RESEARCH ARTICLE

GENETIC DIVERSITY ANALYSIS IN ADVANCED BREEDING LINES (ABLS) OF RICE (*ORYZA SATIVA* L.) UNDER IRRIGATED LATE CONDITION

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Abstract: The present study was undertaken to estimate the nature and magnitude of genetic diversity among 53 diverse breeding lines of rice. The genotypes were grouped into 7 clusters based on Euclidean cluster analysis. The largest cluster, Cluster VI comprised of 17 genotypes followed by Cluster I comprised of 10 genotypes in it, Cluster IV and VI included 9 genotypes each. The maximum intra cluster distance was observed for Cluster VI and minimum for Cluster III. The maximum diversity was observed between the Cluster III and Cluster V while minimum diversity was observed between Cluster I and Cluster IV. There is maximum inter-cluster distance between Cluster I and V, hence the hybridization between the genotypes of these clusters will be rewarding and would generate maximum variability and transgressive segregants.

Keywords: Genetic diversity, Analysis of variance, Cluster analysis

INTRODUCTION

Rice is the staple cereal food crop next to wheat in world crop production. India ranks topped in area under rice cultivation accounting about 44 m ha with production 118.43 m tons per ha as per advance estimates for 2019-20 (Anonymous, 2020). The levels of rice grain yield have reached its plateau due to use of concentrated parent genotypes in breeding programmes for several decades. Narrow genetic base of rice genotypes also makes plants vulnerable to many biotic and abiotic stresses. To improve grain yield, crop improvement programmes should zoom in broadening the genetic base of existing genotypes for yield and other important traits as well. The success of breeding program depends on collection of diverse genotypes following their evaluation and utilization in breeding programmes. Genetic diversity represents the heritable variation existing within population species since, hybridization between genotypes belonging to wide genetic diversity yields maximum variability accumulating favourable alleles in a common background in segregating generations present effort has been made to study genetic diversity among 53 breeding lines of rice (*Oryza sativa* L.).

MATERIALS AND METHODS

The present study was conducted at the Research Cum Instructional Farm, Department of Genetics and Plant Breeding, Indira Gandhi Krishi Vihswavidyalaya, Raipur (India), during the *Kharif*, (wet season) 2020, in a randomized block design (RBD) with two replications. Geographically the experimental site is situated between 17.14 and 24.45° North latitude and 79.16 and 84.15° East latitude and 289.60 m above mean sea level. A set of 53 diverse late-duration breeding lines of rice including 4 checks were taken as experimental materials. Twenty-five days young seedlings were transplanted adopting a row spacing 20 cm between rows and 15 cm between plants. The genotypes used in the present investigation are given in Table-1. The recommended standard agronomic package of practices was followed with plant protection measures. The observation was recorded for both quantitative traits (days to 50 % flowering, days to maturity, plant height (cm), total tillers per plant, effective tillers per plant, Panicle length (cm), number of spikelet per panicle, filled spikelet per panicle, spikelet fertility %, 1000 seed weight (g), harvest index (%), grain yield per plant)as well as qualitative traits *viz.*, Grain length (mm), grain breadth (mm), grain length: breadth ratio, kernel length (mm), kernel breadth (mm), kernel length: breadth ratio, hulling %, milling %, head rice recovery % and amylase content (%) during the peak crop growth stage. Mahalanobis D^2 statistics was used to study nature and magnitude of genetic diversity among the genotypes following clustering of genotypes based on.

RESULTS AND DISCUSSION

The experimental materials displayed considerable variability for all qualitative traits and among quantitative traits except total tillers per plant, effective tillers per plant, spikelet fertility percentage and grain yield per plant (Table-2).
Quantitative traits were utilized to estimate cluster diversity analysis. 53 rice genotypes were grouped into seven separate clusters. The composition of different clusters obtained from the D^2 analysis has been presented in Table-3. The largest cluster formed is Cluster VII, comprised of 17 genotypes which are followed by Cluster I with 10 genotypes, Cluster IV

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and VI includes 9 genotypes each and Cluster III, II and V comprised of 4, 2, 2 genotypes respectively.

The average cluster distance within the cluster (intra) and between the two clusters (inter) in rice genotypes are presented in Table -4. The maximum intra cluster distance was observed for Cluster VI (D^2=135.33) and minimum for Cluster III (D^2=37.96). Cluster VI (D^2=135.33) was recorded with maximum intra cluster distance followed by Cluster VII (D^2=129.22), Cluster IV (D^2=100.93) and Cluster I (D^2=88.87). The genotypes present in cluster with wide intra distance relatively have more diverse genotypes than those in the other clusters.

The maximum inter-cluster distance was observed between the Cluster III and V (D^2=329.27). These findings suggested the existence of wide diversity among the genotypes present in this cluster. Where, Cluster III includes the genotypes distinguished by minimum plant height, shorter panicle length, lowest number of spikelet per panicle, filled spikelet per panicle while Cluster V had genotypes with maximum number of spikelet per panicle, filled spikelet per panicle, spikelet fertility percentage and minimum number of tillers per plant, effective tillers per plant and lowest grain yield per plant. This result was followed by between Cluster IV and V (D^2=295.55) and Cluster I and V (D^2= 270.40). The minimum inter-cluster distance was observed between Cluster I and Cluster IV (D^2=51.71). Since, hybridization between most diverse genotypes is likely to generate large variability and desirable transgressive segregants, genotypes from these clusters should be considered for their use as parents in hybridization programs aimed at developing high-yielding rice varieties. Cluster IV is distinguished by genotypes which had longer duration for 50 % flowering, day to maturity, larger plant height, maximum effective tillers per plant, high harvest index and higher grain yield and Cluster I for maximum 1000 seed weight.

Analysis of cluster means indicates existence of considerable differences in the mean values of different traits (Table-5). Cluster I exhibited highest mean values for 1000 seed weight (22.19) while Cluster II exhibited high mean values for total tillers per plant (9.15), maximum panicle length (27.15) and lowest mean values for days to 50 % flowering (96.50), days to maturity (123.50), spikelet fertility percentage (71.65) and harvest index (24.65). On the contrary, Cluster III had genotypes with minimum mean values for plant height (103.20), panicle length (23.90), number of spikelet per panicle (146.25) and filled spikelet per panicle (11475). Cluster IV exhibited a high mean value for days to 50 % flowering, days to maturity, plant height, effective tillers per plant, harvest index and high grain yield and Cluster V exhibited highest mean values for number of spikelet per panicle, filled spikelet per panicle and spikelet fertility % and low cluster mean values for total tillers per plant, effective tillers per plant, 1000 seed weight and grain yield displayed. Whereas, cluster VII and Cluster VII had shown intermediate mean value for all the characters. Similar results in rice were also by Rahman et al. (1997) and Singh et al. (1996). Basher *et al.* (2007) also reported.

CONCLUSION

Since, selection of accessions from clusters having wider inter cluster distance would produce maximum variability parents should be selected from cluster III for shorter plant height and panicle length and from cluster V for maximum number of spikelet per panicle, filled spikelet per panicle, harvest index and high grain yield per plant would be successful in accumulating favorable genes.

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Table 1. List of 53 rice genotypes used as experimental material.

Sl. No.	Entry number	Sl. No.	Entry number	Sl. No.	Entry number
1	R 2307-76-1-39-1	**19**	R 2405-376-1-188-1	**37**	R 2419-1272-1-630-1
2	R 2303-38-1-19-1	**20**	R 2405-283-1-192-1	**38**	R 2408-739-2-438-1
3	R 2307-53-1-28-1	**21**	R 2405-391-200-1	**39**	R 2408-739-3-439-1
4	R 2307-59-1-31-1	**22**	R 2406-418-2-219-1	**40**	R 2408-739-4-440-1
5	R 2321-97-1-54-1	**23**	R 2406-422-1-222-1	**41**	R 2408-740-4-444-1
6	R 2325-104-1-59-1	**24**	R 2408-424-1-223-1	**42**	R 2408-740-5-445-1
7	R 2326-108-1-61-1	**25**	R 2409-467-1-252-1	**43**	Swarna (Check)
8	R 2328-129-1-69-1	**26**	R 2409-469-1-254-1	**44**	Mahsuri (Check)

9	R 2340-143-1-73-1	**27**	R 2409-487-1-258-1	**45**	Pooja (Check)
10	R 2370-263-1-114-1	**28**	R 2409-4809-1-260-1	**46**	Jaldubi (Check)
11	R 2370-265-1-116-1	**29**	R 2409-490-1-261-1	**47**	DH-19-1-1
12	R 2370-268-1-117-1	**30**	R 2409-490-1-262-1	**48**	DH-19-1-2
13	R 2370-268-2-118-1	**31**	R 2409-493-1-263-1	**49**	DH-19-1-3
14	R 2370-272-1-122-1	**32**	R 2409-494-264-1	**50**	DH-19-1-4
15	R 2373-277-1-123-1	**33**	R 2409-494-1-267-1	**51**	DH-19-1-5
16	R 2372-292-1-131-1	**34**	R 1771-529-1-274-1	**52**	DH-19-1-6
17	R 2374-299-1-135-1	**35**	R 2419-1248-1-610-1	**53**	DH-19-1-7
18	R 2404-346-1-164-1	**36**	R 2419-1250-611-1		

Table 2. Analysis of variance (ANOVA) for different traits in 53 rice genotypes

Sl. No	**Characters**	**Source of Variation**		
		Replication	**Treatments**	**Errors**
		d.f. (1)	*d.f.*(52)	*d.f.*(52)
1	Days to 50 % flowering	5.434	170.653**	0.434
2	Days to maturity	6.377	238.269**	0.416
3	Plant height	103.614	1004.020**	9.325
4	Total tillers per plant	0.666	1.666	1.041
5	Effective tillers per plant	0.085	1.670	0.940
6	Panicle length	0.097	5.094**	0.622
7	Number of spikelet per panicle	2.123	5987.378**	611.392
8	Number of filled spikelet per panicle	744.915	4610.430**	640.550
9	Spikelet fertility %	135.171	146.975	62.937
10	1000 seed weight	0.604	46.697**	0.421
11	Harvest index	72.064	163.058*	34.530
12	Kernel length	0.006	0.724**	0.006
13	kernel breadth	0.000	0.082**	0.006
14	kernel L:B	0.002	0.199**	0.010
15	Grain length	0.059	1.854**	0.010
16	Grain breadth	0.046	0.143**	0.004
17	Grain L:B	0.031	0.389	0.010
18	Head rice recovery %	5.056	191.572**	2.923
19	Amylose content	2.325	14.930**	0.957
20	Hulling percentage	0.452	60.511**	1.519
21	Milling percentage	2.223	51.725**	2.504
22	Grain yield per plant	21.917	40.600	10.754

**=Singificance level at 0.05%

* = Singificance level at 0.01%

Table 3. Cluster pattern of 53 rice genotypes

Cluster number	No of genotypes	Lines Included
Cluster I	10	R 2307-76-1-39-1, R 2303-38-1-19-1, R 2328-129-1-69-1, R 2405-376-1-188-1, R 2405-283-1-192-1, R 2405-391-200-1, R 2406-418-2-219-1, Swarna, DH-19-1-6, DH-19-1-7
Cluster II	2	R 2409-487-1-258-1, R 1771-529-1-274-1
Cluster III	4	R 2307-53-1-28-1, DH-19-1-1, DH-19-1-2, DH-19-1-5
Cluster IV	9	R 2307-59-1-31-1, R 2372-292-1-131-1, R 2409-467-1-252-1, R 2408-739-3-439-1, R 2408-739-4-440-1, R 2408-740-4-444-1, R 2408-740-5-445-1, Mahsuri, Pooja
Cluster V	2	R 2409-490-1-261-1, R 2409-490-1-262-1
Cluster VI	9	R 2340-143-1-73-1, R 2370-263-1-114-1, R 2370-268-1-117-1, R 2370-268-2-118-1, R 2408-424-1-223-1, R 2409-4809-1-260-1, R 2409-493-1-263-1, R 2409-494-264-1, DH-19-1-3
Cluster VII	17	R 2321-97-1-54-1, R 2325-104-1-59-1, R 2326-108-1-61-1, R 2370-265-1-116-1, R 2370-272-1-122-1, R 2373-277-1-123-1, R 2374-299-1-135-1, R 2404-346-1-164-1, R 2406-422-1-222-1, R 2409-469-1-254-1, R 2409-494-1-267-1, R 2419-1248-1-610-1, R 2419-1250-611-1, R 2419-1272-1-630-1 , R 2408-739-2-438-1, Jaldubi, DH-19-1-4

Table 4. Intra (diagonal and bold) and inter cluster D^2 values and distances among 5 clusters

		Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
Cluster	I	**88.87**	68.10	60.13	51.71	270.40	115.53	54.09
Cluster	II		**39.21**	99.15	75.92	261.67	107.07	66.35
Cluster	III			**37.96**	64.16	329.2	173.34	110.77
Cluster	IV				**100.93**	295.55	134.07	72.17
Cluster	V					**45.00**	162.52	224.38
Cluster	VI						**135.33**	64.40
Cluster	VII							**129.22**

Table 5. Cluster means values of different characters in 53 genotypes

Clusters	**Days to 50 % flowering**	**Days to maturity**	**Plant height**	**Total tillers per plant**	**Effective tillers per plant**	**Panicle length**	**Number of spikelet per panicle**	**Filled spikelet per panicle**	**Spikelet fertility %**	**1000 seed weight**	**Harvest index**	**Grain yield per plant**
I	97.90	124.70	113.75	7.98	7.15	24.73	187.80	156.15	83.4	22.19	31.84	13.95
II	96.50	123.50	134.35	9.15	7.10	27.15	239.50	120.75	71.65	13.10	24.65	12.00
III	100.00	126.75	103.20	7.75	7.35	23.90	146.25	114.75	78.17	18.90	28.92	11.10
IV	112.61	141.94	152.94	8.20	7.40	26.68	173.22	136.72	78.62	20.46	31.86	15.95
V	103.00	130.00	125.20	6.85	6.00	26.40	392.00	332.50	84.85	11.65	29.55	10.35

VI	106.88	135.00	144.12	7.20	6.58	26.17	278.16	218.72	74.73	13.90	29.18	12.44
VII	106.61	134.97	137.61	8.09	7.38	25.85	226.00	182.44	80.98	18.06	31.66	14.54
Avg.	103.36	130.98	130.17	7.89	6.99	25.84	234.70	180.29	78.91	16.89	29.67	12.90

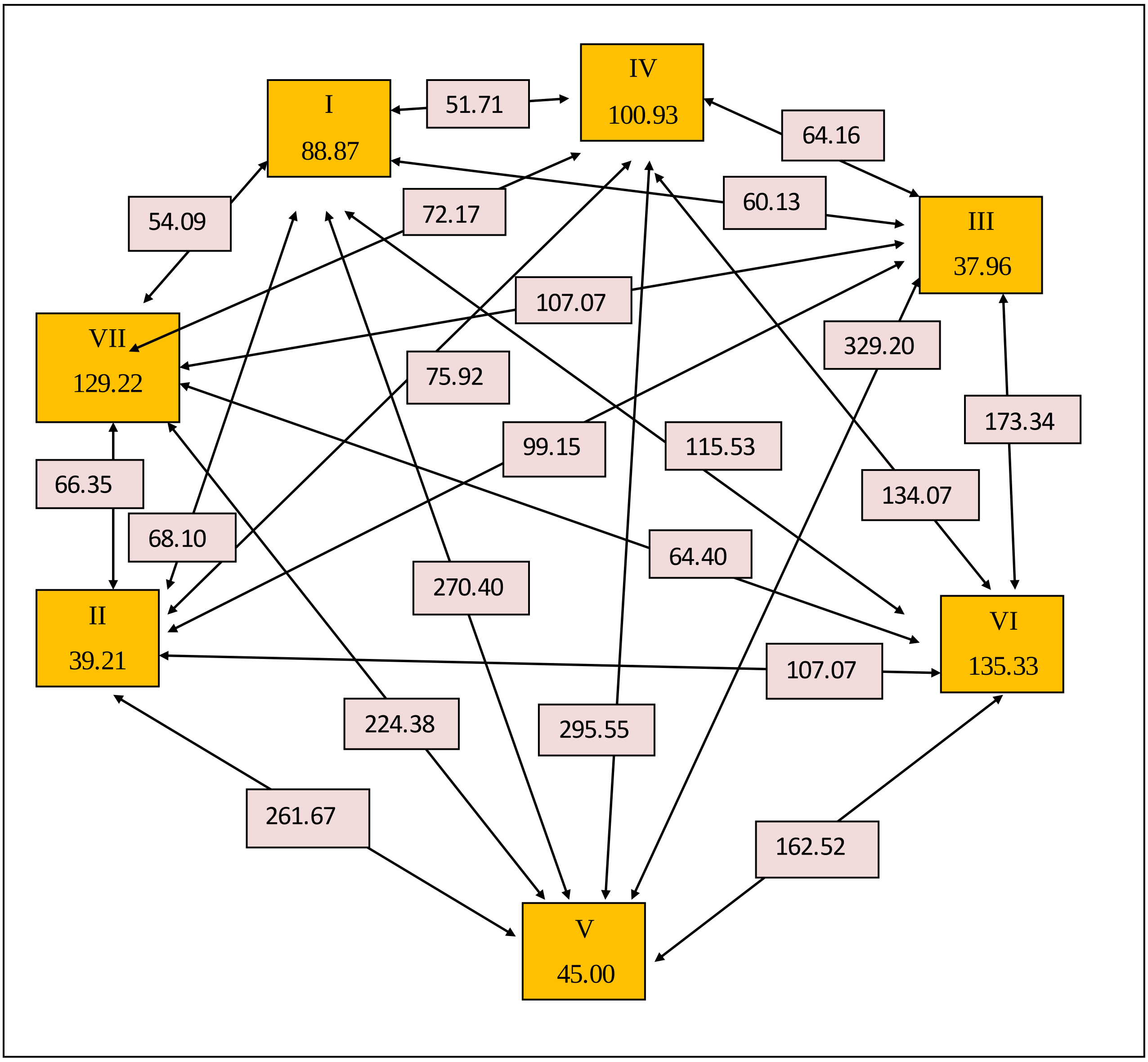

Fig-1. Cluster diagram with Intra and inter cluster distance

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