

Genetic Variability and Divergence Studies on Yield under Delayed Sowing Conditions in Rice (*Oryza sativa* L.)

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Authors' contributions

This work was carried out in collaboration among all authors. Authors SV and VIL designed the study, performed the statistical analysis, wrote the protocol and wrote the first draft of the manuscript. Authors KCW and BP managed the analyses of the study. Authors MS and SR managed the literature searches. All authors read and approved the final manuscript.

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ABSTRACT

Timely sowing is a critical factor in realizing the yield as it ensures the vegetative growth to crop up during a period of satisfactory temperatures and fits the cultivar maturity length and growing season. In the present investigation, 38 cold tolerant rice genotypes were studied under delayed sowing conditions at College Farm, Professor Jayashankar Telangana State Agricultural University, Hyderabad. The genotypes were evaluated for yield attributing traits with a view of understanding the extent of variability and diversity present among the genotypes that could be suitable for delayed sowing conditions with cold tolerance. Analysis of variance (ANOVA) indicated significant differences for all the characters with high genotypic coefficient of variation (GCV) and phenotypic

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coefficient of variation (PCV) values for tillers per plant, spikelet fertility, filled grains per panicle and seed yield per plant. High heritability coupled with high genetic advance as percent of the mean was observed for plant height, spikelet fertility, filled grains per panicle with higher variability indicating the presence of fixable gene action which may suggest a reliable crop improvement through selection of these traits. As association analysis could help the breeder to design selection strategies to improve grain yield, correlation studies were carried out which revealed the trait to be having positive relation with all the traits except panicle exertion and panicle length. Path coefficient analysis showed all the traits except panicle exertion and test weight to be exhibiting a direct positive effect on yield, selection for which should be emphasized on these positively associated traits for yield enhancement. Principal component analysis and D^2 analysis together determined plant height, grain yield, panicle exertion, panicle length and yield per plant having higher contributions to the total variability, which could be taken into consideration in rice breeding programmes for further improvement in production.

Keywords: *Delayed sowing; cold tolerant rice genotypes; genetic variability; correlation; path analysis; principal component analysis; D^2 analysis.*

1. INTRODUCTION

Rice, *Oryza sativa* L. (2 n=24) is one of the most important cereals supplying more than half of the total world's population with major source of calories [1]. Besides its significance, it is rich also in genetic diversity in the form of many land races and progenitor species [2]. The onset of the rainy season is the most decisive factor in deciding the yield and quality of rice. Erratic rainfall can trigger extreme climatic events such as floods and drought, which may decline rice production by 8-17% expectedly by 2050 [3]. Delay in rains may cause a water deficit condition affecting the crop at morphological (reduced germination, plant height, plant biomass, number of tillers, various root and leaf traits), physiological (reduced photosynthesis, transpiration, stomatal conductance, water use efficiency), biochemical (accumulation of osmo-protectants) and molecular (altered expression of genes which encode transcription factors and defence related proteins) levels thereby affecting its yield and quality [4].

Seasonal shift and *delayed onset* of the monsoon season evolving as a regular phenomenon due to climate change. Understanding the variability and development of adaptable rice varieties that can give assured yields are to be emphasized. The success of any breeding program depends upon the quantum of genetic variability available for exploitation in the species and the extent to which the desirable traits are heritable [5]. Genetic variability is represented by the occurrence of variation among the plant species due to differences either in their genetic constitution or in environments. For the prediction of gain under selection,

heritability estimates along with genetic advance are more helpful as selection parameters. Estimates of relation among yield attributing traits and their effects on yield are useful in designing an efficient plant breeding program. However, simple correlation may not represent the exact relationship of cause and effect between grain yield and its components [6]. Thus, this effect of yield attributing traits on yield is further separated to identify the direct and indirect selection criteria through path coefficient analysis. This strategy is useful in determining indirect selection criteria for yield when the related component traits show high heritability to the next generation [7].

Genetic diversity of parents is a pre-requisite for a successful breeding programme, since crosses involving parents with maximum genetic divergence would more likely to yield desirable and superior recombinants in the population [8]. The multivariate analysis using Mahalanobis D^2 statistics and principal component analysis provides a powerful tool for measuring the genetic diversity in germplasm lines with respect to the traits considered together [9]. Hence, in this study, 38 cold tolerant genotypes were evaluated to assess the variability and magnitude of genetic diversity for utilization in breeding programmes.

2. MATERIALS AND METHODS

The experiment was conducted with 38 genotypes in Randomized Block Design (RBD) with 2 replications at College Farm, Professor Jayashankar Telangana State Agricultural University (PJTSAU), Rajendranagar, Hyderabad. Weather conditions prevailing during

Table 1. Materials used under the study and their source

S. no	Germplasm lines	Code	Centres/ Source
1	CHINA-1039	G1	SKAU, Khudwani, Kashmir.
2	SKAU-382	G2	SKAU, Khudwani, Kashmir.
3	K-116	G3	SKAU, Khudwani, Kashmir.
4	K-475	G4	SKAU, Khudwani, Kashmir.
5	CHINA-988	G5	SKAU, Khudwani, Kashmir.
6	JHELUM	G6	SKAU, Khudwani, Kashmir.
7	SKAU-5	G7	SKAU, Khudwani, Kashmir.
8	CHINA-1007	G8	SKAU, Khudwani, Kashmir.
9	SHALIMAR-1	G9	SKAU, Khudwani, Kashmir.
10	SKAU-389	G10	SKAU, Khudwani, Kashmir.
11	CHENAB	G11	SKAU, Khudwani, Kashmir.
12	K-332	G12	SKAU, Khudwani, Kashmir.
13	SKAU-339	G13	SKAU, Khudwani, Kashmir.
14	SKAU-341	G14	SKAU, Khudwani, Kashmir.
15	K-429	G15	SKAU, Khudwani, Kashmir.
16	HIMALAYA-1	G16	KVV, Malan, Himachal Pradesh.
17	HIMALAYA-741	G17	KVV, Malan, Himachal Pradesh.
18	HIMALAYA-2216	G18	KVV, Malan, Himachal Pradesh.
19	RP-2421	G19	KVV, Malan, Himachal Pradesh.
20	HPR-2143	G20	KVV, Malan, Himachal Pradesh.
21	HPR-1068	G21	KVV, Malan, Himachal Pradesh.
22	SUKARADHAN-1	G22	KVV, Malan, Himachal Pradesh.
23	HPR-2373	G23	KVV, Malan, Himachal Pradesh.
24	HPR-2336	G24	KVV, Malan, Himachal Pradesh.
25	HPR-2513	G25	KVV, Malan, Himachal Pradesh.
26	VIVEK DHAN-85	G26	VPKS, Almora, Uttarkand.
27	VIVEK DHAN-82	G27	VPKS, Almora, Uttarkand.
28	VIVEK DHAN-62	G28	VPKS, Almora, Uttarkand.
29	VIVEK DHAN-65	G29	VPKS, Almora, Uttarkand.
30	V L DHAN-86	G30	VPKS, Almora, Uttarkand.
31	V L DHAN-206	G31	VPKS, Almora, Uttarkand.
32	V L DHAN-207	G32	VPKS, Almora, Uttarkand.
33	V L DHAN-208	G33	VPKS, Almora, Uttarkand.
34	V L DHAN-209	G34	VPKS, Almora, Uttarkand.
35	V L DHAN-221	G35	VPKS, Almora, Uttarkand.
36	MTU 1010	G36	APRRI, Maruteru.
37	TELLAHAMSA	G37	Andhra Pradesh.
38	RAJENDRA	G38	Rice section, Rajendranagar.

the cropping season with average maximum temperature of 31.1°C and avg. minimum of 19.4°C and total rainfall of 246 mm with 15 rainy days. Nursery was raised during first week of August 2018 and plantings were done during first week of September. In each replication, data was recorded on five randomly selected plants for the following traits.

I. Days to 50% flowering: The total number of days were taken from the date of sowing to the complete exertion of the panicle tip above the sheath of the flag leaf in 50 per cent of the total plants in the net plot.

II. Plant height (cm): The plant height was recorded by measuring the total height from base of the plant to tip of the main panicle at the time of harvest.

III. Tillers/plant: The number of tillers which produced healthy panicles were counted on each plant at the time of maturity.

IV. Panicle length (cm): The length of panicles from each plant was measured in centimeters from the neck node to the tip of top most grain.

V. Panicle exertion: The length of panicle base exerted from the boot leaf is measured and mean was calculated.

VI. Spikelet fertility: Spikelet fertility is calculated using the formula

Spikelet fertility = no of filled grains/total grains ×100.

VII. Spikelets per panicle: The numbers of filled spikelets were counted from five panicles in each selected plant and their mean was taken.

VIII. Test weight (g): One thousand well filled grains were counted from a random sample of each entry in each replication and weighed with the help of electronic top pan balance in grams.

IX. Seed yield per plant: Panicles from a single plant were harvested at maturity, threshed, cleaned and sun dried to optimum content and the weight was recorded in kg per plot converted into kg/ha.

According to the formula given by Allard [10], Heritability (h^2) in the broad sense was calculated and the heritability estimates, the genetic advance were calculated according to Burton [11]. Genotypic and phenotypic correlation coefficients (significance at both 1% and 5% probability) were estimated as per Singh and choudhary [9], path coefficient analysis per Dewey and Lu [12], Mahalanobis D^2 distances through INDOSTAT software and Principal component analysis (PCA) analysis using XLSTAT software.

3. RESULTS AND DISCUSSION

3.1 Genetic Variability Studies

Analysis of Variance indicated significant differences for all the characters of the genotypes studied. The trait plant height had a mean of 91.94 cm and ranged from 53.8 cm (HIMALAYA-1) to 115.3 cm (VL DHAN-209). Similarly, days to 50% flowering varied from 105 days (K-116) to 130 days (VL DHAN-207), while number of tillers per plant had a mean of 11.53. Panicle exertion was highest in the genotype V L DHAN-206 with a general mean of 1.43, while panicle length ranged from 13.10 cm (HPR-2373) to 23.20 cm (VIVEK DHAN-82). The trait, spikelet fertility was highest in the genotype K-475 and filled grains per panicle in VIVEK DHAN-65. Test weight varied between 18.35 g (HPR-2143) to 25.40 g (HPR-2336), while seed yield from 3.79 g (K-116) to 19.67) g (RP-2421). The characters, tillers per plant, spikelet fertility, filled grains per panicle and seed yield per plant recorded high genotypic coefficient of variation (GCV) and

phenotypic coefficient of variation (PCV) values (Table 2, Fig. 1), while, high heritability coupled with high genetic advance as percent of the mean was observed for plant height, spikelet fertility, filled grains per panicle indicated the preponderance of additive type of gene action in the inheritance of these traits suggesting high heritability and paving a way for genetic change which can be further improved by following simple selection procedure. A similar result was reported by Kumar et al., 2017 [13] while working with nine rice genotypes that included seven advance lines and two rice varieties (RC Maniphou-5, Ginaphou).

The frequency distribution for the nine yield and attributing traits was depicted in the form of box plots (Fig. 2) representing a vast genetic variability. The traits, plant height, spikelet fertility and filled grains had higher variability compared to other traits as supported by heatmap (Fig. 3), while grain yield showed an outlier indicating highest mean for the trait. With respect to Quantile-Quantile plots, (Fig. 4) normal distribution for days to 50% flowering, ear bearing tillers, spikelet fertility, panicle exertion and test weight was depicted. While the remaining traits had had few genotypes slightly deviating determining the presence of variability in those genotypes.

3.2 Correlation Analysis

Correlation studies (Table 3, Fig. 5) depicted grain yield to be positively correlated with plant height, days to 50% flowering, tillers per plant, spikelet fertility and filled grains per panicle, while, panicle exertion, panicle length and had a negative association with yield as reported by Thippani et al. [14]. Significant positive associations were found for plant height with tillers per plant, panicle exertion, and panicle length and negatively significant with spikelet fertility which had negative associations with almost all the traits similar to filled grains per panicle. Thus, for improving grain yield, the traits plant height, days to 50% flowering, tillers per plant, spikelet fertility and filled grains per panicle should be improved simultaneously by selection.

3.3 Path Coefficient Studies

Path coefficient analysis (Table 4) revealed that all the traits except panicle exertion and test weight exhibited direct positive effect on yield. Hence, selection should be practiced for these traits in order to obtain superior plant types for

improvement of yield of the plant. Though panicle exertion exhibited negative direct effect, its indirect effect through spikelet fertility and filled grains per panicle was positive. Similarly, for test

weight, all indirect effects on grain yield were negative except for days to 50% flowering, spikelet fertility and filled grains that can improve the grain yield [15].

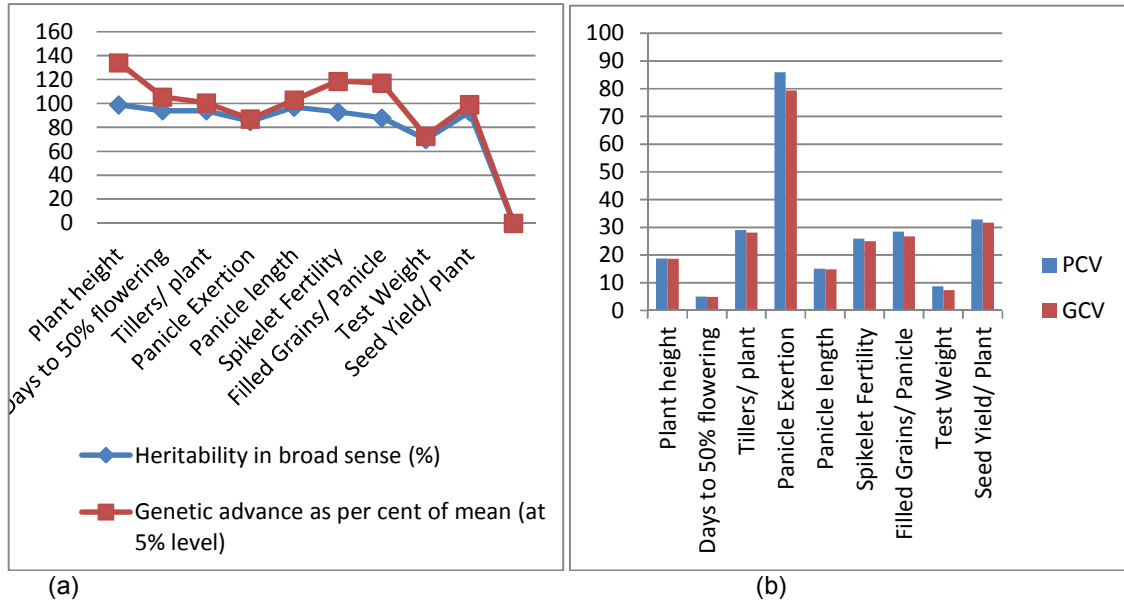


Fig. 1. Histogram of (a) heritability in broad sense (h^2), genetic advance and (b) phenotypic and genotypic co-efficient of variation (GCV) for grain yield and its component characters in rice

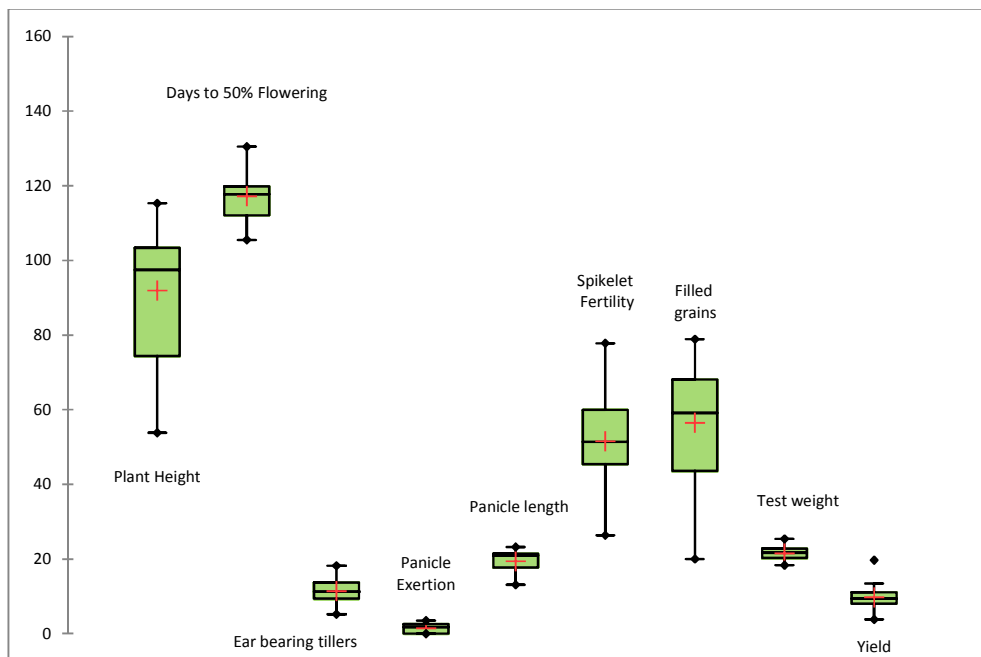


Fig. 2. Box-plots showing variation of the data from the nine quantitative variables evaluated in 38 rice genotypes

The upper, median and lower quartiles represent the 75th, 50th and 25th percentiles of the accessions respectively. The vertical lines represent the variation in the population. Dots represent the outliers

Table 2. Estimates of range, variability, heritability, genetic advance for grain yield and its components

Characters	Mean	Range		Coefficient of variation		Heritability in broad sense h^{2bs} (%)	Gen adv. As per cent of mean (at 5% level)
		Min	Max	Phenotypic	Genotypic		
Plant height (cm)	91.94	53.8	115.3	18.80	18.66	99.00	35.09
Days to 50% flowering	117.2	105.5	130.5	5.04	4.89	94.00	11.44
Tillers/ plant	11.53	5.20	18.2	28.98	28.11	94.00	6.47
Panicle Exertion	1.43	0.00	3.50	85.99	79.33	85.00	2.16
Panicle length	19.40	13.10	23.20	15.13	14.88	97.00	5.85
Spikelet Fertility	51.55	26.35	77.81	25.88	24.96	93.00	25.57
Filled Grains/ Panicle	56.61	20.0	78.90	28.53	26.70	88.00	29.08
Test Weight	21.51	18.35	25.40	8.76	7.31	70.00	2.70
Seed Yield/ Plant	9.73	3.79	19.67	32.79	31.70	93.00	6.14

Table 3. Phenotypic (P) and Genotypic (G) correlation coefficient analysis of yield and yield contributing characters in rice

Character		Plant height (cm)	Days to 50% flowering	Tillers/ Plant	Panicle Exertion	Panicle Length (cm)	Spikelet Fertility	Filled grains/panicle	Test weight (g)	Seed yield /plant (g)
Plant height (cm)	G	1.0000	0.2245	0.2510	0.6459	0.8981	-0.2374	-0.1283	0.2125	0.0722
	P	1.0000	0.2146	0.2562*	0.5836**	0.8761**	-0.2332**	-0.1305	0.1797	0.0620
Days to 50% Flowering	G		1.0000	0.2220	0.2821	0.1555	0.0495	0.1887	-0.2364	0.3239
	P		1.0000	0.2083	0.2594*	0.1536	0.0436	0.1803	-0.1548	0.3015
Tillers/ Plant	G			1.0000	0.1741	0.2548	-0.2573	-0.1595	-0.0091	0.0133
	P			1.0000	0.1453	0.2445*	-0.2441*	-0.1512	0.0127	0.0131
Panicle Exertion	G				1.0000	0.5602	-0.1134	-0.1446	0.0377	-0.0266
	P				1.0000	0.5027**	-0.1124	-0.1090	0.0529	-0.0309
Panicle Length (cm)	G					1.0000	-0.3777	-0.2345	0.1962	-0.0540
	P					1.0000	-0.3596**	-0.2056	0.1516	-0.0574
Spikelet Fertility	G						1.0000	0.8922	-0.0494	0.7382
	P						1.0000	0.8044**	-0.0420	0.7412
Filled grains/panicle	G							1.0000	-0.1154	0.8243
	P							1.0000	-0.0567	0.7353
Test weight(g)	G								1.0000	-0.1414
	P								1.0000	-0.1280

* indicates significant at 5% ** indicates significant at 1% probability

Table 4. Phenotypic (P) and Genotypic (G) Path coefficient analysis of yield and yield contributing characters in rice

Character		Plant height (cm)	Days to 50% flowering	Tillers/ Plant	Panicle Exertion	Panicle Length (cm)	Spikelet Fertility	Filled grains/panicle	Test weight (g)	Seed yield /plant (g)
Plant height (cm)	G	0.2712	0.0336	0.0272	-0.0965	0.0040	-0.0860	-0.0635	-0.0176	0.0722
	P	0.2510	0.0367	0.0296	-0.0896	0.0280	-0.1429	-0.0321	-0.0189	0.0620
Days to 50% Flowering	G	0.0609	0.1495	0.0240	-0.0422	0.0007	0.0179	0.0934	0.0196	0.3239
	P	0.0539	0.1711	0.0241	-0.0398	0.0049	0.0267	0.0443	0.0163	0.3015
Tillers/ Plant	G	0.0681	0.0332	0.1083	-0.0260	0.0011	-0.0932	-0.0789	0.0008	0.0133
	P	0.0643	0.0357	0.1157	-0.0223	0.0078	-0.1496	-0.0372	-0.0013	0.0131
Panicle Exertion	G	0.1751	0.0422	0.0188	-0.1495	0.0025	-0.0411	-0.0715	-0.0031	-0.0266
	P	0.1465	0.0444	0.0168	-0.1534	0.0161	-0.0689	-0.0268	-0.0056	-0.0309
PanicleLength (cm)	G	0.2435	0.0232	0.0276	-0.0837	0.0044	-0.1368	-0.1160	-0.0163	-0.0540
	P	0.2199	0.0263	0.0283	-0.0771	0.0320	-0.2204	-0.0505	-0.0159	-0.0574
Spikelet Fertility	G	-0.0644	0.0074	-0.0279	0.0169	-0.0017	0.3622	0.4415	0.0041	0.7382
	P	-0.0585	0.0075	-0.0282	0.0172	-0.0115	0.6128	0.1976	0.0044	0.7412
Filled grains/panicle	G	-0.0348	0.0282	-0.0173	0.0216	-0.0010	0.3232	0.4948	0.0096	0.8243
	P	-0.0328	0.0309	-0.0175	0.0167	-0.0066	0.4929	0.2457	0.0060	0.7353
Test weight (g)	G	0.0576	-0.0353	-0.0010	-0.0056	0.0009	-0.0179	-0.0571	-0.0830	-0.1414
	P	0.0451	-0.0265	0.0015	-0.0081	0.0049	-0.0258	-0.0139	-0.1051	-0.1280

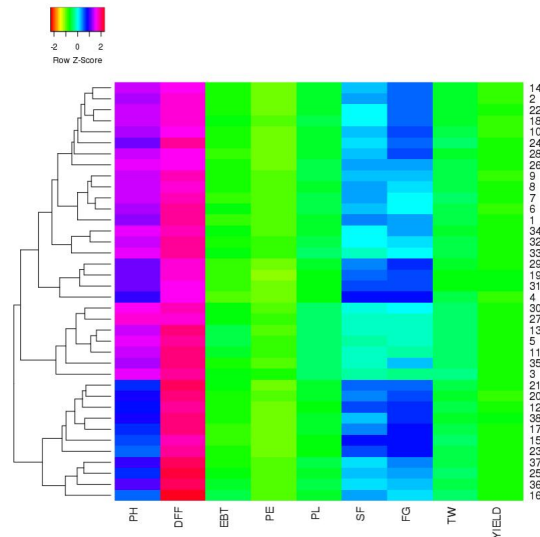


Fig. 3. Heatmap depicting the genetic variability in 38 rice genotypes for yield and its attributing traits

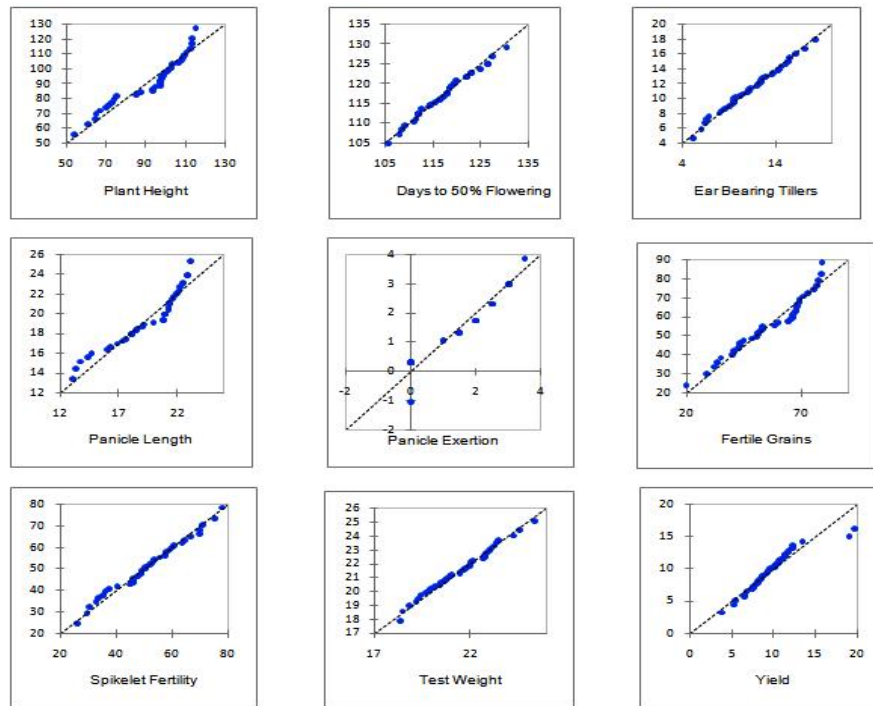


Fig. 4. Q-Q plots showing the distribution of rice genotypes for yield and its attributing traits

3.4 Diversity Studies

Principal component analysis revealed five most informative principal components with Eigen values of 2.961, 2.361, 1.230, 0.915 and 0.640 which accounted for 90.063% of the total variance for all the traits studied (Table 5).

According to principal component 1, traits such as spikelet fertility (0.818) and fertile grains (0.750) had relatively higher contributions to the total variability, while the second principal component accounted for 26.231% of the total variation with maximum contributions from plant height (0.643), days to 50% flowering (0.584),

panicle exertion (0.539), panicle length (0.525) and seed yield (0.700) for principal component 3 and principal component 4 contribute for test weight (0.755) and tillers per plant (0.725) respectively. Scree plot (Fig. 6) depicted Principal component 1 showing 32.897% variability followed by principal component 2 showing 26.231% variability which then declined gradually. Biplot diagram derived from first and second factor components with 59.13% variability is shown in Fig. 8. The first and fourth regions of biplot, which have positive values, are suitable regions to identify the high performing genotypes and traits having high variability. The

first PC, which explained more than 32.90 % of total variation, revealed that traits seed yield per plant, filled grains per panicle and spikelet fertility were the most important contributing traits. The most important traits in the PC2 are plant height, panicle length, panicle exertion and tillers per plant with 26.23% of total variation. The genotypes VL DHAN-206, VIVEK DHAN-65, RP-2421, VIVEK DHAN-62 and HPR-1068 being cold tolerant accessions these performed well in the cold temperature and these genotypes are best in trait seed yield per plant. Selection of these will be helpful in the future breeding programmes.

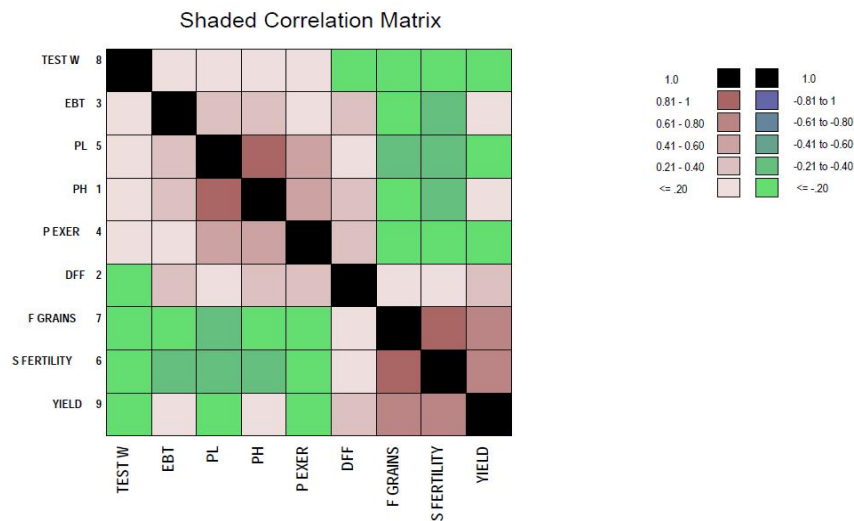


Fig. 5. Correlogram showing correlation of grain yield with yield related traits in 38 genotypes of rice

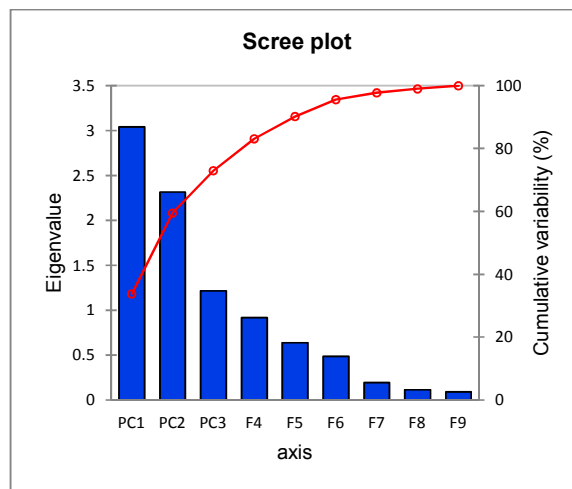


Fig. 6. Scree plot depicting Eigen value and percentage of cumulative variability in 38 rice genotypes

Table 5. Eigen vectors and factor loadings of four principal components for 9 characters in rice genotypes

	PC1	PC2	PC3	PC4	PC5
Eigen value	3.041	2.314	1.213	0.915	0.640
Variability (%)	33.793	25.711	13.481	10.164	7.109
Cumulative %	33.793	59.503	72.984	82.954	90.063
Plant Height (cm)	-0.669	0.633	0.217	-0.029	-0.157
Days to 50% Flowering	-0.042	0.580	-0.556	-0.081	0.575
Ear Bearing Tillers	-0.366	0.223	-0.468	0.725	-0.124
Panicle Exertion	-0.523	0.533	0.085	-0.400	0.118
Panicle Length (cm)	-0.739	0.511	0.180	0.000	-0.225
Spikelet Fertility	0.820	0.424	0.238	-0.042	-0.038
Fertile Grains	0.751	0.551	0.127	0.068	-0.063
Test Weight (g)	-0.224	-0.024	0.725	0.454	0.427
Yield (g)	0.594	0.706	-0.002	0.094	-0.128

Table 6. Grouping of 38 genotypes of rice into different clusters based on yield and yield contributing traits by D² analysis

Clusters	No. of Entries	Accessions
I	15	CHINA-988, SKAU-339, SKAU-389, JHELMUM, SHALIMAR-1, V L DHAN-86, SKAU-382, CHINA-1007, HIMALAYA-2216, SKAU-5, SKAU-389, V L DHAN, SKAU-341, VIVEK DHAN-85, VIVEK DHAN-82
II	6	V L DHAN-207, V L DHAN-208, V L DHAN-209, SUKARADHAN-1, VIVEK DHAN-65, VIVEK DHAN-62
III	8	MTU 1010, TELLAHAMSA, K-332, HIMALAYA-741, HPR-2143, HPR-1068, HPR-2513, HPR-2373
IV	1	CHINA-1039
V	1	K-429
VI	1	RP-2421
VII	1	RAJENDRA
VIII	1	HIMALAYA-1
IX	1	K-475
X	1	HPR-2336
XI	1	V L DHAN-206
XII	1	K-116

D² values grouped the genotypes into 12 clusters using the Tocher method. Out of the 12 clusters, (Table 6 and Fig. 7), cluster I was the largest comprising of 15 accessions followed by cluster III and II with eight and six genotypes respectively. All the remaining clusters had only one genotype indicating a high degree of diversity among the accessions [16]. Thus, the single genotypes of each cluster namely, CHINA-1039, K-429, RP-2421, RAJENDRA, HIMALAYA-1, K-475, HPR-2336, V L DHAN-206 and K-116 can be directly used as parents for crossing programmes. Intra cluster D² values ranged from zero to 67.40 9 (Table 7). Maximum intra cluster distance was observed in cluster III (67.40),

followed by cluster I (53.89) indicating presence of some kind of genetic divergence among the genotypes. From the inter cluster D² values of the twelve clusters, highest divergence was noticed between cluster II and XIII (890.50) followed by cluster I and XIII (615.92). Thus, hybridization is suggested between the genotypes of clusters I, III and VIII. The contribution of plant height was highest towards genetic divergence (39.68%) followed by yield per plant (16.07%), days to 50 % flowering (13.08%), spikelet fertility (11.23%), panicle length (10.09%), ear bearing tillers (4.55%), fertile grains (3.27%), panicle exertion (1.28%) and test weight (0.71%) respectively (Table 8).

Table 7. Average inter and intra cluster distances of 38 genotypes of rice obtained by D² analysis using 9 yield and yield contributing traits

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster 7	Cluster 8	Cluster 9	Cluster 10	Cluster 11	Cluster 12
Cluster 1	53.89	105.82	300.00	83.62	496.94	172.93	188.18	615.92	196.92	79.22	202.10	127.27
Cluster 2		51.79	453.82	198.81	739.66	132.12	293.01	890.50	331.93	118.95	98.82	313.18
Cluster 3			67.40	137.00	109.23	409.97	111.91	137.12	144.55	191.26	490.32	214.14
Cluster 4				0.00	226.26	225.68	106.74	363.89	55.64	84.23	246.45	68.23
Cluster 5					0.00	673.26	255.78	127.39	132.68	380.50	761.00	304.11
Cluster 6						0.00	164.38	797.15	325.79	103.96	62.97	377.92
Cluster 7							0.00	270.30	179.26	83.98	294.20	177.20
Cluster 8								0.00	369.99	483.91	956.43	376.78
Cluster 9									0.00	162.96	345.53	167.73
Cluster 10										0.00	162.97	162.18
Cluster 11											0.00	466.91
Cluster 12												0.00

The traits plant height, yield per plant, and days to fifty per cent flowering with spikelet fertility alone contributed 80.06 % towards total divergence. Similar results for maximum contribution by days to 50% flowering, grain yield and plant height was reported by

Tejaswini et al. [17] while studying 114 F₅ families of rice obtained from six different crosses with seven parents in rice (*O. sativa* L.). Therefore, these traits should be given prime importance during hybridization programmes.

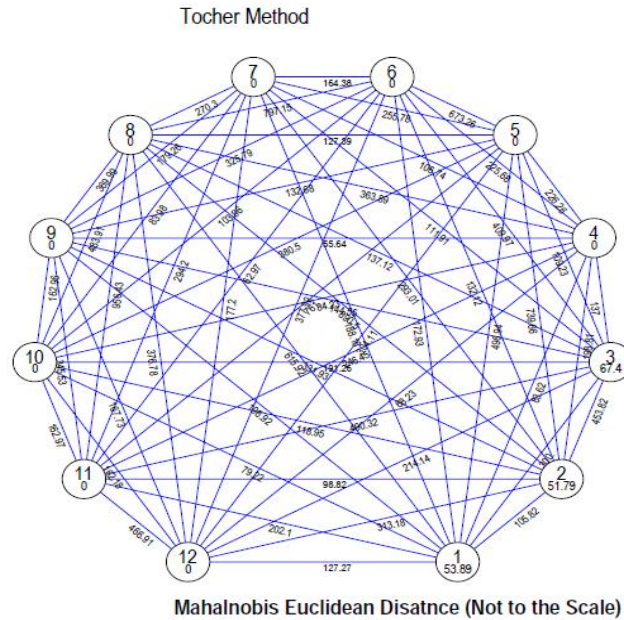


Fig. 7. Cluster diagram of 38 genotypesbased on D2 values by Tocher method

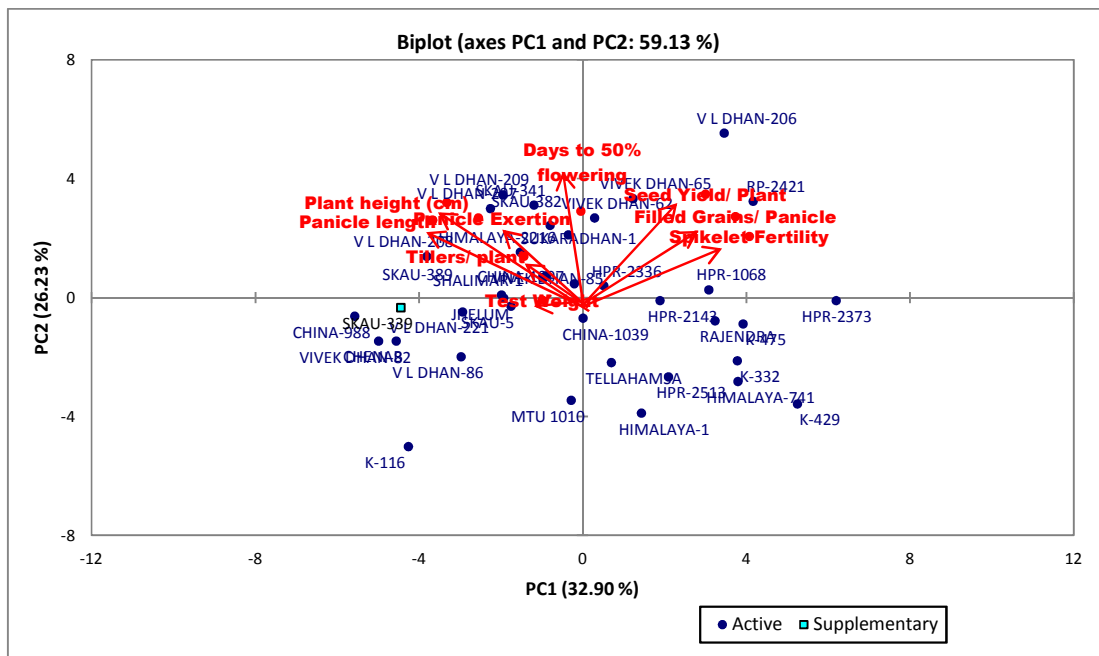


Fig. 8. Biplot of principal component

Table 8. Relative contribution of different characters to genetic diversity in 38 genotypes of rice

S. No	Characters	Contribution (%)
1	Plant height (cm)	39.68
2	Yield per plant (g)	16.07
3	Days to 50 % flowering	13.08
4	Spikelet fertility	11.23
5	Panicle length (cm)	10.09
6	Ear bearing tillers	4.55
7	Fertile grains	3.27
8	Panicle exertion	1.28
9	Test weight (g)	0.71

4. CONCLUSION

Genetic variability, association and diversity studies in crop species are the fundamental requirements for any crop breeding program in order to breed superior cultivars. Thus, present study identified the traits viz. plant height, spikelet fertility and filled grains with high variability, heritability and positive association with grain yield and thus could be emphasized during selection process for improving grain yield. Also, the genotypes VL DHAN-206, VIVEK DHAN-65, RP-2421, VIVEK DHAN-62 and HPR-1068 being cold tolerant were also found to be diverse with optimum yield. Thus, the present study was useful in identifying key traits and genotypes, selection of which could be beneficial under delayed sowing conditions.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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