



Evaluation of genetic divergence existing in the rice germplasm collections

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Abstract

The present investigation was conducted during Kharif 2017-18 at the Central research station (Masodha, Faizabad) and lab experiments were conducted in Seed Testing Laboratory, Seed Technology Section, N. D. University of Agriculture and Technology, Narendra Nagar (Kumarganj), Faizabad (U.P.) India. The experimental materials of studies comprised of twenty seven Rice varieties/ lines/ genotypes excluding three check varieties viz., NDR97, Baranideep and Shushk Samrat these varieties were procured from genetic stock available in Rice section, Department of genetics and Plant Breeding, N. D. University of Agriculture and Technology, Narendra Nagar (Kumarganj), Faizabad (U.P.) India. The non-hierarchical Euclidean cluster analysis was employed to study the genetic diversity existing among 30 rice germplasm collections on the basis of 14 quantitative and qualitative characters. The pseudo F-test revealed that 6 clusters arrangement was most appropriate for grouping the 30 genotypes therefore the 30 genotypes were accepted to the group into 6 non overlapping clusters the distribution of 30 rice line in 6 clusters is presented in the investigation. It indicated the existence of high degree of genetic diversity present in the genotypes. Therefore, these genotypes may serve as valuable source for selection of diverse parents. Maximum intra-cluster distance was found for cluster III (4.685), followed by cluster VI (1.673). Crosses should be made between these widely related genotypes located in intra and inter cluster distances. Seed yield showed high contributions towards total genetic divergence. The contribution of eleven characters in genetic divergence showed variation whose highest contribution was given by Yield per plant (72.41%) followed by 1000-seed weight (9.89%) and days to maturity (7.36%) and minimum contribution was given by no. of tiller per plant, germination percentage, panicle length and harvest index, rest of the characters very low average contribution towards genetic divergence.

Keywords: hierarchical, divergence, stock, genotypes

Introduction

Rice (*Oryza sativa* L.) is the most important staple food crop of the world because of being the major source of calories of more than half of the total global population. More than 90 per cent of the world's rice is grown and consumed in Asia, known as rice bowl of the world, where 60 per cent of the earth's people and two third of world's poor live. Rice being the staple food for more than 70 per cent of our national population and source of livelihood for 120-150 million rural households is backbone to the Indian Agriculture.

Rice (*Oryza sativa* L.) is a semi-aquatic annual grass plant belongs to the genus *Oryza*, tribe Oryzeae and family Poaceae. It is the second largest principal food crop in the world after wheat and is one of the main staple food crops in India. Besides being the staple food crop, it has been the cornerstone of food and culture for our people. Among seven billion people on the earth, more than half of them depend on this crop for principal source of energy in their daily diet. Rice is distributed over a wider range of latitude from 50° N to 40° S and is being grown up to an altitude of 2500 meters. It evolved in humid tropics as a semi aquatic plant and it has got unique adaptive nature to hot humid environment, which is not seen in any other major cereal crop.

Protein content of milled rice is 6-7 per cent, rice however, compares favorably with other cereals in amino acid content. The biological value of protein is high, the fat content of rice is low (2.0-2.5%) and much of the fat is lost during milling. Rice grain contains as much B group vitamin as wheat. Milled rice losses valuable proteins, vitamins and minerals in the milling process during which embryo and aleuronic layers are removed and much of the loss of nutrients can avoid through parboiling process. The by-products of rice milling are used for a variety of purposes. Rice bran is used as cattle and poultry feed. Rice hull can be used in manufacture of insulation materials, cement and cardboard as well as a litter in poultry keeping. Rice straw can be used as cattle feed as well as litter during winter. Rice is grown almost throughout the year in hot and humid regions of eastern and southern parts of India where two or three crops in a year is uncommon. It is being the staple food for more than 70 percent of our national population as well as the source of livelihood for 120-150 million rural households. It is a backbone to the Indian agriculture. Rice production (according to USDA 2016/2017) is forecast higher at 105 MMT from 43.5 million hectare compared to 2016/17 production of 103.5 million tons in India (Grain report 2016).

Materials and Methods

The study was designed to work out the status of association of different seed yield traits and direct and indirect effects of these different traits on seed yield per plant among twenty seven rice genotypes at field experiment under present investigation was conducted during Kharif 2017-18 at the Central research station (Mashodha, Faizabad) and lab experiments were conducted in Seed Testing Laboratory, Seed Technology Section, N. D. University of Agriculture and Technology, Narendra Nagar (Kumarganj), Faizabad (U.P.) India. The experimental materials of studies comprised of twenty seven Rice varieties/ lines/ genotypes excluding three check varieties *viz.* NDR97, Baranideep and Shushk Samrat these varieties were procured from genetic stock available in Rice section, Department of genetics and Plant Breeding, N. D. University of Agriculture and Technology, Narendra Nagar (Kumarganj), Faizabad (U.P.) India. The experiment was laid out in Randomized Block Design. The observation were recorded on Fourteen different seed yield traits *viz.*, days to 50% flowering, days to maturity, plant height, number of seeds per panicle, panicle length, harvest index, number of tillers per plant, number of panicle bearing tillers per plant, 1000-seed weight, biological yield, Germination percent, Seedling length, Vigour index and Seed yield per plant. Standard statistical measures such as genetic divergence Pseudo f-test and Euclidean cluster analysis were in operation during the investigation.

Seed germination percentage was investigated under lab condition germination was estimated on the basis of 100 randomly selected seeds kept for germination in germination paper at room temperature in germinator. The samples were kept in seed germinator maintained at $20^{\circ} \text{C} \pm 1$. Ten seedlings were randomly taken from each replication. On 8th day seedlings were measured on meter scale, the unit of length was in cm. The vigour index was conducted as per the method prescribed by Abdul-Bali and Anderson (1973) ^[1] and expressed in whole number. The seed were kept for germinate following ISTA method. The seedlings were measured for seedling length to obtain seedling length.

Results and Discussion

Genetic divergence analysis

The non-hierarchical Euclidean cluster analysis was employed to study the genetic diversity existing among 30 rice germplasm collections on the basis of 14 quantitative and qualitative characters. The pseudo F-test revealed that 6 clusters arrangement was most appropriate for grouping the 30 genotypes therefore the 30 genotypes were accepted to the group into 6 non overlapping clusters the distribution of 30 rice line in 6 clusters is presented in Table (2).

1. Clustering pattern on the basis D² analysis

The highest number of genotypes appeared in cluster-III, which contained 11 entries, followed by cluster V having 6 entries. Cluster IV and I possessed 5 genotypes each, while cluster VI was represented by 3 entries. Cluster II was constituted by 1 lines.

2. Intra and Inter-cluster distance

To estimate of intra and inter cluster distance for 14 cluster are

presented in Table 3. The highest intra cluster distance was observed in case of cluster III (4.685), followed by cluster IV (1.637) and cluster I (1.017) while the lowest value was recorded for cluster VI (0.00) followed by cluster V (0.126). The maximum inter-cluster distance was found between cluster VI and cluster III (304.232) followed by cluster distance between cluster I and VI (195.002) and cluster V and cluster III (133.003), and Cluster VI and II (129.697), cluster IV and III (80.608), cluster VI and IV (73.618), cluster V and I (64.635), cluster III and II (38.446), cluster VI and V (35.329), cluster I and IV (30.171) and cluster II and V (29.903). The minimum cluster distance was found between cluster I and II (7.389) followed by cluster V and VI (7.389).

3. Cluster mean on the basis of D² analysis

The cluster means for fourteen characters are presented in Table 3. The highest cluster mean for harvest index was recorded for cluster V (42.83) Followed by cluster-III (41.43) which indicated that genotypes having high harvest index were concentrated in these two groups. The lowest cluster mean for harvest index was noted for cluster II (39.17) days followed by cluster VI (40.06).

The genotype of cluster V was responsible for highest cluster mean for seeds per panicle (200.00), followed by entries cluster IV (200.00), cluster I (189.95), cluster III (183.38) and cluster I (180.26). The genotype with early maturity were concentrated in cluster VI (98.00) followed by cluster IV (102.67) days and cluster II (106.76). The highest cluster mean for plant height was recorded in case of cluster III (100.82 cm) followed by cluster II (100.49 cm). The lowest cluster mean for this character was found in case of cluster VI (96.00 cm), followed by cluster V (96.19 cm), while remaining cluster had moderate mean for plant height. The highest cluster mean for number of tillers per plant was observed in cluster-IV (11.93), followed by, cluster-V (11.65) and cluster-I (11.04), and The minimum number of tillers per plant was noted in cluster-II (10.35), followed by cluster III (10.71), whereas the rest of characters had moderate mean for number of tillers per plant. The cluster-IV showed highest mean for panicle length (22.36), followed by cluster-V (22.11) and cluster-I (21.27). The lowest mean for number of secondary branches per plant was exhibit by cluster II (19.97), followed by cluster III (20.58). The genotypes occurring in cluster-VI produced highest cluster mean (27.93 g) for 1000-seed weight followed by cluster-V (21.83 g), while lowest mean was recorded in cluster-IV (19.90 g), followed by cluster III (20.41 g). The rest of the cluster showed moderate mean for 100-seed weight.

Highest cluster mean for seed germination was exhibited by cluster-IV (92.00%), and cluster-VI (91.00%). Cluster-I (87.14%) showed lowest mean for this character, while remaining cluster had moderate mean seed germination. The maximum cluster mean for seedling length was observed in case of cluster-IV (28.46cm) and cluster-VI (26.26cm), whereas lowest mean was noted in cluster-III (25.33cm). The rest of clusters were characterized by medium seedling length means. The highest cluster mean for biological yield was observed in case of cluster-IV (84.53) and cluster-VI (82.08), which indicated that, these traits having very high biological yield were concentrated in these clusters. The genotypes

which had very low biological yield were grouped in cluster-II (79.92) and cluster-III (80.03). Remaining clusters had average biological yield. The maximum cluster mean for seed yield per plant was observed in case of cluster IV (35.03) which indicated that lines having higher seed yield were concentrated in this cluster. The cluster mean for seed yield was also higher order in case of cluster V (35.01 g). The genotypes with very low seed yield were found to be grouped in cluster II (31.31). While the remaining cluster had moderate values.

4. Percent contribution

The contribution of eleven characters in genetic divergence showed variation whose highest contribution was given by Yield per plant (72.41%) followed by 1000-seed weight (9.89%) and days to maturity (7.36%) and minimum contribution was given by no. of tiller per plant, germination percentage, panicle length and harvest index, rest of the characters very low average contribution towards genetic divergence (Table 4).

Summary and Conclusion

Genetic divergence analyses

An examination on the estimates of within and between cluster genetic diversity revealed that the genotypes of same cluster had little genetic divergence from each other with

respect to aggregate effect of fourteen characters studied (table 2). In this context, the highest inter-cluster distance was recorded between cluster VI and cluster III (304.232) followed by cluster distance between cluster I and VI (195.002) and cluster V and cluster III (133.003), and Cluster VI and II (129.697), cluster IV and III (80.608), cluster VI and IV (73.618), cluster V and I (64.635), cluster III and II (38.446), cluster VI and V (35.329), cluster I and IV (30.171) and cluster II and V (29.903). The minimum cluster distance was found between cluster I and II (7.389) followed by cluster V and VI (7.389) indicating that members of these clusters were genetically close to each other. The inter-cluster distance ranged between 7.389 (cluster-V and VI) to 304.232 (cluster-VI and III). The highest intra-cluster was recorded for cluster-VI followed by cluster-I, II, III, V and IV.

Using D² statistics, the thirty genotypes of rice were grouped into six distinct non-overlapping clusters. This indicated considerable diversity among the genotype collection evaluated in the present study. III had 10 genotypes, Cluster-V having 6 genotypes, Cluster-I and IV having 5 genotypes, VI having 3 genotypes and cluster II having single genotype. The genotype existing in Cluster-V The genotype of cluster V was responsible for highest cluster mean for seeds per panicle (200.00), days to 50% flowering, seed germination, seedling length, plant height and number of seeds/pod.

Table 1: Clustering pattern of thirty rice varieties on the basis of D² analysis

Cluster No.	No. of genotype	Genotypes
1	5	NDR-118,NDR1104-3,NDR-1127,NDR-1170-1-4,Sahbhagidhan
2	1	NDR-1132-2
3	10	NDR-1023-3,NDR-1176,NDR1161-1-1,NDR-1018-1-1-2,NDR1169-1-1,NDR1164-1-5,NDR-80, NDR-1055-6, IR-87707-446-B-B-B-M-2
4	5	NDR-1075-2,NDR-97,NDR1132-5,NDR1177,IR-87707-445-B-B-B-2
5	6	NDR-1132-6,NDR1159,Shusk Samrat,CBOG-510-M1, IR-78997-B-16-B-7-10-B-8-B-2,IR-87705-14-11-B-M-2
6	3	NDR-119,NDR1130-1, NDR-1140

Table 2: Estimates of average intra and inter-cluster distances for the six clusters in rice varieties

Cluster No.	1 Cluster	2 Cluster	3 Cluster	4 Cluster	5 Cluster	6 Cluster
1 Cluster	1.017	7.434	14.232	30.171	64.635	195.022
2 Cluster		0.819	38.446	8.869	29.903	129.697
3 Cluster			4.685	80.608	133.003	304.232
4 Cluster				1.637	7.389	73.618
5 Cluster					0.126	35.329
6 Cluster						0.000

Bold figures represent intra-cluster distances

Table 3: Cluster means for 14 characters of Rice varieties by D² analysis

Characters	Days to Maturity	Plant Height cm	Tillers/Plant	Panicle Length cm	Seeds/Panicle	Test Weight	Biological Yield/Plant	Harvest Index	Germination %	Seedling Length	Yield/Plant	Days to Maturity	Plant Height cm	Tillers/Plant
Cluster 1	108.190**	96.855	11.043	21.271	189.952**	20.652	81.766*	41.271	87.143	26.198	33.754	108.190**	96.855*	11.043
Cluster 2	106.767**	100.495**	10.357	19.975	180.267**	21.010	79.929*	39.172	88.000*	25.875	31.315	106.767**	100.495**	10.357
Cluster 3	111.778**	100.825**	10.717	20.586	183.389**	20.411	80.037*	40.350	88.167*	25.333	32.300	111.778**	100.825**	10.717
Cluster 4	102.667**	68.000	11.933	22.367	200.000**	19.900	84.533*	41.433	92.000*	28.467	35.033	102.667**	68.000	11.933
Cluster 5	109.600	96.197	11.657	22.113	200.000**	21.833	81.720*	42.833	88.800*	27.410	35.010	109.600**	96.197*	11.657
Cluster 6	98.000*	94.000	10.833	20.983	180.667**	27.933	82.083*	40.067	91.000*	26.267	32.883	98.000*	94.000*	10.833

*and ** indicates lowest & highest value

Table 4: Contribution of different quantitative characters of rice towards divergence

S. No.	Characters	Contribution in genetic divergence (%)
1	Days to Maturity	7.36
2	Plant Height cm	2.99
3	Tillers/ Plant	0.01
4	Panicle Length cm	0.01
5	Seeds/ Panicle	0.69
6	Test Weight	9.89
7	Biological Yield/Plant	2.53
8	Harvest Index	0.46
9	Germination%	1.61
10	Seedling Length	2.07
11	Yield/ Plant	72.41

While cluster-II exhibited lowest cluster mean for days to maturity, seedling length, seed germination and seed yield/plant. Cluster-III exhibited lowest cluster mean for number of secondary branches/plant, seedling length and vigour index. Cluster-VII exhibited lowest cluster mean for days to maturity and cluster-III for 1000-seed weight. Cluster-IV exhibited lowest cluster mean for 1000 seed weight and plant height. The six clusters in genetic divergence analysis contained frequently the genotypes of heterogeneous origin (Table 3). Although the genotypes originated in the same place or geographic region were also found to be grouped together in same cluster, the instance of grouping of genotypes of different origin or geographic region in the same cluster were observed in case of all the eight clusters. This suggests lack of parallelism between genetic and geographic diversity. This finding is in agreement with the reports advocating lack of definite relationship between genetic and geographic diversity in rice. The contribution of eleven characters in genetic divergence showed variation whose highest contribution was given by Yield per plant (72.41%) followed by 1000-seed weight (9.89%) and days to maturity (7.36%) and minimum contribution was given by no. of tiller per plant, germination percentage, panicle length and harvest index, rest of the characters very low average contribution towards genetic divergence (Table 4).

Conclusion

The thirty rice varieties were grouped into six distinct clusters by using Mahalanobis D^2 cluster analysis. It indicated the existence of high degree of genetic diversity present in the varieties. Therefore, these varieties may serve as valuable source for selection of diverse parents. Maximum intra-cluster distance was found for cluster-V followed by cluster-VI, the minimum intra-cluster distance was recorded for cluster-I followed by cluster-II. The highest inter-cluster distance was observed between cluster-II and cluster-V followed by cluster-IV and cluster-III. The lowest inter-cluster distance was observed between cluster-I and cluster-II followed by cluster-III and cluster-IV.

Seed yield per plant, days to maturity, plant height, 100-seed weight and seed germination showed high contribution towards total genetic divergence. Remaining characters showed low contribution towards total genetic divergence.

Considering the overall result it is apparent that certain information obtained here will help in future for improving existing rice genotypes.

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