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CHARACTERIZATION AND PRINCIPAL COMPONENT ANALYSIS OF RICE GERMPLASM (*ORYZA SATIVA* L.) UNDER SUB-TROPICAL ECOLOGY OF JAMMU REGION OF INDIA

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ABSTRACT

Present study was carried out during *Kharif* 2021 with an aim to assess genetic diversity among rice germplasm lines based on agro-morphological and DUS traits. Thirty rice germplasm lines procured from three different districts of Jammu province were evaluated in Randomized Complete Block Design (RCBD) in three replications having a plot size of 1.6m^2. Analysis of variance revealed significant differences among the germplasm lines for all the traits recorded, while DUS traits were also found to be distinct indicating sufficient variation in the germplasm lines. Estimates of genetic parameters revealed that traits like days to 50 per cent flowering, days to maturity, plant height, 1000 grain weight and grain yield per plant were found to have high heritability coupled with high genetic advance indicating the effectiveness of these traits in selection. Results of D^2 statistics diversified the germplasm lines into 8 clusters and among these cluster 1 was found to have maximum number of germplasm lines (11) followed by cluster 4 (9) and cluster 2 (5) while, clusters 3,5,6,7 and 8 were found to have one germplasm line each. Principal component analysis found characters like kernel length/breadth, panicle length, kernel length, number of days to 50 per cent flowering, number of days to maturity, 1000 grain weight, number of effective tillers per plant, total number of tillers per plant and grain yield per plant were found to be major diversity analysing characters.

Key words : Rice germplasm, Agro-morphological and DUS traits, D^2 analysis, PCA.

Introduction

Rice (*Oryza sativa* L., 2n = 2x = 24) is an essential food grain serving as a staple food for more than 50 per cent of the world's population (Fukagawa and Ziska, 2019). In India, it is one of the predominant food crops, providing remuneration to several households. Primary goal of a plant breeding programme is to develop superior crop varieties with higher yield along with resistance to various stresses. To develop such excellent varieties in crop species like rice, plant breeder thrives for variation to be exploited. India is considered epicentre for rice cultivation with rich and historical background, comprising wide range of local germplasm lines. These germplasm lines are store house for variability and have the potential to be suitable donors in hybridization programmes. The true skill of plant breeder lies in identifying and utilizing the suitable variability present so as to develop superior cultivars. Agro-morphological markers act as a fundamental tool in a plant breeder's quest for variability. Agro-morphological traits provide information with respect to genetic diversity (Lin, 1991) that can be used in plant breeding activities.

Characterization based on agro-morphological variations involves studying and analysing various morphological features and assessing the variability among different germplasm lines. The germplasm lines are grouped based on presence or absence of traits or if present they are further sub-divided based on characteristic of the trait. The amount of variability among the germplasm for phenotypic characters is quantified using estimates of genotypic and phenotypic coefficient of variation, heritability and genetic advance. The

genotypic coefficient of variability (GCV) indicates the inherent capability of a genotype to cause the heterogeneity in a polygenic trait. The estimates of genotypic and phenotypic coefficient of variance together help to decipher the role of environment in causing a trait. Higher estimates of PCV than GCV indicates the apparent role of environment in the expression of a trait. Heritability combined with genetic advance are the fundamental estimates that determine transmissibility of a character from one generation to another. Multivariate analysis using Mahalanobis (D^2) statistics and principal component analysis are two of the most prominent biometrical techniques that help to understand relationship among the variables. Mahalanobis statistics reveals genetic similarities by grouping the germplasm lines based on the multivariate relationships and provide inter and intra cluster differences showcasing the diversification which helps in selection of parents for hybridization. Principal component analysis divides the data into a set of few components and ranks them according to their per cent value and variability and also helps us to interpret data on multiple dimensions.

Materials and Methods

Experimental material

Thirty germplasm lines/landraces/farmers' varieties collected from three intermediate hill districts of Jammu province *viz*., Poonch, Rajouri and Udhampur along with germplasm lines maintained at Division of Plant Breeding and Genetics, SKUAST-J and recently released varieties constitute the experimental material. The details of experimental materials is presented in Table 1.

Experimental design and layout

The present study was conducted at experimental area of the Division of Plant Breeding and Genetics, Faculty of Agriculture, SKUAST-J, Main Campus, Chatha, Jammu during *Kharif* 2021. The seeds of the germplasm lines were sown in nursery during the month of June, 2021 and twenty-five days old healthy seedlings were transplanted in Randomized Complete Block Design (RCBD) with three replications with a plot of 1.6 m^2 having spacing of 20 × 15 cm during the month of July, 2021. Single seedling was transplanted per hill and all the necessary package of practices were followed for the optimum growth.

Table 1 : Description of experimental material used in the present study.

S. no.	Area of collection	Code	S.no.	Area of collection	Code
1.	Village Gulpur Tehsil and Distt. Poonch	VGP	16.	SKUAST-J	SJR 76
2.	Village. Barbeen Distt.Udhampur Tehsil Ramnagar	BAIGMI	17.	SKUAST-J	SJR 80
3.	Village. Barbeen Distt. Udhampur Tehsil Ramnagar	BANJI	18.	SKUAST-J	SJR 82
4.	Village. Barbeen Distt. Udhampur Tehsil Ramnagar	PALM	19.	SKUAST-J	SJR 92
5.	Village Sankari Tehsil and Distt. Rajouri	RUCY	20.	SKUAST-J	SJR 51
6.	Village Khanetar Bela Tehsil and Distt. Poonch	R. RANJAH	21.	SKUAST-J	JB 118
7.	Village Chandak Tehsil and Distt. Poonch	CHANDAKI	22.	SKUAST-J	JB 123
8.	SKUAST-J	SURJEET	23.	SKUAST-J	JB 129
9.	SKUAST-J	KUDRAT	24.	SKUAST-J	JB 138
10.	SKUAST-J	TILAK	25.	SKUAST-J	K 343
11.	Village Rehan Tehsil and Distt. Rajouri	VRR	26.	Village Chaktroo Tehsil and Distt. Poonch	VCP
12.	Village Kalar Tehsil and Distt. Rajouri	VKR	27.	Village Jhullas Tehsil and Distt. Poonch	VJP
13.	Village Dalogra Tehsil and Distt. Rajouri	VDR	28.	Village Ajote Tehsil and Distt. Poonch	VAP
14.	Village Manjakote Tehsil and Distt. Rajouri	VMR	29.	VillageKhanetar BelaTehsil and Distt. Poonch	VKBP
15.	SKUAST-J	SJR 70	30.	Village Qazi Morah Tehsil and Distt. Poonch	VQMP

Agro-morphological traits studied

Agro-morphological observations were recorded by randomly choosing 5 plants from each germplasm line from each replication for the characteristics like plant height (cm), total number of tillers per plant, number of effective tillers per plant, panicle length (cm) and descriptors for traits including leaf blade colour, presence of awn, panicle type, flag leaf colour and ligule colour were recorded for each germplasm line in each replication. The characters like number of days to 50 per cent flowering and number days to maturity were observed by counting the days from sowing till the advent of the characters. The post-harvest characters like 1000 grain weight (g), grain yield per plant, kernel length (mm), kernel breadth (mm), length/ breadth ratio and seed coat colour were recorded after harvesting, threshing and drying the seeds.

Data analysis

The recorded data for various parameters understudy were analysed using WINDOSTAT 9.2 and principal component analysis was performed using MINITAB 20.4.

Results and Discussion

Analysis of variance

Analysis of variance (Table 2) for all the traits was found to be significant indicating the presence of significant variation among the germplasm lines. Results of similar kind were reported by Htwe *et al*. (2019), Sarif *et al*. (2020), Usman *et al*. (2022). The significant values of analysis of variance for all the characters determines the diverseness among the germplasm lines and also can be recommended for selection of superior parents for hybridization.

Variability among the germplasm lines for qualitative traits

The germplasm under present study was classified based on the quantitative traits *viz.*, seed coat colour, panicle type, leaf blade colour, awn character, flag leaf colour and ligule colour. The observations recorded are presented in Table 3. Among the germplasm lines, white seed coat and brown seed coat each were observed in 47 per cent of the lines and red seed coat and variegated purple seed coat were observed in rarity with one germplasm line (3 per cent) each. With respect to panicle type, deflexed type was observed in majority (18) germplasm lines covering 60 per cent of the population, followed by drooping type (8 lines) and semi-straight type (5 lines). For leaf base colour, 56.7 per cent (17 lines) of the germplasm lines showed light green colour and rest

Table 2 : Analysis of variance among germplasm lines under present study.

Source of variation	df	Number of days to 50 per cent flowering	Plant height (cm)	Total number of tillers per plant	Number of effective tillers per plant	Number of days to maturity	Panicle length (cm)	1000 grain weight(g)	Grain yield per plant (g)	Kernel length (mm)	Kernel breadth (mm)	Length/ breadth
Replications	2	2.43	3.26	8.61	7.81	1.54	1.88	8.19	1.21	0.03	0.01	0.02
Treatments	29	371.16**	589.89**	18.99**	13.26*	353.51**	26.91**	45.84**	22.18**	3.42**	0.34**	2.65**
Error	58	1.46	1.71	2.61	2.39	2.10	1.52	1.16	2.75	0.01	0.01	0.01

**, * represents significance level at 1 per cent and 5 per cent, respectively.

Table 3 : Descriptors in rice germplasm lines based on DUS characteristics.

Character	Descriptors	Germplasm lines	Frequency
Seed Coat colour	White	VGP,PALM,SURJEET,VRR,SJR 82, SJR 51, JB 118, JB 123, JB 129, JB 138, VCP, VAP, VKBP, VQMP	0.47
	Brown	BAIGMI, RUCY, CHANDAKI, KUDRAT, TILAK, VKR, VDR, VMR, SJR 70, SJR 76, SJR 80, SJR 92, K343, VJP	0.47
	Red	R. RANJAH	0.03
	Variegated Purple	BANJI	0.03
Panicle Type	Straight	-	0.00
	Semi-Straight	BANJI, KUDRAT, TILAK, VMR, JB 138	0.16
	Drooping	PALM, RUCY, R. RANJAH, CHANDAKI, SURJEET, K 343, VAP, VKBP	0.26
	Deflexed	VGP, BAIGMI, VRR, VKR, VDR, VMR, SJR 70, SJR 76, SJR 80, SJR 82, SJR 92, SJR 51, JB 118, JB 123, JB 129, VCP, VJP, VQMP	0.60
Leaf blade colour	Light	BANJI,PALM,RUCY,R. RANJAH, CHANDAKI,VKR, VDR,VMR, SJR 70,SJR 80,SJR 82,SJR 92,JB 118,JB 123,K 343,VCP, VKBP	0.57
	Medium	VGP, BAIGMI, SURJEET, KUDRAT, TILAK, VRR, SJR 76, SJR51, JB129, JB138, VJP, VAP, VQMP	0.43
	Dark	-	0.00
Presence of awn	Present	BAIGMI, SURJEET, TILAK, SJR 70, SJR 76, SJR 80, SJR 82, JB 118, JB123, JB 138, VCP, VJP, VAP	0.43
	Absent	VGP, BANJI, PALM, RUCY, R. RANJAH, CHANDAKI, KUDRAT, VRR, VKR, VDR, VMR, SJR 92, SJR 51, JB 129, K 343, VKBP, VQMP	0.57
Flag leaf colour	Green	VGP, BAIGMI, BANJI, PALM, RUCY, R. RANJAH, CHANDAKI, SURJEET, KUDRAT, TILAK, VRR, VKR, VDR, VMR, SJR 70, SJR 76, SJR 80, SJR 82, SJR 92, SJR 51, JB 118, JB 123, JB 129, JB 138, K 343, VCP, VJP, VAP, VKBP, VQMP	1.00
	Purple	-	0.00
Ligule Colour	Green	VGP, BAIGMI, BANJI, PALM, RUCY, R. RANJAH, CHANDAKI, SURJEET, KUDRAT, TILAK, VRR, VKR, VDR, VMR, SJR 70, SJR 76, SJR 80, SJR 82, SJR 92, SJR51, JB 118, JB 123, JB 129, JB 138, K 343, VCP, VJP, VAP, VKBP, VQMP	1.00
	Purple	-	0.00

43.3 per cent showed medium green coloured leaf base. Majority of germplasm lines (17 lines) was observed to have no awn attached to the grain whereas; rest of the 13 lines has awn attached to the grain. Characters like flag leaf colour and ligule coloured were found to be monomorphic.

Estimates of genetic parameters

Genetic parameters (Table 4) revealed that phenotypic and genotypic variance estimates are more or less similar with phenotypic variance slightly higher than genotypic variance for most of the traits indicating that the environment has less influence in expression of the characters and the variation so observed is by virtue of the germplasm lines itself. Results and conclusions of similar kind were also reported by Govintharaj *et al*. (2018) and Htwe *et al*. (2019). Estimates of coefficients of variation at genotypic and phenotypic levels were observed to be higher in kernel length/breadth ratio and total number of tillers per plant. Moderate estimates of coefficients of variation at genotypic and phenotypic levels was observed in number of effective tillers per plant, 1000 grain weight, kernel breadth, kernel length, grain yield per plant, panicle length and plant height. Lower estimates of PCV and GCV were observed in number of days to 50 per cent flowering and number of days to maturity. Results of similar kind were also reported by Islam *et al*. (2015), Dey *et al*. (2019), Patel *et al*. (2021). The estimates of PCV were observed to be higher than

GCV indicating the influence of environment in developing phenotype. The higher estimates of GCV and PCV indicate the scope of these traits for selection. Relatively lower difference between PCV and GCV indicates the character expression is mainly due to genotype itself.

Heritability determines the transmissibility of that character from one generation to another. Results of present study revealed that all the traits exhibited high heritability (> 60 per cent). Results of similar kind were reported by Kumar *et al*. (2018), Hake and Bhoite (2021), Hasan *et al*. (2022). High heritability coupled with high genetic advance provides reliable results of presence of additive genetic effects in the germplasm lines. High heritability coupled with high genetic advance was observed in characters *viz.*, plant height, number of days to 50 per cent flowering and number of days to maturity. Results of similar kind were reported by Srujana *et al*. (2017), Sandeep et al. (2018). The inclusion of high heritability with genetic advance as per cent mean gives precise results of additive gene effect and selection shall be effective for these characters (Larik *et al.*, 2000). High heritability coupled with high genetic advance as percent of mean was observed for all the characters studied (> 20 per cent) except for number of days to maturity which has moderate genetic advance as percentage of mean. Results of similar kind were observed by Tuhina-Khatun *et al*. (2015), Singh and Verma (2018), Lipi *et al*. (2020).

Table 4 : Estimates of genetic parameters among germplasm lines.

Characters	Genotypic variance (σ^2_g)	Phenotypic variance (σ^2_p)	Genotypic coefficient of variance (per cent)	Phenotypic coefficient of variance (per cent)	Heritability(bs) (per cent)	Genetic advance	Genetic advance as percent of mean (per cent)
No of days to 50 per cent flowering	123.23	123.72	10.75	10.77	99.61	22.82	22.09
Plant height (cm)	199.06	199.63	11.62	11.64	99.72	29.19	24.04
Total number of tillers per plant	5.46	6.33	19.89	21.42	86.27	4.47	38.06
No. of effective tillers per plant	3.62	4.41	17.92	19.79	81.98	3.55	33.43
No. of days to maturity	117.14	117.84	7.92	7.94	99.41	22.23	16.26
Panicle length(cm)	8.46	8.97	11.73	12.07	94.35	5.82	23.46
1000 grain weight	14.89	15.28	18.04	18.28	97.47	7.85	36.69
Grain yield per plant(g)	6.47	7.39	12.35	13.2	87.58	4.91	23.81
Kernel length(mm)	1.13	1.14	16.34	16.45	98.63	2.17	33.43
Kernel breadth(mm)	0.11	0.11	16.94	17.04	98.83	0.69	34.68
Length/Breadth	0.87	0.88	27.37	27.50	99.02	1.92	56.10

Genetic diversity studies

The diversity among the 30 germplasm lines with respect to traits is elucidated using Mahalanobis (D^2) statistics and principal component analysis.

Mahalanobis (D^2) statistics

Divergence analysis using D^2 statistics and clustering of 30 germplasm lines using Tocher's method (Rao, 1952) a total of 8 clusters were generated (Table 5 and Fig. 1). Results of similar kind were reported by Kumari *et al*. (2019), Parimala *et al*. (2020), Kumari *et al*. (2022). Out of 8 clusters, 3 clusters (1, 2 and 4) were major clusters and remaining 5 clusters (3, 5, 6, 7 and 8) were minor clusters with one germplasm line each. The maximum germplasm lines were observed in cluster 1(11) followed by cluster 4

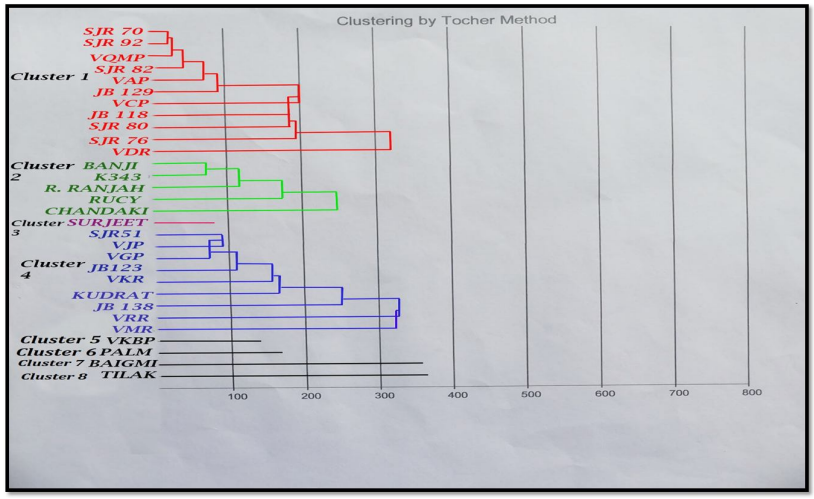

Fig. 1 : Clustering of germplasm lines based on Tocher's Method.

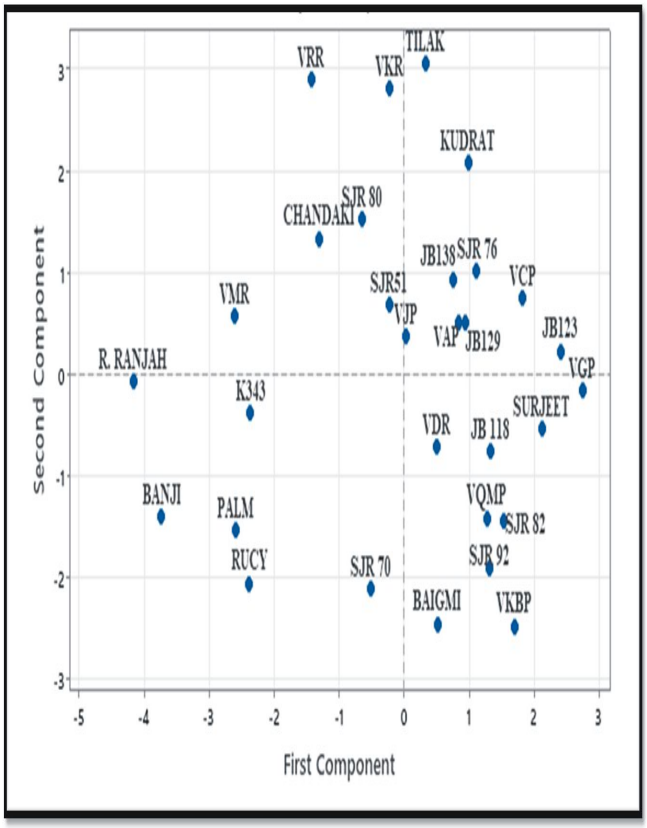

Fig. 2 : Principle component analysis.

(9) and cluster 2 (5). The high intra-cluster values indicated the presence of high genetic diversity among the germplasm lines within each cluster, which can be used in selecting phenotypically superior germplasm lines. The average D^2 distances among the different clusters were calculated and the distance found between lines within a cluster is presented in Table 6. The maximum inter- cluster distance between 2 clusters was found to be 103.09 between cluster 6 and 8, followed by 86.40 between cluster 2 and 8, 76.03 between cluster 4 and 6, 71.75 between cluster 5 and 8, 69.73 between cluster 3 and 6, 62.89 between cluster 7 and 8, 59.79 between cluster 2 and 4, 54.50 between cluster 1 and 8 and 52.13 between cluster 1 and 8. The high inter-cluster distance indicated the presence of high divergence among the germplasm lines. Results and conclusions of similar trends were reported by Kumar *et al.* (2014) and Koli *et al.* (2022). Selecting superior germplasm within the clusters and attempting hybridization between germplasm of maximum inter-cluster distance yields promising heterotic segregants (Roy and Panwar, 1993; Vivekanandan and Subramanian, 1993). Cluster analysis identified all the released varieties and pre-breeding lines in clusters 1 and 4 and also identified germplasm lines TILAK, PALM and BAIGMI to be most diverse among the germplasm lines. Hence, hybridization among the said lines may yield superior sergeants.

Based on the cluster means (Table 7), cluster 8 (124.33) took maximum days to 50 per cent flowering, cluster 7 (168.39) has taller plants, total number of tillers per plant are highest in cluster 2 (14.02), number of effective tillers per plant are highest in cluster 6 (12.47), cluster 8 took maximum days to mature (161.00), panicle length was found highest in cluster 5 (28.60), cluster 7 recorded highest 1000 grain weight (30.40), grain yield per plant was found highest in cluster 4 (21.82), kernel length was highest in cluster 5 (8.12) , kernel breadth was found highest in cluster 6 (2.21) and highest kernel length/breadth was observed in cluster 3 (4.97). Grain yield per plant, 1000 grain weight, number days to 50 per cent flowering and number of days to maturity are relatively higher contributors for total divergence implicating selection of genotypes based on these characters are ideal (Bose and Pradhan, 2006). Results and conclusions of similar kind was observed by Singh *et al.* (2020) and Sudeepthi *et al.* (2020).

Principal component analysis (PCA)

Principal component analysis in the present study resulted a total of 11 principal components (Table 8) out of which 5 principal components are with eigen values greater than 1 and has variability (per cent) more than 5 are considered (Brejda *et al.*, 2000). The variability (%) contributed by these PCs is 87.74 per cent out of which PC1 accounts for maximum variability (30.51 per cent) followed by PC2 (22.69 per cent), PC3 (13.22 per cent), PC4 (11.19 per cent) and PC5 (10.14 per cent). Results of similar trends were observed by Nachimuthu *et al.*

Table 5 : Distribution of germplasm lines in clusters.

Clusters	Number of lines	Nomenclature of germplasm lines
1	11	SJR 70, SJR 92, VQMP, SJR 82, VAP, JB 129, VCP, JB 118, SJR 80, SJR 76, VDR
2	5	BANJI, K 343, R. RANJAH, RUCY, CHANDAKI
3	1	SURJEET
4	9	SJR 51, JB 138, VJP, VRR, VGP, VMR, JB 123, VKR, KUDRAT
5	1	VKBP
6	1	PALM
7	1	BAIGMI
8	1	TILAK

Table 6 : Inter and Intra (diagonal) cluster distances among germplasm lines.

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster 7	Cluster 8
Cluster 1	14.29	36.34	22.42	29.79	21.71	52.13	22.21	54.50
Cluster 2		15.30	53.93	59.79	22.90	21.30	35.15	86.40
Cluster 3			0.00	17.54	37.08	69.73	31.23	36.82
Cluster 4				16.48	45.81	76.03	36.70	30.93
Cluster 5					0.00	37.12	22.72	71.75
Cluster 6					37.12	0.00	48.39	103.09
Cluster 7							0.00	62.89
Cluster 8								0.00

Table 7 : Cluster means and contribution by individual traits towards total genetic divergence.

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster 7	Cluster 8	Contrib-ution (percent)
No. of days to 50 per cent flowering	103.03	87.73	110.00	113.07	95.00	78.33	100.00	124.33	15.37
Plant height (cm)	116.18	114.6	122.33	124.51	110.85	134.65	168.39	111.51	7.37
Total number of tillers per plant	10.98	14.02	10.8	11.41	10.00	14.00	11.80	12.20	1.23
No. of effective tillers per plant	10.03	12.33	9.73	10.33	9.40	12.47	11.07	10.93	1.23
Number of days to maturity	135.42	122.60	145.00	146.81	128.33	118.00	131.00	161.00	12.99
Panicle length (cm)	25.88	22.19	26.80	24.03	28.6	21.84	27.51	27.65	1.23
1000 grain weight	20.74	22.73	18.83	20.86	27.37	19.23	30.4	16.37	20.40
Grain yield per plant (g)	20.91	20.28	18.47	21.82	18.5	19.52	21.09	20.66	22.43
Kernel length (mm)	7.30	5.65	8.07	5.97	8.12	5.81	6.97	5.29	8.57
Kernel breadth (mm)	1.88	2.14	1.62	2.07	1.85	2.21	1.94	2.19	5.82
Length/breadth	3.97	2.69	4.97	3.02	4.40	2.66	3.60	2.42	3.46

(2014), Pachauri *et al*. (2017), Krishna *et al*. (2022). The first two principal components accounted for the cumulative variance more than 50 per cent and hence can be further utilized in understanding the genetic diversity among the germplasm lines as represented in a 2-dimensional loading plot with PC1 as x-axis and PC2 as y-axis in Fig. 2.

Rotated component matrix studies revealed that PC1 is significantly associated with characters like length/ breadth, panicle length, kernel length, number of days to

Table 8 : Eigen values and per cent variability.

	PC 1	PC 2	PC 3	PC 4	PC 5	PC6	PC 7	PC 8	PC 9	PC 10	PC 11
Eigen value	3.36	2.50	1.45	1.23	1.11	0.54	0.44	0.34	0.02	0.01	0.00
Variance (percent)	30.51	22.69	13.22	11.19	10.14	4.89	4.00	3.06	0.19	0.08	0.04

Table 9 : Principal component scores observed for germplasm lines.

Germplasm lines	PC 1	PC 2	PC 3	PC 4	PC 5
VGP	2.75	0.16	-0.53	0.13	-0.92
BAIGMI	0.52	2.45	-0.60	3.55	0.59
BANJI	-3.74	1.39	0.70	-1.20	-0.83
PALM	-2.59	1.53	-0.25	-0.19	1.00
RUCY	-2.39	2.05	0.39	0.81	-0.49
R. RANJAH	-4.17	0.06	-1.06	0.22	-0.56
CHANDAKI	-1.31	-1.34	-1.15	-1.06	1.66
SURJEET	2.12	0.54	-0.27	-0.10	-1.35
KUDRAT	0.98	-2.09	0.75	-0.56	-1.06
TILAK	0.32	-3.05	1.08	0.56	-1.15
VRR	-1.43	-2.91	-0.10	-0.64	-0.37
VKR	-0.22	-2.82	-1.60	1.08	-1.36
VDR	0.50	0.71	0.60	-0.01	-1.28
VMR	-2.61	-0.58	2.07	1.20	0.63
SJR 70	-0.52	2.11	1.29	-0.48	-0.92
SJR 76	1.12	-1.01	-0.64	-0.47	0.64
SJR 80	-0.66	-1.52	-1.15	0.11	0.69
SJR 82	1.53	1.44	0.31	-1.43	0.64
SJR 92	1.31	1.89	0.17	-1.09	-0.47
SJR 51	-0.23	-0.69	1.81	0.20	-0.37
JB 118	1.33	0.75	1.86	-0.54	1.14
JB 123	2.40	-0.23	2.17	1.31	1.81
JB 129	0.95	-0.51	0.82	-2.56	1.54
JB 138	0.75	-0.94	0.28	1.79	1.40
K 343	-2.37	0.38	-1.54	-0.17	1.27
VCP	1.83	-0.75	-1.75	0.44	0.50
VJP	0.03	-0.38	0.90	0.14	-1.82
VAP	0.85	-0.52	-1.56	-0.45	0.69
VKBP	1.69	2.47	-1.99	-0.26	-0.69
VQMP	1.28	1.41	-1.01	-0.33	-0.54

50 per cent flowering and number of days to maturity with positive loading values and associated with total number of tillers per plant, number of effective tillers per plant and kernel breadth with negative loading values. Similarly, PC2 was positively associated with kernel length, length/breadth, 1000 grain weight, number of effective tillers per plant and total number of tillers per plant and is negatively associated with number of days to 50 per cent flowering, number of days to maturity and kernel breadth and PC3 was found to be positively associated with grain yield per plant, total number of tillers per plant, number of effective tillers per plant, number of days to maturity and number of days to 50 per cent flowering whereas negatively associated with 1000 grain weight and kernel breadth. Characters associated with PC1, PC2 and PC3 are principal discriminatory characters as these PCs contribute maximum towards variation (Sanni *et al*., 2012). The PCA revealed the contribution of both yield attributing characters as well as qualitative characters in genetic variation among the germplasm. Results are in positive association with Sinha and Mishra (2013) and Pachauri *et al*. (2017. PC scores analysed the germplasm lines that are positively associated with each principal component were depicted in Table 9. The germplasm lines with high positive scores in each principal component are highly associated with the respective variables and germplasm lines with negative values; indicate negative correlation with respect to characters associated (Singh and Chaudhary, 1977). Germplasm lines with high positive principal component scores with values > 1.5 in each principal component are considered to be of high value (Rahangdale *et al*., 2021). Hence, germplasm lines VGP, SURJEET, SJR 82, JB1 23, VCP, VKBP, BAIGMI, PALM, RUCY, SJR70, SJR 92, VMR, JB 123, JB 138 and JB 129 are highly positive for the yield and yield attributing as well as grain quality characters.

Conclusion

The present study successfully identified genetic diversity among the 30 germplasm lines based on studied agro-morphological characters. D^2 analysis by Tocher's method classified the germplasm lines into 8 clusters with high intra and inter cluster distances revealing vast diversity among the germplasm lines. The maximum inter-cluster distance was observed between cluster 6 and 8, followed by cluster 2 and 8 and cluster 4 and 6 indicating diversity among the lines. Cluster analysis identified germplasm lines TILAK, PALM and BAIGMI to be diverse from other germplasm lines and also inferred characters like grain yield per plant, 1000 grain weight, number of days to 50 per cent flowering and number of days to maturity had higher contribution in genetic diversity. Principal component analysis of 30 germplasm lines for agro-morphological characters resulted in 11 principal components and also characters like kernel length/

breadth, panicle length, kernel length, number of days to 50 per cent flowering, number of days to maturity, 1000 grain weight, number of effective tillers per plant, total number of tillers per plant and grain yield per plant were found to be major diversity analysing characters.

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