratio; YPP: Yield per plant

index showed the greatest direct influence on seed yield, followed by panicle length. Among all the traits having significant positive correlation with yield, in the case of total tillers per plant and harvest index, it was because of the high direct effects, whereas the positive correlation of productive tillers per plant was due to its indirect effect via spikelets per plant, harvest index and grain breadth. Similarly, the positive correlation of panicle length with grain yield was because of its indirect effect via spikelets per panicle, grain breadth and harvest index. The residual effect obtained from path coefficient analysis was 0.187, indicating that the characters included in the study explained a major proportion of the variability in grain yield. The low magnitude of residual effect suggests that most of the important yield-contributing traits were considered in the analysis, and only a small proportion of variation remained unexplained.

Table 4. Eigenvectors for the components of quantitatively measured traits

	Eigen variables									
	PC1	**PC2**	**PC3**	**PC4**	**PC5**	**PC6**	**PC7**	**PC8**	**PC9**	**PC10**
Eigenvalue	5.66	3.94	3.01	1.54	1.24	0.90	0.56	0.32	0.30	0.19
Variability (%)	31.5	21.9	16.8	8.62	6.92	5	3.1	1.8	1.7	1.1
CUM. (%)	31.5	53.4	70.1	78.7	85.7	90.7	93.8	95.6	97.3	98.3
DF	0.31	-0.01	-0.04	0.01	0.40	-0.34	-0.04	-0.19	-0.52	0.33
DM	0.31	-0.13	0.15	-0.04	0.21	-0.10	0.48	-0.26	-0.14	-0.21
PH	-0.22	0.30	-0.04	0.06	0.38	0.07	0.17	0.31	-0.16	-0.62
FLL	-0.21	0.18	0.15	0.03	0.56	-0.06	-0.44	-0.02	0.15	0.11
FLW	-0.17	-0.10	0.35	-0.34	-0.35	-0.16	-0.05	0.25	-0.19	-0.16
FLA	0.03	0.01	0.46	-0.35	0.03	-0.19	-0.38	0.20	-0.04	-0.08
TTP	-0.39	-0.08	0.03	0.01	-0.07	-0.15	0.09	0.04	-0.05	0.33
PTP	-0.39	-0.10	0.06	-0.02	-0.01	-0.12	0.19	0.05	0.04	0.17
PL	-0.19	-0.26	0.20	0.20	-0.13	0.23	-0.36	-0.61	-0.17	-0.31
SPP	0.03	0.32	0.12	0.47	-0.26	-0.30	-0.05	0.01	-0.12	-0.06
GPP	0.01	0.36	0.34	0.23	-0.09	0.01	0.12	-0.14	-0.12	0.01
SF	-0.05	0.09	0.39	-0.33	0.19	0.45	0.29	-0.20	0.06	0.17
HI	-0.37	-0.12	0.02	-0.01	-0.03	-0.14	0.17	0.08	-0.32	0.01
TGW	-0.02	-0.33	-0.20	-0.20	0.09	0.01	-0.16	0.02	-0.24	-0.23
GL	0.13	-0.27	0.37	0.37	0.08	0.44	-0.06	0.42	-0.27	0.18
GB	0.01	0.37	-0.15	-0.15	-0.17	0.41	-0.13	0.05	-0.45	0.17
GLB	0.08	-0.39	0.32	0.32	0.14	0.02	0.05	0.23	0.12	-0.01
YPP	-0.39	-0.12	-0.03	-0.03	0.12	-0.08	0.11	-0.05	-0.28	-0.01

DFF: Days to 50% flowering, **DM**: Days to maturity; **PH:** Plant height; **FLL:** Flag leaf length; **FLW:** Flag leaf width; **FLA**: Flag leaf area; **TTP:** Total tillers per plant; **PTP**: Productive tillers per plant; **PL:** Panicle length; **SPP**: Spikelets per panicle; **GPP:** Grains per panicle; **SF**: Spikelet fertility; **HI:** Harvest index; **TGW:** Thousand grain weight; **GL:** Grain length; **GB:** Grain breadth; **GLB**: Grain length width ratio; **YPP**: Yield per plant

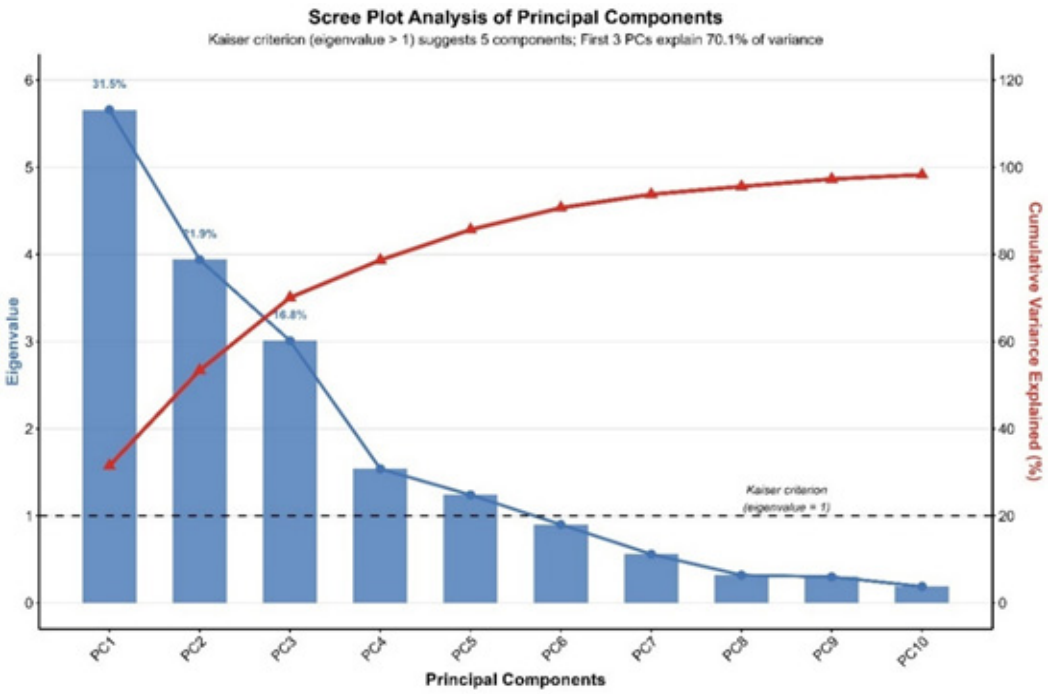


Figure 1. Scree plot for analysis of principal components.

Principal Component Analysis (PCA) showed that the first five Eigenvectors are the most important, as they have eigenvalues greater than one. (Table 4). Eigenvalues reflect how much variance each Principal Component (PC) explains. First Principal Component (PC1) explained 31.5% of total variance, and PC2 accounted for 21.94% of total variance. Taken together, the first two PCs cover 53.4% of the variance, and the first five PCs cover around 85.7%. For the first principal Component (PC1), the strongest positive loadings are observed on Days to 50% Flowering (DF, 0.311) and Days to Maturity (DM, 0.317), while the strongest negative loadings appear on total tillers per panicle (TTP, -0.395), productive tillers per panicle (PTP, -0.392), harvest index (HI, -0.379), and yield per plant (YPP, -0.39). These key findings are in line with those of Behera *et al.*[25]. This suggests that PC1 captures a trade-off between maturity-related timelines and yield-related performance traits. IN PC2, Plant Height (PH, 0.307), Grain Per Panicle (GPP, 0.362) and Grain Weight (GW, 0.374) dominate positively, whereas Grain Length Breadth ratio (GLB, -0.39) and Thousand-Grain Weight (TGW, -0.33) contribute negatively, indicating a contrast between structural growth and grain dimensions, For PC3, the highest positive loadings are seen for Flag Leaf Area (FLA, 0.469) and Grain Length (GL, 0.379), with Spikelet Fertility (SF, 0.391) also contributing noticeably- suggesting that PC3 represents variation in leaf and grain morphology. The remaining components (PC4-PC10) capture increasingly finer trait combinations, such as PC5 reflecting Days to Flowering (DF=0.405) and PC6 emphasizing negative maturity effects (DM=-0.345). Figure 1 illustrates the screen plot analysis of principal components.

The findings advocate for selection strategies focusing on tillering capacity, harvest index, and grain weight to enhance yield performance. Future breeding efforts should emphasise these traits, leveraging their high heritability, pronounced genetic advance, and demonstrated direct influence on yield potential.

CONCLUSIONS

The present investigation revealed significant genetic variability among rice genotypes for all the traits under study. High heritability coupled with high genetic

advance for flag leaf width, flag leaf area, productive tillers per plant, grains per panicle and grain yield per plant suggest strong additive gene action suitable for selection. Correlation analysis identifies total tillers per plant, productive tillers per plant, panicle length and harvest index as major positive yield contributors. Path coefficient analysis further confirmed that total tillers and harvest index exerted high positive direct effects on grain yield, indicating that selection for these traits will aid in improvement of grain yield. The principal component analysis revealed that the traits related to flowering, maturity, tillering and grain characteristics play a major role in determining overall variability among the rice genotypes. The rice genotypes studied exhibited remarkable genetic variability, making them invaluable resources for breeding programs aimed at improving yield and other yield-related traits.

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AUTHORS CONTRIBUTION

KB: conducted the experiment, analyzed the data and wrote the original manuscript. NB: conceptualized the research programme, methodology and provided resources. PB and VN: reviewed and edited the manuscript.