Genetic Diversity Analysis of Rice Germplasm (*Oryza sativa* L.) Using Morphological Markers

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Abstract

The present investigation was carried out to assess the genetic diversity among 35 rice germplasm lines for 19 different traits including quantitative and grain quality traits. The genotypes were grouped into 8 clusters and out of these maximum number of genotypes were placed in cluster I (25 genotypes) followed by Cluster II (4 genotypes). The highest intra-cluster distance was observed for cluster I whereas, highest inter-cluster distance was recorded between cluster VII and cluster VIII. Cluster III, cluster V and cluster VIII showed the highest cluster mean values for most of the traits studied. The maximum contribution towards the genetic divergence was exhibited by spikelets per panicle followed by 1000 grain weight, days to 75% maturity and plant height. These traits, hence could be focused for selection improving grain yield. The germplasm lines falling in different clusters with high mean for grain yield and other component traits can be utilized for hybridization programme to obtain elite segregants.

Introduction

Rice is the staple food for more than half the world's population of 7.8 billion people and plays a pivotal role in food security of many countries. More than 90% of the global production and consumption of rice is in Asia. It is the primary food source for more than one-third of the world's population and is grown on 11% of the world's cultivated area. It provides minerals, vitamins and fiber. To meet the challenge of producing more rice from limited available lands, we need varieties or hybrids which grow better under adverse conditions and possess high yield potential. Genetic diversity is the pre-requisite for any crop improvement programme because it helps in the development of superior recombinants, through selection of parents having wider variability for different characters. Since, the last few centuries, rice has faced loss in diversity due to replacement of native varieties with high yielding varieties (Choudhary *et al.,* 2013). Genetic divergence analysis evaluates the genetical distance among the selected genotypes and shows the relative contribution of specific traits towards the total divergence. A higher heterosis could be achieved from crosses between genetically distant parents (Falconer, 1960). Therefore, the present investigation is aimed to assess the nature and magnitude of genetic divergence present in the 35 germplasm lines of basmati rice and to select suitable diverse genotypes as parents for further utilization in crop improvement programmes.

Materials and Methods

Experimental Material and Plan

Experiment was conducted during *kharif,* 2022 at Chaudhary Sarwan Kumar Himachal Pradesh Krishi

Vishvavidyalaya Rice and Wheat Research Centre, Malan. The experimental material comprised of 35 germplasm lines of rice. The nursery was sown on 28th May and 21 days old seedlings were transplanted in the field in Randomized block design with three replications. Standard agronomic practices and plant protection measures were taken as per schedule. Each germplasm line was raised in a 3 rowed plot of 3 m length with a spacing of 20 × 15 cm respectively.

Morphological Markers

Observations were recorded on five randomly selected plants per replication for different quantitative traits: days to 50 per cent flowering (DF), days to maturity (DM), total tillers per plant (TT), effective tillers per plant (ET), plant height (PH), panicle length (PL), spikelets per panicle (SPP), grains per panicle (TG), spikelet fertility per centage (SFP), 1000- grain weight (TW) biological yield per plant (g), harvest index per cent and grain yield per plant (GYPP); four quality traits: grain length (GL), grain breadth (GB), L/B ratio (LB) and amylose content (AC).

Statistical analysis

Genetic divergence was estimated by Mahalanobis' D^2 statistics (1936). The germplasms lines were grouped into a number of clusters by Tocher's method described by Rao (1952). Each character was ranked on the basis of values in all the combination of genotype for estimation of contribution of individual characters towards divergence.

Results and Discussions

Cluster distances and composition

It is the task of grouping a set of genotypes in which accessions falling in the same group are more similar to each other than to those in other groups or clusters which is very helpful in diversity analysis. In the present investigation with nonhierarchical Euclidean cluster analysis, 35 rice germplasm lines were grouped into eight different clusters based on the *inter se* genetic distances. Out of eight clusters two clusters were polygenotypic while six were monogenotypic based on genetic divergence. Maximum number of genotypes were placed in cluster I (25 genotypes) followed by cluster II (4 genotypes), cluster III (1 genotype) and cluster IV (1 genotype), cluster V (1genotype), cluster VI (1 genotype), cluster VII (1 genotype), cluster VIII (1genotype). Genotypes falling under each cluster are presented in **Table 1** which indicates cluster 1 represent maximum genotypes. Similar studies were taken up by Chakravorty *et al.,* (2013) who assessed genetic divergence among 51 rice genotypes and grouped them into 11 clusters using D^2 analysis and Akhter *et al.,* (2022) who assessed genetic divergence among rice genotypes and grouped them into different clusters using D^2 analysis. Rao *et al.,* (2018) conducted diversity analysis in rice germplasm and divided the genotypes into 8 clusters. Tushara *et al.,* (2022) also conducted similar studies on grouping of rice germplasm into different clusters.

Table 1: Grouping of rice genotypes into different clusters on the basis of Mahalanobis D^2 -analysis

Clusters	No. of genotype	Genotypes
Cluster 1	25	HPR-5021, HPR-5024, HPR-2612, HPR-5022, HPR-5007, HPR-5015, HPR-5008, PB-1509, HPR-3221,Kasturi,HPR-5020, HPR-2750, HPR-5023, HPR-5016, HPR-5001, HPR-5018, HPR5017, HPR-5003, HPR5012, HPR-5009, HPR-5013, HPR-5026,HPR- 2749,HPR-5019, HPR-5025
Cluster 2	4	HPR-5004,HPR-5005, HPR-5002, HPR-5006
Cluster 3	1	HPR-2696
Cluster 4	1	HPR-5014
Cluster 5	1	HPR-5010
Cluster 6	1	HPR-3225
Cluster 7	1	HPR-5011
Cluster 8	1	HPR-5027

The average intra and inter-cluster distances are presented in **Table 2**. The highest intra-cluster distance is observed for cluster I (18.31), followed by cluster II (12.62) and no intra-cluster distance is observed for cluster III, cluster IV, cluster V, cluster VI, cluster VII and cluster VIII as these clusters possess only one genotype each. Presence of high intra-cluster distances revealed that genotypes within the same cluster were quite diverse; hence the selection of parents within the cluster would be effective. The highest inter-cluster distance was 42.92, which was observed between clusters VII and cluster VIII followed by VI and VII (39.80), V and VIII (35.02), V and VI (34.53), IV and VIII (34.17), II and VIII (33.01), I and VIII (32.02) and III and V (31.71) indicating that, hybridization between the most diverse genotypes would yield desirable segregants with the accumulation of favorable genes in the segregating generations, while, least inter cluster distance was observed between cluster V and VII (18.48) indicating that the genotypes belonging to these clusters were comparatively less diverse. Similar studies were also conducted by Kishore *et al.,* (2018), Vennila *et al.,* (2011), Chakravorty *et al.,* (2013) and Devi *et al.,* (2015).

Table 2: Average intra and inter-cluster distance

Clusters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII
Cluster I	**18.31**	21.67	22.78	22.39	23.19	23.65	22.93	32.03
Cluster II	0	12.62	26.43	26.38	24.48	30.09	30.18	33.01
Cluster III		0	0	29.97	31.78	21.17	30.99	28.55
Cluster IV				0	21.95	25.22	22.87	34.17
Cluster V					0	34.53	18.48	35.02
Cluster VI						0	26.14	39.80
Cluster VII							0	**42.92**
Cluster VII								0

Cluster means for different characters:

The cluster means of rice genotypes falling under different clusters are presented in **Table 3**. Analysis of cluster means indicates existence of considerable differences in the mean values of different traits. The highest values of total tillers per plant, effective tillers per plant, biological yield per plant and amylose content were observed in cluster III. Cluster V showed highest value for plant height, flag leaf length, 1000-grain weight and grain breadth. Cluster VIII showed highest value for days to 50% flowering, days to 75% maturity, harvest index and grain yield per plant Cluster IV showed highest values for flag leaf breadth, grain length, L/B ratio. Cluster VI showed highest value for panicle length and spikelets per plant and cluster VII showed highest value for spikelet fertility and grains per panicle. The cluster IV exhibited minimum values for most of the traits *viz.*, days to 75% maturity, flag leaf length, total tillers per plant, effective tillers per plant, spikelet fertility, biological yield per plant and grain yield per plant while, cluster VI showed minimum values for plant height, grain length and grain breadth. Thus, various traits contribute to the total divergence in cluster, III, V and VII and the genotypes comprising these clusters seem to be quiet promising for many of the traits under study. Similar studies in rice were also done by Sharma *et al.,* (2011), Chakravorty *et al.,* (2013), Kumar (2015) and Amudha and Ariharasutharsan (2021).

Table 3: Cluster means of eight clusters for yield and yield related traits of rice genotypes

Cluster/ Character	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Mean	Min	Max
Days to 50% flowering	87.78	88.58	94.00	82.33	87.00	86.00	80.00	108.00	89.21	80.00*	108.00**
Days to 75% maturity	121.01	120.75	118.00	108.00	122.67	119.33	122.00	124.67	119.55	108.00*	124.67**
Plant height (cm)	120.69	128.74	108.13	122.20	146.87	85.93	112.53	134.93	120.00	85.93*	146.87**
Flag leaf Length (cm)	36.05	36.48	33.83	29.53	37.30	30.20	32.77	34.37	33.82	29.53*	37.30**
Flag leaf width (cm)	1.48	1.48	1.53	1.87	1.73	1.50	1.73	1.43	1.59	1.43*	1.87**
Total tillers per plant	8.39	8.02	11.47	6.60	8.53	11.30	9.27	7.60	8.90	6.60*	11.47**
Effective tillers per plant	7.93	7.34	10.47	6.47	8.13	10.40	8.47	7.47	8.34	6.47*	10.47**
Panicle length (cm)	25.64	25.42	24.30	24.97	24.07	26.70	23.80	23.13	24.75	23.13*	26.70**
Spikelets per plant	180.87	136.27	182.90	193.73	182.47	199.40	195.67	172.40	180.46	136.27 *	199.4 0**
Spikelet fertility (%)	91.96	94.29	94.57	76.23	97.10	78.07	98.17	96.03	90.80	76.23 *	98.17**
Grains per panicle	166.29	128.31	172.93	147.73	177.13	155.63	192.00	165.60	163.20	128.31*	192.00**
1000 grain weight (g)	23.73	23.23	20.63	26.20	31.13	22.73	30.17	26.23	25.51	20.63*	31.13**
Harvest index (%)	34.95	34.45	26.07	37.83	25.90	34.30	37.37	40.17	33.88	25.90*	40.17
Biological yield per plant (g)	43.82	37.13	58.63	33.23	55.27	40.6	39.6	44.93	44.15	33.23*	58.63**
Grain length (mm)	6.33	5.63	5.70	7.17	6.60	5.13	6.50	6.63	6.21	5.13*	7.17 **
Grain breadth (mm)	1.82	1.82	1.93	1.73	2.20	1.60	2.13	1.97	1.90	1.60*	2.20**
L/B ratio	3.52	3.12	2.96	4.15	3.00	3.22	3.06	3.39	3.30	2.96*	4.15**
Amylose content (%)	23.31	22.04	25.89	24.85	22.99	24.50	25.40	21.53	23.81	21.53*	25.89**
Grain yield per plant (g)	15.23	12.66	15.30	12.60	14.33	13.97	14.40	17.73	14.53	12.60*	17.73**

Trait contribution towards the divergence

A comparison of contribution of different traits towards genetic diversity was estimated based on ranking method. Contribution of different traits to total divergence is presented in **Table 4**. The maximum contribution towards the genetic divergence was exhibited by spikelets per panicle followed by 1000 grain weight, days to 75% maturity, plant height, days to 50% flowering, spikelet fertility, grain yield per plant, amylose content, grains per panicle, flag leaf length, grain length, flag leaf width, grain breadth, L/B ratio, harvest index and biological yield. Hence, spikelets per panicle, 1000 grain weight, plant height and days to 50% flowering, were found to be potential contributors to genetic divergence. The results are supported by the earlier findings of Devi *et al.,* (2015) and Rachappanavar (2017) who revealed similar findings.

Table 4: Relative contribution of individual trait towards divergence among rice genotypes

Traits	Rank	Contribution
Days to 50% flowering	48	7.62%
Days to 75% maturity	74	11.75%
Plant height	74	11.75%
Flag leaf Length	22	3.49%
Flag leaf width	8	1.27%
Total tillers	0	0.00%
Effective tillers	0	0.00%
Panicle length	0	0.00%
Spikelets per panicle	**185**	**29.37%**
spikelet fertility	31	4.92%
Grains per panicle	24	3.81%
1000 grain weight	88	13.97%
Harvest index	2	0.32%
Biological yield	1	0.16%
Grain length	10	1.59%
Grain breadth	6	0.95%
L/B ratio	5	0.79%
Amylose content	25	3.97%
Grain yield per plant	27	4.29%

Conclusion

A significant range of variation is evident among thirty-five rice genotypes evaluated in the present study. The thirty-five rice genotypes were grouped into eight clusters which was in consonance with the clustering pattern obtained by Mahalanobis D^2 statistics. The parents for hybridization program should be selected on the basis of magnitude of genetic distance, contribution of different characters towards the total divergence and magnitude of cluster means for different characters performance having maximum heterosis. Genetic diversity studies revealed that maximum number of genotypes were placed in cluster I. The highest intra-cluster distance was observed for cluster I, whereas, highest inter-cluster distance was recorded between cluster VII and cluster VIII followed by V and VII, IV and VIII, II and VIII, I and VIII and III. Hence, crosses between the genotypes of these clusters are expected to manifest high heterosis along with, accumulation of favorable genes in subsequent segregating generations.

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