Original Research Article   https://doi.org/10.20546/ijcmas.2020.910.013

Genetic Divergence Analysis in Elite Rice (*Oryza sativa* L.) Germplasm using Agro-morphological Traits

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A B S T R A C T

The current experimentation was carried out at the field experimentation centre, Department of Genetics and Plant Breeding, Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj, U.P. Thirty two genotypes which include, 29 advanced breeding lines and three checks, were examined for several genetic parameters and genetic divergence among them using D^2 statistics for 13 quantitative characters. The analysis divided the 32 genotypes into seven clusters based on Tocher's clustering method. Out of the seven clusters formed, cluster I was the largest with eight genotypes and cluster VI and VII were monogenotypic. Highest inter cluster distance was found between cluster II and cluster IV indicating higher diversity between the genotypes of those clusters. Cluster II had highest mean for test weight character and cluster IV had highest mean for number of tillers per hill, number of panicles per hill and number of spikelets per panicle. Hence, hybridization between genotypes of these clusters would yield transgressive segregants. Highest intra-cluster distance was recorded in cluster V. Test weight had the highest heritability and maximum contribution towards divergence where as number of panicles per hill, flag leaf width, number of spikelets per panicle, biological yield and grain yield per hill had no contribution towards divergence.

Introduction

Rice belongs to the genus *Oryza* and the tribe *Oryzeae* of the family Gramineae (Poaceae). The genus *Oryza* contains 24 recognized species, of which 22 are wild species and two cultivated species are *O. sativa* and *O. glaberrima*. Rice (*Oryza sativa* L.) is one of the staple cereal crops of the world, directly feeding more people than any other crop. It is considered as the 'Grain of Life' because it is not only the stable food for more than 70% of the Indians but also a source of livelihood for about 120 million households. In India, rice is grown in 44.16 m.ha, the production level is 115 million tonnes and the productivity is about 2700kg/ha during 2018-19 (Annual report - NRRI-2019). In India, West Bengal stands top in the production of rice with an area of 5.12 m.ha. (11.68% of entire area across India) with production of 14.97 million tonnes (13.26% of entire production) and productivity of 2926kg/ha. (Agriculture statistics at a glance – 2018, DAC&FW, GoI). Uttar Pradesh ranks second in the country in production of rice covering 5.91 m.ha.

(13.28% of nation's share) with a production of 13.27 million tons (11.75% of entire production) and productivity of the state is around 2.2 t/ha (Agriculture statistics at a glance – 2018).

Knowledge of existing genetic divergence in a plant population is of utmost importance in any any crop improvement programme. Parents identified on the basis of divergence for any breeding programme would be more promising (Kwon *et al.,* 2002). Thus, the present study aims at studying the genetic variability using parameters like GCV, PCV, heritability, genetic advance and identifying parents with high genetic divergence to use them in future hybridization programmes.

Materials and Methods

The present investigation was carried out in the Field Experimentation Centre of Department of Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj, U.P during *kharif*-2019. The experimental materials for the present study consisted of 29 ABLs and three check varieties namely NDR-359, Jaya and SHIATS DHAN 1 of rice received from the Department of Genetics and Plant Breeding, SHUATS, Prayagraj conducted during *kharif*-2019. Standard agronomic practices were followed to ensure a good crop. Seedlings were transplanted at a spacing of 15 x 20 cm. observations were recorded on five randomly selected plants per replication for 13 quantitative characters namely days to 50% flowering, plant height (cm), number of tillers per hill, number of panicles per hill, panicle length(cm), flag leaf length (cm), flag leaf width (cm), number of spikelets per panicle, days to maturity, biological yield (g), harvest index (%), test weight (g) and grain yield per hill (g). The experimental data thus recorded on these

characters were subjected to statistical and biometrical analysis for analysis of variance (Fisher, 1936), different genetic parameters like Coefficient of variation (GCV, PCV) (Burton, 1952),estimation of heritability (Burton and De Vane, 1953), genetic advance (Johnson, *et al.,* 1995), and genetic divergence among the advanced breeding lines based on Mahalanobis D^2 statistics. The 32 genotypes under study were divided into seven clusters based on Tocher's method of clustering. Statistical analysis was performed using Windostat version 9.3

Results and Discussion

The analysis of variance revealed that there was sufficient amount of variability in the population for selection to act upon. The study of genetic parameters reveals that high GCV and PCV were recorded for number of spikelets (28.29 and 35.22 respectively) per panicle where as higher variation between GCV and PCV was also seen for the same character indicating higher amount of environment on it. Test weight character had the highest heritability (99.9%) followed by days to 50% flowering (97.2%) and days to maturity (96.5%). High heritability coupled with high range of genetic advance as percent mean was recorded for the characters number of tillers per hill, number of panicles per hill, number of spikelets per panicle, biological yield and test weight. However, days to 50% flowering, plant height, panicle length and days to maturity showed high heritability but moderate genetic advance. Similar observations were noted by Prajapati *et al.,* (2011). The table of ANOVA and summary of genetic parameters under study has been enlisted in table 1 and table 2 respectively.

The divergence studies revealed that the genotypes were divided into 7 clusters (Table 3) with cluster being the largest with 8 genotypes and cluster VI and VII had single

genotypes each. The highest inter cluster distance was found between cluster II and cluster IV (2633.03) followed by cluster II and cluster VI (2308.08). This indicates that the genotypes in these clusters were highly divergent and a crossing programme between these genotypes would yield transgressive segregants (Fig. 1–3).

Table.1 ANOVA for 13 characters of 32 rice germplasm evaluated during *kharif* 2019

S.no.	Characters	Mean sum of squares		
		Replication (df=2)	Treatments (df=31)	Error (df=62)
1.	Days to 50% flowering	1.34	174.43**	1.66
2.	Plant Height	25.78	273.29**	7.40
3.	Tillers per hill	0.54	10.93**	1.16
4.	Panicles per hill	0.66	8.12**	0.94
5.	Panicle length	0.98	8.67**	0.68
6.	Flag Leaf Length	1.002	57.65**	4.09
7.	Flag Leaf width	0.001	0.044**	0.004
8.	Spikelets per panicle	566.94	7199.82**	1114.79
9.	Days to maturity	11.46	122.75**	1.44
10.	Biological yield	73.39	285.24**	48.55
11.	Harvest Index(%)	11.53	81.81**	16.77
12.	Test Weight	0.35	70.62**	0.03
13.	Grain yield per hill	0.24	66.48**	17.11

** Significant at 1% Level of Significance

Table.2 Estimation of variability parameters for 13 quantitative traits of rice genotypes evaluated during *kharif*-2019

S.no.	Character	V_g	V_p	GCV	PCV	h^2 (bs) (%)	GA	GA as % mean
1.	Days to 50% flowering	57.58	59.25	8.13	8.25	97.2	15.41	16.52
2.	Plant height(cm)	88.62	96.03	8.06	8.39	92.3	18.63	15.95
3.	Number of tillers per hill	3.25	4.42	19.26	22.45	73.6	3.19	34.06
4.	Number of panicles per hill	2.39	3.34	18.15	21.44	71.7	2.69	31.66
5.	Panicle length (cm)	2.66	3.35	6.65	7.46	79.4	2.99	12.21
6.	Flag leaf length(cm)	17.85	21.94	12.65	14.02	81.4	7.85	23.50
7.	Flag leaf width(cm)	0.01	0.018	8.98	10.38	74.7	0.20	15.99
8.	No. of spikelets per panicle	2028.34	3143.14	**28.29**	**35.22**	64.5	**74.52**	**46.82**
9.	Days to maturity	40.43	41.88	5.13	5.23	96.5	12.87	10.40
10.	Biological yield(gm)	78.89	127.45	16.67	21.19	61.9	14.39	27.02
11.	Harvest index(%)	21.68	38.45	8.65	11.52	56.38	7.2	13.38
12.	Test weight (g)	23.53	23.56	20.84	20.86	**99.9**	9.98	42.91
13.	Grain yield per hill(g)	16.45	33.57	14.74	21.06	49	5.85	21.27

Table.3 Distribution of 32 genotypes into various clusters

S.no.	Cluster number	Number of genotypes	Genotypes included
1.	I	8	SHUATS DHAN (ABL)-03, SHUATS DHAN (ABL)-05, SHUATS DHAN (ABL)-06, SHUATS DHAN (ABL)-09, SHUATS DHAN (ABL)-17, SHUATS DHAN (ABL)-20, SHUATS DHAN (ABL)-21, SHUATS DHAN (ABL)-25
2.	II	4	SHUATS DHAN (ABL)-02, SHUATS DHAN (ABL)-11, SHUATS DHAN (ABL)-15, SHUATS DHAN (ABL)-24
3.	III	4	SHUATS DHAN (ABL)-01, SHUATS DHAN (ABL)-04, SHUATS DHAN (ABL)-07, SHUATS DHAN (ABL)-27
4.	IV	7	SHUATS DHAN (ABL)-12, SHUATS DHAN (ABL)-13, SHUATS DHAN (ABL)-16, SHUATS DHAN (ABL)-18, SHUATS DHAN (ABL)-19, NDR-359©,SHIATS DHAN-1©
5.	V	7	SHUATS DHAN (ABL)-10, SHUATS DHAN (ABL)-14, SHUATS DHAN (ABL)-22, SHUATS DHAN (ABL)-23, SHUATS DHAN (ABL)-26, MTU-1001, JAYA©
6.	VI	1	BPT-5204
7.	VII	1	SHUATS DHAN (ABL)-08

Table.4 Intra and Inter cluster distances among the seven clusters

Clusters	I	II	III	IV	V	VI	VII	
I	**32.21**	590.27	278.29	824.27	141.76	765.89	253.14	
II		**43.94**	1508.44	2633.03	512.37	2308.08	1312.96	
III			**71.48**	248.31	468.11	354.78	113.05	
IV				**77.82**	1033.67	194.79	302.57	
V					**139.56**	797.57	304.35	
VI						**0**	192.42	
VII							**0**	

Table.5 Cluster Mean values for 13 quantitative traits in 32 rice genotypes evaluated during *kharif* – 2019

	Days to 50% flowering	Plant Height (cm)	No. of Tillers per hill	No. of panicles per hill	Panicle length (cm)	Flag Leaf Length (cm)	Flag leaf width (cm)	No. of spikelets per panicle	Days to Maturity	Biolo gical yield (g)	Harv est Index (%)	Test Weight (g)	Grain yield per hill (g)
Cluster 1	**86.96**	111.02	9.42	8.38	24.01	30.88	1.16	135.13	**118.5**	48.59	54.22	24.96	26.2
Cluster 2	89.17	124.55	8.92	8.08	25.7	35.79	1.25	110.08	121.42	56.47	51.81	**31.62**	29.31
Cluster 3	90.42	126.28	8.67	7.83	23.22	**37.88**	1.29	195.5	119.25	51.06	**55.95**	20.41	28.86
Cluster 4	95.86	116.02	**10.57**	**9.62**	24.45	32.26	1.31	**210.1**	126.14	**56.74**	50.12	16.89	27.74
Cluster 5	97.62	116.07	9	8.38	**25.98**	34.32	**1.36**	138.19	127.95	53.2	49.03	25.66	26.58
Cluster 6	111.67	**99.83**	9.67	9	21.47	29.45	1.5	163.67	141	60.4	48.2	18.03	**30.73**
Cluster 7	105	121.8	7.33	7	22.77	31.63	1.4	188.67	129.67	55.87	48.47	20.95	27

Table.6 Percent contribution of each character towards divergence

S.no	Source	Contribution (%)	Times ranked 1st
1	Days to 50% flowering	9.27	46
2	Plant height (cm)	1.41	7
3	Number of tillers/hill	0.2	1
4	Number of panicles per hill	0	-
5	Panicle length (cm)	0.81	4
6	Flag leaf length (cm)	0.2	1
7	Flag leaf width (cm)	0	-
8	No. of spikelets/panicle	0	-
9	Days to maturity	5.04	25
10	Biological yield (gm)	0	-
11	Harvest index(%)	0.2	1
12	Test weight (g)	**82.86**	411
13	Grain yield per hill(g)	0	-

Fig.1 Histogram depicting percent contribution of each character towards genetic divergence
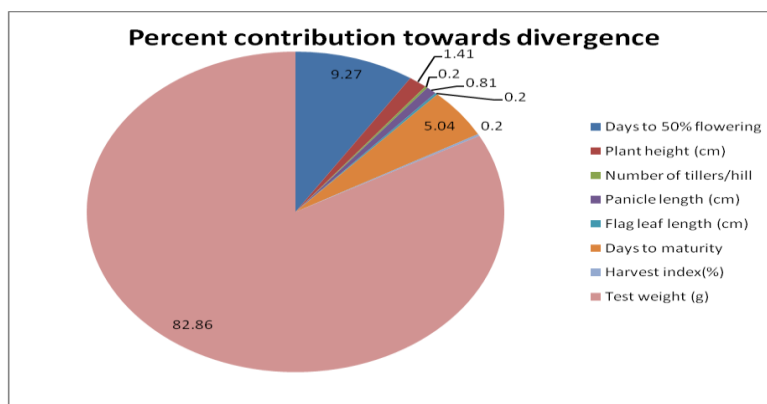
Fig.2 Cluster Diagram depicting relative position of different clusters with intra and inter cluster distances among them
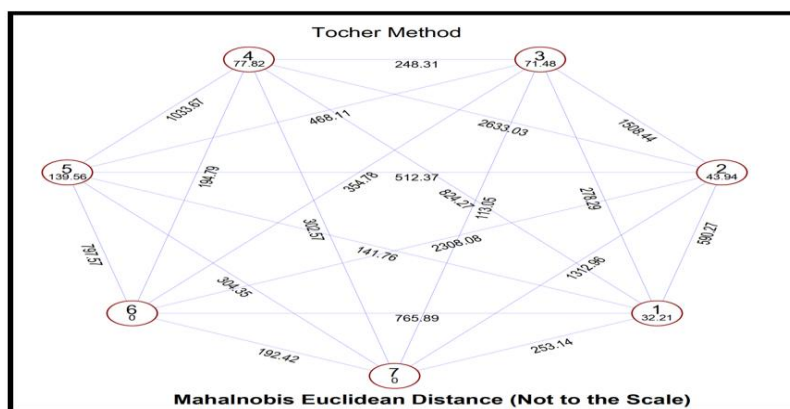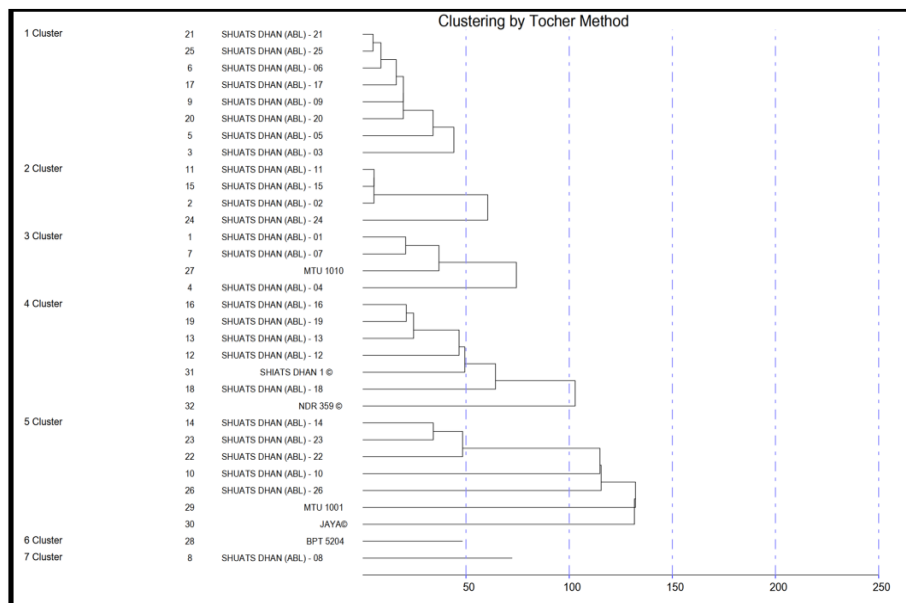
Fig.3 Dendrogram showing clustering pattern of 32 rice genotypes in *kharif*-2019 using Tocher's method

Cluster II showed superiority for test weight (for which the opposite distant cluster IV was inferior) and cluster IV was superior for number of spikelets per panicle, number of tillers per hill and number of panicle per hill. Thus a crossing between these clusters will yield desirable results. Highest intra cluster distance was found for cluster V. Different clusters showed superiority for different characters which indicates that a single cluster can't be used for development of all characters. The intra and inter cluster distances have been tabulated in table 4.

Mean performance of a cluster is the mean values of individual characters of the genotypes included in it. Analysis of cluster means indicates the existence of considerable differences for mean values in different traits. High cluster mean indicates that the genotypes of the cluster can be used for development of that particular character e.g. Cluster II showed highest mean for test weight which means genotypes of cluster II can be used to develop the test weight

character. Per cent contribution of each character towards divergence revealed that test weight (82.86%) and days to 50% flowering (9.27%) were the major contributors towards divergence and accounted for about 92.13% of contribution towards total divergence. These observations come in agreement with the findings of Ramesh Chandra *et al.,* (2010), Iftekharuddaula *et al.,* (2010), Rajesh *et al.,* (2010), N. Chamundeswari (2016) (Table 5 and 6).

In conclusion the current investigation revealed that the genotypes under study had considerable variability among them which enables selection to act upon. The genotype SHUATS DHAN (ABL)-02 was observed the best in terms of grain yield per hill where as SHUATS DHAN (ABL)-20 was the earliest maturing variety (115 days). High GCV and PCV were recorded for number of spikelets per panicle. High magnitude of difference for GCV and PCV were recorded for the same character which indicates higher

environmental influence. High heritability coupled with high genetic advance as percent mean was recorded for the characters number of tillers per hill, number of panicles per hill, number of spikelets per panicle, biological yield and test weight. This indicates preponderance of additive gene action for these characters. Such combination is desirable as direct selection can be practiced for such characters due to their high heritability and high genetic advance. Highest intra cluster distance was recorded for cluster V and highest inter cluster distance was recorded between cluster II and cluster IV. Cluster II showed high cluster mean for test weight and cluster IV showed high mean for superior for number of tillers per hill, number of panicles per hill, number of spikelets per panicle. These clusters can be used for development of these characters. Out of all the characters, test weight had the highest contribution towards divergence. The genotypes of clusters II, III, IV, VI can be used for crossings in future hybridization programmes as they have high genetic diversity among them.

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How to cite this article:

Ankit Kumar, Rajashekar Reddy, Meghana Devi, B. Jalandhar Ram and Suresh, B. G. 2020. Genetic Divergence Analysis in Elite Rice (*Oryza sativa* L.) Germplasm using Agro-morphological Traits. *Int.J.Curr.Microbiol.App.Sci.* 9(10): 92-99.
doi: https://doi.org/10.20546/ijcmas.2020.910.013