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GENETIC VARIABILITY, CORRELATION, PATH AND PCA FOR YIELD AND ITS COMPONENT TRAITS IN PAN INDIA ELITE CULTIVARS OF RICE (*ORYZA SATIVA* L.)

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ABSTRACT

The experiment was carried out at the Agricultural Research Farm, SAGR, LPU, Jalandhar (Punjab). Fifty pan India elite cultivars of rice (*Oryza sativa* L.), which were gathered from different states of India for investigation. Analysis of variance showed significant variation among the genotypes for all ten quantitative traits under evaluation, indicated presence of variation in the populations. The genotypes showed high variability for most traits, reflecting high potential for selection to enhance yield. The investigation recorded high Genetic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV) for biological yield, which was trailed by harvest index, seed yield per plant, and test weight, implying large genetic variation for these traits and thus effective direct selection. The traits had high heritability and genetic advance, showing that they are regulated by additive gene effects, making them ideal for selection. Correlation analysis indicated seed yield per plants had moderate positive correlations with biological yield and harvest index. The phenological traits had negative and significant associations with seed yield per plant, indicated desirability of earliness. The same traits also had maximum direct effects on seed yield at both genotypic and phenotypic levels. Principal component analysis resulted in three principal components, which accounted for 55% of the total variation. These traits pinpointed yield-related characteristics, including biological yield, harvest index, and test weight, that are utilized to separate genotypes by their potential for yield.

Key words : Variability, Correlation and Path coefficient analysis, PCA.

Introduction

Rice (*Oryza sativa* L.), a Gramineae family member and Oryzoideae subfamily member, has 24 chromosomes and is one of the world's most significant cereal crops. Known colloquially as the "Global Grain," it is responsible for feeding almost half of the world's population. In India, the yield of rice averages about 45 tonnes per hectare, with an overall harvested area of about 47.8 million hectares. (FAOSTAT, 2023). Rice is commonly known to be a calorie-dense high-energy food but also a great source of highly biological value protein. Nutrition-wise, it has approximately 7.5% protein, 1.9% fat, 0.9% crude fiber, and 76.5% carbohydrate. Every 100 grams includes around 1.2 mg of ash content, along with essential minerals calcium, phosphorus, iron, sodium and potassium. Furthermore, rice contains good amounts of significant vitamins, such as thiamine, riboflavin, niacin and tocopherol (Abid *et al.*, 2024). India's fast-growing population has picked up the demand for national food security, with a high demand for rice varieties that have both high quality and yield. Raising rice productivity and production has therefore become a priority. This can only be achieved if plant breeders have a good understanding of the nature and extent of genetic variation controlling the inheritance of quantitative traits in rice. The creation of high-yielding, superior varieties is crucial for enhancing overall productivity. To this end, breeders must maintain a diverse and healthy pool of desirable donor parents (Murali *et al.*, 2023).

Evaluating genetic variability is a fundamental step in any plant breeding program. The existence of variability among different traits is crucial, as it enables the identification and selection of promising genetic material. This selection process is essential for the development of high-yielding varieties, which remains the primary objective of plant breeding efforts (Tiwari *et al.*, 2019). Effective genetic improvement of a genotype relies on a comprehensive understanding of key genetic parameters. These include the Phenotypic Coefficient of Variation (PCV), Genotypic Coefficient of Variation (GCV), broad-sense heritability, and genetic gain. These parameters provide valuable insights into the extent of genetic diversity and the potential for successful selection and breeding in a given crop or plant (Kishore *et al.*, 2015).

Correlation analysis is a useful technique for determining relationships among various variables, allowing researchers to know about associations and make logical predictions. Expanding on this, path analysis provides a more extensive method by determining the cause-and-effect relationship. It enables correlation to be partitioned into direct and indirect effects and shows how independent variables affect a dependent variable. This method is particularly useful in agronomic and breeding research, where knowledge of the contribution of individual traits to yield or other critical outcomes is vital for efficient selection and improvement. (Mahendran *et al.*, 2024).

Principal Component Analysis (PCA), on the other hand, is concerned with dimensionality reduction of complicated data sets with the intention to retain the most significant variations in the data. PCA is therefore particularly valuable for the revelation of underlying structures, clustering comparable observations, and identifying significant characteristics worthy of further examination. When combined with correlation and path analysis, PCA helps bring more effective and enlightened decision-making (Edukondalu *et al.*, 2024).

Materials and Methods

Experimental site and materials

The experiment was conducted at the Agricultural Research Farm, School of Agriculture, Lovely Professional University, Jalandhar (Punjab). This location lies in (31° 15' 47" North, 75° 41' 20" East). The study was focused on 50 different rice genotypes (Table 1), evaluated using a randomized block design (RBD) with three replications. Nursery sowing took place on May 27, 2024, and 31-day-old seedlings were transplanted into the main field on July 1, 2024. The crop was cultivated using a row spacing of 20 cm and a plant spacing of 15 cm, following recommended agronomic practices to ensure optimal growth. A set of recommended practices was implemented to maintain crop health.

Observations recorded

Total ten biometrical traits *viz.*, plant height (cm), the number of productive tillers per plant, panicle length (cm), grains per panicle, 100 grain weight (g), biological yield, harvest index and seed yield per plant (g) were observed and recorded at appropriate stages from the five randomly selected plants from each replication. Characters days to 50 per cent flowering and days to maturity were recorded on plot basis.

Statistical analysis

The statistical analysis was carried out using latest version of R software. Analysis of variance, variability, correlation coefficient, path analysis and PCA parameters were calculated in accordance to Robinson *et al.* (1955), Allard (1960), Singh and Choudhury (1979), Al-Jibouri *et al.* (1958), Wright (1934), Dewey and Lu (1959), Pearson (1901).

Table 1 : List of rice genotypes used in the present experiment with the source/pedigree/origin.

S. no.	Genotypes	Source/Pedigree/Developed by
1	CO-51	ADT 43 and RR 272-1745
2	HUR -105	Banaras Hindu University (BHU), Varanasi, India
3	HUR-917	Banaras Hindu University (BHU), Varanasi, India
4	PUSA-1509	Indian Agricultural Research Institute (IARI), New Delhi
5	PUSA SAMBA 1850	Indian Agricultural Research Institute (IARI), New Delhi
6	PUSA SL-03	Indian Agricultural Research Institute (IARI), New Delhi
7	SAMBA MASURI	Indian Institute of Rice Research (ICAR-IIRR), Hyderabad
8	SWARNA	ICAR-NRRI
9	HUR-1309	Banaras Hindu University (BHU) in Varanasi
10	HUR-1322	Banaras Hindu University (BHU) in Varanasi
11	PUSA 1776	Indian Agricultural Research Institute (IARI), New Delhi
12	ASGST-11	TNAU, Coimbatore.
13	ASGST-16	TNAU, Coimbatore.
14	ASGST-26	TNAU, Coimbatore.

Table 1 continued...

Table 1 continued...

15	ASGST-34	TNAU, Coimbatore.
16	ASGST-39	TNAU, Coimbatore.
17	GOPAL BHAG	B C K V, Kolkata
18	PUSA 1638	Indian Agricultural Research Institute (IARI).
19	SURJOO-52	Indian Agricultural Research Institute (IARI).
20	LALAAT	Indian Agricultural Research Institute (IARI).
21	BIRSMATI	Indian Agricultural Research Institute (IARI).
22	MTU-1010	Andhra Pradesh Rice Research Institute (APRI)
23	NAVEEN	Indian Agricultural Research Institute (IARI), New Delhi, India.
24	RAJENDRA MAHSURI	Bihar Agricultural University, Sabour, Bihar, India.
25	BIRDPUR KALA NAMAK	-NA-
26	IR 167 1662	-NA-
27	IR 9578-15-1-1-4	-NA-
28	IR 82635-B-B-75-2	-NA-
29	RAJENNDRA KASTURI	Bihar Agricultural University, Sabour, Bihar, India.
30	PR 121	Punjab Agricultural University (PAU), Ludhiana, India.
31	JGL 384	Prof. Jayashankar Telangana State Agril. Uni. (PJTSAU), Hyderabad, India
32	URG 27	-NA-
33	DRR 50	ICAR-Indian Institute of Rice Research (ICAR-IIRR), Hyderabad
34	IR 64 DUB-1	International Rice Research Institute (IRRI)
35	SWARNA SUB 1	International Rice Research Institute (IRRI)
36	CR DHAN 800	National Rice Research Institute (NRRI), Cuttack, India
37	HUR-36	Haryana Agricultural University, Hisar, India.
38	HUR-1304	Haryana Agricultural University, Hisar, India.
39	URG 28	-NA-
40	URG 19	-NA-
41	HUR 917	Developed at Banaras Hindu University (BHU), Varanasi, India.
42	URG 1	-NA-
43	URG 15	-NA-
44	URG 49	-NA-
45	URG 14	-NA-
46	URG 29	-NA-
47	URG 37	-NA-
48	URG 38	-NA-
49	CRD-202	National Rice Research Institute (NRRI), Cuttack
50	HUR-2-1	Banaras Hindu University (BHU) in Varanasi

Results and Discussion

Analysis of variance (ANOVA)

For development of varieties plant breeders depends on natural variations exists in the populations or they have to explore new ways to create it through different plant breeding techniques. In the materials collected and evaluated from pan India regions, the mean sum of squares due to genotypes were found to be significant for all the traits under study indicating the presence of significant differences in the traits across the genotypes (Table 2). While mean squares due replications were non-significant for all the traits.

Mean performance

Comparison between genotypic and overall populations means helps breeder identify the higher and poor performers based on the phenotypic data recorded (Table 3). Similarly, the mean data comparisons in between 50 genotypes for seed yield per plant revealed that there are a few genotypes out performing above overall population mean *viz.*; HUR-1304 (41.77 g), HUR 917 (39.58 g), URG 1 (39.06 g), BIRDPUR KALA NAMAK (37. 01 g) and RAJENNDRA KASTURI

Table 2 : Analysis of variance (ANOVA) for ten quantitative traits of fifty rice genotypes.

Characters	Replication	Genotypes	Error
Df	**2**	**49**	**98**
Days to 50% flowering (DFF)	0.78	263.56**	6.45
Days to maturity (DM)	15.86	231.96**	6.90
Plant height (cm) (PH)	44.11	507.25**	24.60
Productive tiller (PT)	0.84	4.57**	0.44
Panicle length (cm) PL)	3.39	20.86**	1.45
1000 seed weight (g) (TSW)	0.01	28.28**	0.01
Grains per panicle (GPP)	51.09	660.15**	25.42
Biological yield/plant (BY)	6.34	297.57**	3.37
Harvest Index (HI)	1.04	216.48**	6.28
Seed yield per plant (g) (SYP)	0.89	94.73**	2.66

* Significance at 1% level.

Table 3 : Top 5 performers for seed yield per plants along with the supporting traits.

Genotypes	DFF	DM	PH	PT	PL	TSW	GPP	BY	HI	SY
BIRDPUR KALA NAMAK	92.00	124.67	103.64	15.73	22.32	22.57	125.49	94.46	39.18	37.01
RAJENNDRA KASTURI	109.33	138.33	145.32	14.14	22.34	18.3	122.28	117.72	31.35	36.9
HUR-1304	87.33	122.67	109.54	8.66	26.76	21.72	157.7	102.57	40.75	41.77
HUR 917	90.33	116.67	114.15	15.12	23.24	25.32	129.02	52.27	75.76	39.58
URG 1	90.33	123	140.62	13.9	19.16	24.81	127.66	102.37	38.16	39.06
Overall Mean	97.06	127.56	122.844	14.2	22.694	23.224	132.074	79.549	38.311	29.517
Max	118	145	145.32	16.84	28	29.42	167.61	117.72	75.76	41.77
Min	87	115	99.5	8.66	15.63	15.55	104.07	43.51	21.03	17.91
SE(d) ±	9.54	9	13.55	1.34	2.8	3.05	15.31	18.21	8.68	5.74
CD at 5%	4.12	4.26	8.04	1.08	1.95	0.18	8.17	2.97	4.06	2.64
CV%	2.62	2.06	4.04	4.67	5.31	0.48	3.82	2.31	6.54	5.53

(36.90 g). The top five performers also had satisfactory performances in desirable traits for selection. The genotype HUR-1304 stands out as a high-yielding, early-maturing variety with a high harvest index and strong grain production traits like GPP and PL. Its combination of early flowering and maturity with excellent yield and agronomic efficiency makes it a highly promising genotype for cultivation, especially in areas where early harvesting is needed or multiple cropping is practiced.

Genotypic and phenotypic coefficient of variations (GCV and PCV)

Analysis of genotypes reported that the PCV was found to be marginally higher than the GCV for all the traits studied which reveals the environmental influence on the expression of characters. PCV and GCV were high for the traits *viz*., biological yield 22.92% and 23.04%, Harvest index 21.84% and 22.8%, The traits like seed yield per plant (18.76% and 19.56%), grain per panicle (11.01% and 11.65%), test weight (13.21% and 13.22%), panicle length (11.2% and 12.4%) and plant height (10.32% and 11.08%) exhibited moderate GCV and PCV, while days to 50% flowering (9.53% and 9.89%), days to maturity (6.79% and 7.09%) and panicle length (11.2% and 12.4%) showed lowest GCV and PCV value. These results were in accordance in rice with (Sree *et al*., 2023), and (Singh *et al*., 2024) for high GCV and PCV, (Kushwaha *et al*., 2024) for seed yield per plant, (Kerketta *et al*., 2024) for panicle length (Aklilu *et al*., 2024) for days to maturity, (Sao *et al*., 2024) for days to 50% flowering, (Yadav *et al*., 2024) for productive tillers (Table 4).

Heritability and genetic advance

High heritability coupled with high genetic advance as per cent of mean was recorded for biological yield (99.00%, 46.99%), harvest index, test weight (99.8%, 27.21%) and seed yield per plant (92.00%, 37.08%). These results were in accordance in rice with (Nagoo *et al*., 2024), (Kerketta *et al*., 2024) for test weight (Naik *et al*., 2022) for harvest index and (Kumar *et al*., 2024) for seed yield per plant. High heritability along with moderate genetic advance was found for days to 50 percent flowering (93.00%, 18.94%), days to maturity (91.50%, 13.38%) and plant height (86.70%, 19.80%) (Table 4). Similar findings were also reported by Anusha *et al*. (2024), Nagoo *et al*. (2024) for days to 50% flowering (Soundharya *et al*., 2024) for days to maturity, (Pardhi *et al*., 2025; Yadav and Chetariya, 2022) for plant height.

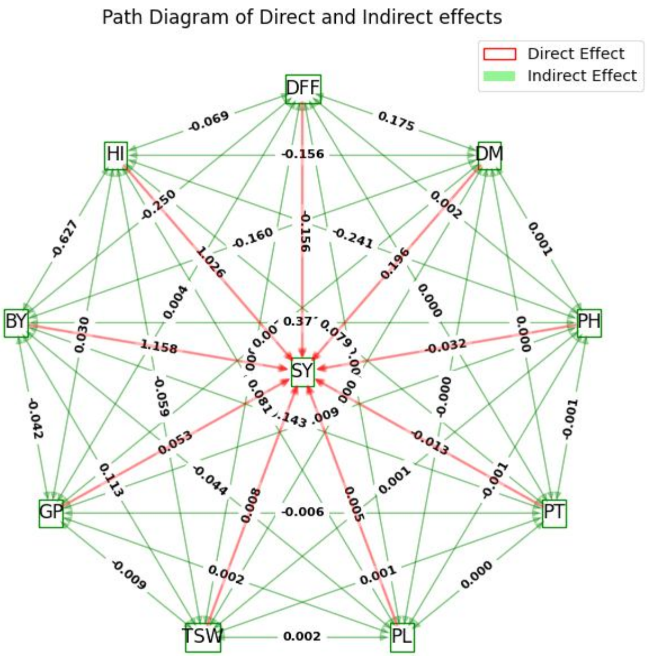

Fig. 1 : Phenotypic path diagram indicating direct and indirect effect.

Residuals effect at GL = 0.0583

Residual effect at PL= 0.0765

Table 4 : Genetic variability parameters for 10 characters of rice under study.

S. no.	Traits	Hbs%	Vg	Vp	GCV	PCV	GA	GA%
1	**DFF**	93.00	85.70	92.16	9.54	9.89	18.39	18.94
2	**DM**	91.50	75.01	81.92	6.79	7.09	17.07	13.38
3	**PH**	86.70	160.88	185.48	10.32	11.08	24.33	19.80
4	**PT**	75.80	1.37	1.81	8.27	9.50	2.10	14.83
5	**PL**	81.60	6.46	7.92	11.20	12.40	4.73	20.86
6	**TSW**	99.80	9.42	9.43	13.21	13.22	6.31	27.21
7	**GPP**	89.20	211.57	236.99	11.01	11.65	28.31	21.43
8	**BY**	99.00	332.66	336.02	22.92	23.04	37.38	46.99
9	**HI**	91.70	70.06	76.35	21.84	22.80	16.51	43.11
10	**SYP**	92.00	30.68	33.35	18.76	19.56	10.94	37.08

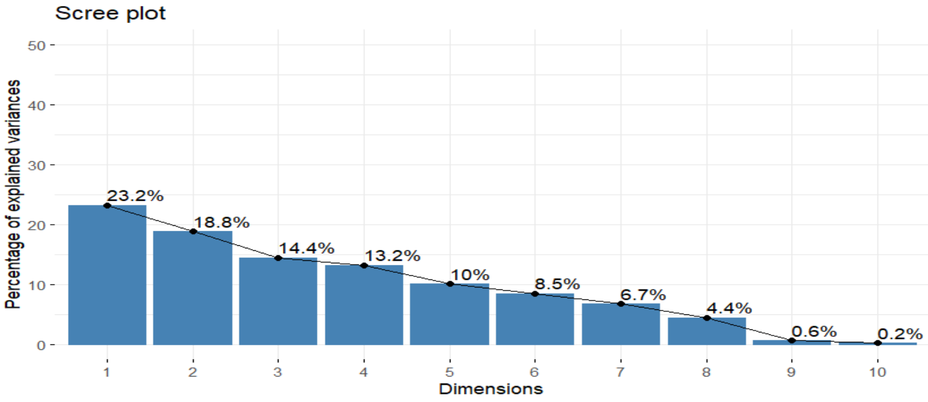

Fig. 2 : Scree plot showing principal components and percentage of variation explained.

Character association

Establish phenotypic and genotypic relationships between all combinations of traits to evaluate the nature, degree, and direction of variation, to enable efficient selection for useful and favorable breeding results, this study revealed that there is a moderate and positive correlation between biological yield (0.526) and seed yield per plant, and a moderately weak positive correlation between harvest index (0.307) and seed yield per plant. On the other hand, characters like days to 50% flowering (-0.293) and days to maturity (-0.251) showed a weak negative correlation with seed yield per plant (Table 5). These findings are consistent with the studies of (Shrivastav and Op, 2023; Prajapati *et al.*, 2022 and Saketh *et al.* (2023), where days to 50% flowering and days to maturity were negatively correlated with seed yield. Similar results were also reported by Kalpande *et al.* (2024).

Direct and indirect effects

Path coefficient analysis helps a breeder understand the effects of interrelated traits on dependent trait (yield) by partitioning effects into two components, direct and indirect effects. The direct and indirect effects of revealed that biological yield exerted the highest positive direct effect on seed yield at both genotypic and phenotypic levels followed by harvest index, days to maturity, days to 50% flowering (Fig. 1). Plant height depicted negative direct effect at both the levels. Thus, biological yield, harvest index, days to maturity, days to 50% flowering directly emerged as major yield contributor. The identification of days to maturity, days to 50% flowering as important direct yield contributing characters is in conformity with the reports of Shende *et al.* (2025), Salunkhe *et al.* (2024), Babu *et al.* (2024).

Principal component analysis (PCA)

In the present study, first three principal components had eigen value greater than one and they cumulatively explained 55.00 per cent of the total variation present in the original data set (Fig. 2). The PC1 explained 23.62 percent the characters which contributed for the variation were days to 50 per cent flowering and days to maturity, while the PC2 exhibited 18.31 percent

Table 5 : Character correlation at genotypic and phenotypic levels among ten metric traits of rice.

Characters	Level	DM	PH	PT	PL	TSW	GPP	BY	HI	SYP
DFF	r_g	0.9638 **	-0.0712	0.0041	-0.0195	0.0482	0.0880	-0.2205	-0.0862	-0.3248 *
	r_p	0.8942 **	-0.0693	-0.0033	-0.0342	0.0464	0.0811	-0.2158 **	-0.0677	-0.2937 **
DM	r_g	1 **	-0.0416	-0.0253	-0.0270	0.0394	0.1488	-0.1436	-0.1631	-0.2716
	r_p	1 **	-0.0372	-0.0122	-0.0404	0.0357	0.1406	-0.1384	-0.1517	-0.2510**
PH	r_g		1 **	0.1529	-0.3144 *	0.1730	-0.1871	0.3499 *	-0.2773	0.0836
	r_p		1 **	0.1023	-0.2623 **	0.1619 *	-0.1623 *	0.3207 **	-0.2349 **	0.0914
PT	r_g			1 **	0.0749	0.1592	-0.1314	-0.1488	0.0947	-0.0989
	r_p			1 **	0.0638	0.1388	-0.1053	-0.1236	0.0769	-0.0862
PL	r_g				1 **	0.3339 *	0.0524	-0.0417	0.0962	0.0653
	r_p				1 **	0.2998 **	0.0470	-0.0377	0.0786	0.0521
TSW	r_g					1 **	-0.1729	0.0983	-0.0604	0.0488
	r_p					1 **	-0.1646 *	0.0974	-0.0574	0.0472
GPP	r_g						1 **	-0.0427	0.0392	0.0625
	r_p						1 **	-0.0362	0.0291	0.0612
BY	r_g							1 **	-0.6321**	0.5519**
	r_p							1 **	-0.6114**	0.5266**
HI	r_g								1 **	0.2554
	r_p								1 **	0.3073**

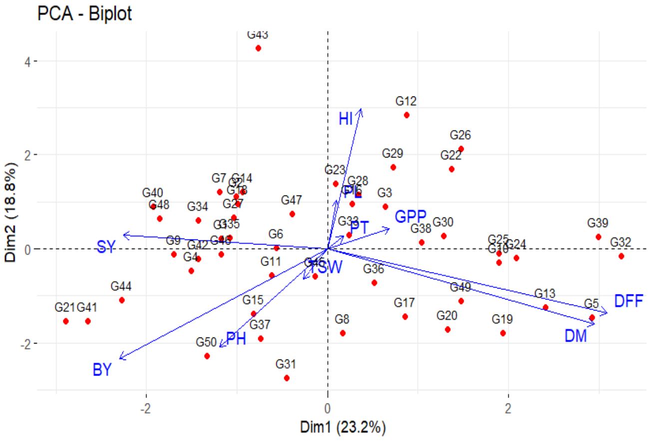

Fig. 3 : PCA biplot graph of different traits for first two principal components.

was mostly contributed by the harvest index and panicle length and PC3 exhibited 14.06 percent variability with major character contributed like test weight, productive tiller and panicle length among the genotypes for the traits under study (Table 6). Similar results were noted earlier by Ratnam *et al*. (2022) for days to 50% flowering, (Islam *et al*., 2024) for days to maturity, (Nivedha *et al*., 2024) for test weight, (Sruthi *et al*., 2024) for panicle length for productive tiller.

Table 6 : Eigen values, percent variance and cumulative eigen values for principal components.

	PC1	PC2	PC3
Eigenvalues	2.3212	1.8793	1.4430
Standard deviation	1.5235	1.3708	1.2013
Proportion of Variance	0.2321	0.1879	0.1443
Cumulative Proportion	0.2321	0.42	0.5643

The character biological yield (-0.415), Seed yield per plant (-0.409), Plant height (-0.213) and TSW (-0.053) showed negative loading in PC1, while the other traits showed positive loadings towards the first principal component. In PC2, positive loadings were showed by productive tiller, panicle length, grain per panicle, harvest index and seed yield per plant whereas other traits showed negative loadings towards PC2. In PC3, characters viz., days to maturity, grain per panicle and seed yield per plant showed negative loadings whereas, other characters showed positive loadings (Table 7).

The biplot diagram of the first two principal components depicted the interaction among the characters and also with each genotype (Fig. 3). The vector length of each character shows how much it contributed to the overall divergence; the longer the vector, the greater the contribution. The character days to 50% flowering and days to maturity showed maximum vector length indicating

Table 7 : Component loading of different characters in rice for yield and its contributing traits.

Characters	PC1	PC2	PC3
DFF	0.557	-0.260	0.025
DM	0.532	-0.313	-0.012
PH	-0.213	-0.408	0.134
PT	0.030	0.057	0.475
PL	0.006	0.195	0.415
TSW	-0.053	-0.138	0.639
GP	0.120	0.080	-0.391
BY	-0.415	-0.479	-0.098
HI	0.054	0.606	0.047
SYP	-0.409	0.066	-0.102

its contribution to the total diversity followed by harvest index, seed yield per plant.

The direction of correlation between the traits is indicated by the angle between the trait vectors. A right angle (90^o) between the vectors indicates no correlation whereas, whereas, the acute angle ($< 90^o$) indicates a positive correlation and obtuse angle (>90) indicates a negative correlation. Out of ten characters under study, the character viz., grain per panicle, panicle length, productive tiller and harvest index showed a positive correlation with single plant yield, whereas the biological yield, test weight and plant height showed negative correlation.

Conclusion

Following the results of this study, enormous genetic variation among the 50 rice genotypes for all the ten quantitative traits was found to show enormous possibilities of selection and genetic improvement. Genotypes HUR-1304, URG 1, and HUR 917 had better mean seed yield, while URG 28 and HUR 917 were revealed as early types of maturing and hence the promising lines of choice for any breeding program. High heritability and genetic advance estimates for such traits as biological yield, harvest index, seed yield per plant, and test weight indicate the dominance of additive gene action, which supports direct selection. Positive correlations and significant direct effects of biological yield, harvest index, earliness to flowering and maturity on seed yield also confirm their significance in improving yield. PCA revealed that three principal components accounted for 55% of the total variability, with certain genotypes like PUSA-1776, HUR-917 and RAJENDRA KASTURI showing significant divergence. These unique genotypes offer valuable potential for hybridization aimed at developing high-yielding rice varieties.

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