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Genetic diversity analysis in JNPT lines of rice (*Oryza sativa* L.)

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Abstract

In present study, sixty-seven JNPT (Jawahar New Plant Type) lines were evaluated for twenty-eight morphological and quality traits planted in Randomized Complete Block Design with three replications. The experiment was conducted during *kharif* seasons of 2018 at Seed Breeding Farm, Department of Plant Breeding and Genetics, College of Agriculture, JNKVV, Jabalpur (M.P.), India. Observations were recorded on the basis of middle five random competitive plants selected from each line in every replication for yield and quality traits. Considerable genetic variability was exhibited by all the yield and quality traits under study. The genotypes of cluster VIII and IX showed higher (19816.1) inter cluster distance followed by cluster IV and VIII (12414.7). Hence genotypes of these clusters may be crossed to broaden the genetic base of rice. Intra cluster distance has been found the highest of cluster V hence, the hybridization among the genotypes of cluster V may also result superior recombinants. The results of this study suggested further hybridization programme should be planned involving the diverse genotype viz. JNPT-1065-3, JNPT-1066-52, JNPT-1065-1, JNPT-1065-2 and JNPT-1068-65 present in Cluster IV, Cluster V, Cluster VII and Cluster VIII on the basis of their greater inter-cluster distances and higher cluster mean values for the yield and quality attributing character.

Keywords: Jawahar new plant type, rice, *Oryza sativa* L.

1. Introduction

Rice (*Oryza sativa* L.) is one of the most important crop, feeding more than half the world's population. Asia, Sub-Saharan Africa, and South America are the largest consuming regions. Globally, India stands first in rice cultivation area and second in rice production, after China. It contributes 26.9 per cent of worldwide rice production. Within the nation, rice occupies one quarter of the total cropped area, contributes around 40 to 43 per cent of total food grain production and continues to play an important role in the national food and livelihood security framework. Ninety per cent of all rice are being grown and consumed in Asia. World production of paddy has risen steadily from about 220 million tonnes in 1960 to over 759.6 million tonnes in 2017 and rice production is 503.9 million tonnes in 2017. At that level, global production would exceed the 2016 record by a modest 0.6 per cent, or 4.5 million tonnes (FAOSTAT, 2018).

Yield of paddy is a complex quantitative character regulated by many genes interacting with the 26 environment and is the result of numerous factors called yield components. Selection of parents based on yield alone is often misleading (Rahman *et al.* 1997) ^[11]. Diversity in crop varieties is important to enhance food production, alleviate poverty, and foster overall economic growth that contributes to agricultural development. This functions as insurance for unknown needs and demands of the future. For the successful selection of parents for hybridization purposes, assessing genetic divergence in the available germplasm is essential. The divergent lines belonging to different and distant clusters are more likely to give heterotic hybrids or superior progenies than those parental lines belonging to the same cluster or group with low genetic distance (Rao 1952) ^[13]. It is quite imperative to group or classify genotypes on the basis of an appropriate scale to understand the usable variability that exists among them.

The present investigation was therefore undertaken to ascertain the genetic divergence among the genotypes and the contribution of characters to genetic divergence studied related to fitness and productivity. A total of sixty-seven NPT line of rice genotypes over 28 yield and yield contributing characters were tested for genetic divergence analysis.

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2. Materials and Methods

The experimental material consists of 67 new JNPT lines (Table 1) derived from *Indica X Japonica* subspecies crosses (F₈-F₉ BC₃ generation) developed by Rice Improvement Project, JNKVV, Jabalpur were grown during *Kharif* season of 2018 at Seed Breeding Farm, JNKVV, Jabalpur (M.P.), India. These lines were planted in Randomized Complete Block Design with three replications. Twenty-one days old seedlings were transplanted in the experimental site with spacing of 15 cm between plant to plant and 20 cm between the rows, keeping single seedling per hill. Gap filling was done within a week so as to keep uniform plant population. Fertilizer dose of 120 kg N, 60 kg P₂O₅ and 60 kg K₂O was applied. The standard agronomic practices were adopted for normal crop growth.

Twenty-eight quantitative and quality characteristics were used to characterize and assess the genetic diversity of JNPT lines as per rice DUS guideline. Five plants were randomly chosen from each replication in each genotype for yield assessment and quality attribute traits. The observations were recorded as per the standard procedure and subjected to statistical analysis using mean values of five randomly selected plants.

Table 1: List of contributing NPT lines of rice in this study

S. No.	Name of NPT lines	S.No.	Name of NPT lines
1	JNPT-1051	35	JNPT-1063-35
2	JNPT-1052	36	JNPT-1063-36
3	JNPT-1053	37	JNPT-1064-1
4	JNPT-1054	38	JNPT-1064-2
5	JNPT-1055	39	JNPT-1064-3
6	JNPT-1056	40	JNPT-1064-4
7	JNPT-1057	41	JNPT-1064-5
8	JNPT-1058	42	JNPT-1064-6
9	JNPT-1059-9	43	JNPT-1064-7
10	JNPT-1059-10	44	JNPT-1064-8
11	JNPT-1059-11	45	JNPT-1064-9
12	JNPT-1059-12	46	JNPT-1064-10
13	JNPT-1060-13	47	JNPT-1065-1
14	JNPT-1060-14	48	JNPT-1065-2
15	JNPT-1060-15	49	JNPT-1065-3
16	JNPT-1060-16	50	JNPT-1065-4
17	JNPT-1060-17	51	JNPT-1065-5
18	JNPT-1060-18	52	JNPT-1066-52
19	JNPT-1060-19	53	JNPT-1066-53
20	JNPT-1060-20	54	JNPT-1066-54
21	JNPT-1060-21	55	JNPT-1066-55
22	JNPT-1060-22	56	JNPT-1066-56
23	JNPT-1060-23	57	JNPT-1066-57
24	JNPT-1060-24	58	JNPT-1067-1
25	JNPT-1061-25	59	JNPT-1067-2
26	JNPT-1061-26	60	JNPT-1067-3
27	JNPT-1061-27	61	JNPT-1067-4
28	JNPT-1061-28	62	JNPT-1067-5
29	JNPT-1062-1	63	JNPT-1068-63
30	JNPT-1062-2	64	JNPT-1068-64
31	JNPT-1063-31	65	JNPT-1068-65
32	JNPT-1063-32	66	JNPT-1068-66
33	JNPT-1063-33	67	JNPT-1068-67
34	JNPT-1063-34		

2.1 Statistical analysis

The data on different characters were analyzed through Mahalanobis' generalized distance D² (1936). Grouping of the populations into various clusters was done by using Tocher's method as described by Rao (1952) [13]. The criterion used in clustering by this method is that any two variables belonging to the same cluster should at least on an average, show a smaller D² value than those belonging to different clusters. For this purpose, D² values of the combinations of each genotype were arranged in ascending order of their magnitudes as described by Singh and Chaudhary (1979).

3. Results and Discussion

3.1 Genetic diversity analysis

The genetic divergence has been studied using Mahalanobis's D² statistics on 67 genotypes over 28 yield and yield contributing characters. Results are presented below.

3.2 Mahalanobis generalize distance (D²)

As per Wilks test, Wilks criterion was obtained as 19349.024 with V statistics as 10228.42 and df as 1848. The analysis of variance showed highly significant differences within the population for all the 28 characters studied. The D² values corresponding to possible comparison among 67 genotypes taking two genotypes at a time were computed separately in the analysis.

3.3 Contribution of individual characters towards genetic divergence

The percentage contribution towards genetic divergence by all the characters is presented in table 2. The results indicated that the character thousand grain weight (72.00%) contributed most towards genetic divergence followed by remaining characters in descending order viz. head rice recovery (18.77%), grain length (6.15%), decorticated grain length (0.68%), days to 50% flowering (0.50%), fertile spikelets/panicle (0.45%), days to maturity (0.36%), Milling percentage (0.36%), grain breadth (0.18%), panicle length (0.14%), biological yield/plant (0.14%), harvest index (0.14%), number of spikelets/panicle (0.09%) and hulling percentage (0.05%). Whereas, number of tillers/plant, number of productive tillers/plant, plant height, stem length, stem thickness, flag leaf length, flag leaf width, panicle weight/plant, spikelet fertility, spikelet density, panicle index, decorticated grain breadth, decorticated grain L/B ratio had no contribution towards divergence.

These results are in conformity with the findings of Shanthi and Singh (2001) [17], Naik *et al.* (2006) [9], Reddy *et al.* (2006) [12] and Jha *et al.* (2014) [4] for thousand grain weight while, grain length contributed towards genetic divergence was in agreement with the finding reported by Shanthi and Singh (2001) [17], Naik *et al.* (2006) [9], Chandra Ramesh *et al.* (2007), Singh *et al.* (2008) and Shahidullah *et al.* (2009). Plant height was not contributed for genetic divergence. This was not in support with the findings of Madhavilatha *et al.* (2005) [6], Bose and Pradhan (2005) [1], Reddy *et al.* (2006) [12], Kumar Dushyantha (2008) [5] and Jha *et al.* (2014) [4], they were of the view that it contributed towards maximum divergence.

Table 2: Percent contribution of characters towards divergence in JNPT lines of rice

S. No.	Character	Times ranked 1st	Percentage (%) contribution of traits towards divergence
1	Thousand grain weight	1592	72.00%
2	Head rice recovery	415	18.77%
3	Grain length	136	6.15%
4	Decorticated grain length	15	0.68%
5	Days to 50% flowering	11	0.50%
6	Fertile spikelets/panicle	10	0.45%
7	Days to maturity	8	0.36%
8	Milling percentage	8	0.36%
9	Grain breadth	4	0.18%
10	Panicle length	3	0.14%
11	Biological yield /plant	3	0.14%
12	Harvest index	3	0.14%
13	Number of spikelets/panicle	2	0.09%
14	Hulling percentage	1	0.05%
15	Number of tillers/plant	0	0.00%
16	Number of productive tillers/plant	0	0.00%
17	Plant height	0	0.00%
18	Stem length	0	0.00%
19	Stem thickness	0	0.00%
20	Flag leaf length	0	0.00%
21	Flag leaf width	0	0.00%
22	Panicle weight/plant	0	0.00%
23	Spikelet fertility	0	0.00%
24	Spikelet density	0	0.00%
25	Panicle index	0	0.00%
26	Decorticated grain breadth	0	0.00%
27	Decorticated grain L/B ratio	0	0.00%
28	Grain yield per plant	0	0.00%

3.4 Grouping of lines into different clusters

On the basis of D^2 values, the 67 lines were grouped into 10 clusters following Tocher's method. The cluster II was polygenotypic (16 lines) followed by Cluster III with 15 lines,

cluster IV with 14 lines, cluster I with 10 lines, cluster V with 4 lines, cluster VI with 3 lines, cluster VIII with 2 lines, cluster VII, IX and X each with 1-line Cluster wise distribution of lines are summarized in Table 3.

Table 3: Distribution of rice genotypes in different clusters

Cluster No.	Number of genotypes	Genotypes
I	10	JNPT-1063-35, JNPT-1063-36, JNPT-1060-13, JNPT-1064-4, JNPT-1067-2, JNPT-1061-25, JNPT-1064-1, JNPT-1064-3, JNPT-1063-32, JNPT-1063-33
II	16	JNPT-1067-1, JNPT-1067-3, JNPT-1064-8, JNPT-1052, JNPT-1064-2, JNPT-1064-9, JNPT-1057, JNPT-1064-5, JNPT-1059-9, JNPT-1064-6, JNPT-1053, JNPT-1056, JNPT-1061-27, JNPT-1059-11, JNPT-1054
III	15	JNPT-1060-14, JNPT-1060-19, JNPT-1060-18, JNPT-1060-22, JNPT-1062-2, JNPT-1060-21, JNPT-1060-15, JNPT-1060-17, JNPT-1060-20, JNPT-1060-24, JNPT-1062-1, JNPT-1055, JNPT-1059-9, JNPT-1063-34, JNPT-1063-31
IV	14	JNPT-1061-26, JNPT-1061-28, JNPT-1064-7, JNPT-1065-3, JNPT-1066-52, JNPT-1066-53, JNPT-1066-54, JNPT-1066-55, JNPT-1066-56, JNPT-1066-57, JNPT-1067-4, JNPT-1067-5, JNPT-1068-66, JNPT-1068-67
V	4	JNPT-1051, JNPT-1058, JNPT-1059-12, JNPT-1065-1
VI	3	JNPT-1065-4, JNPT-1065-5, JNPT-1068-63
VII	1	JNPT-1065-2
VIII	2	JNPT-1068-64, JNPT-1068-65
IX	1	JNPT-1060-23
X	1	JNPT-1060-16

3.5 Inter and intra cluster divergence D^2 values

The average intra and inter-cluster D^2 values estimated as per the procedure given by Singh and Choudhary (1979) are presented in table 4 and the cluster mean values are summarized in table 5.

Intra cluster D^2 values are minimum (0.00) in cluster VII, IX and X as these were mono-genotypic clusters and genotypes falling in these clusters were more divergent and they could be utilized as parents for hybridization. Maximum intra cluster distance was observed in cluster V (773.17), followed by cluster IV (573.8) and cluster VI (437.61), indicating that

some genetic divergence still existed among the genotypes within each of these clusters. Selection within such clusters might be executed based on maximum mean value for the desirable characters.

The inter cluster distance was higher than intra cluster distance, indicating the presence of wide genetic diversity among the genotypes under study. The highest inter cluster divergence was found between genotypes of cluster VIII and IX ($D^2 = 19816.1$), followed by cluster IV and VIII ($D^2 = 12414.7$), cluster III and IX ($D^2 = 11086.97$), cluster IX and X ($D^2 = 10103.23$), cluster VII and VIII ($D^2 = 9992.08$) whereas

least inter cluster divergence was observed between genotypes of cluster I and V ($D^2 = 550.09$). Clustering pattern revealed that quantum of diversity present in different clusters suggesting the genotypes from two clusters having wider inter-cluster distances could be used as parents in hybridization programme in diallele selective mating system

design since hybridization between divergent parents is likely to produce wide variability and transgressive segregations with high heterotic effects (Pratap *et al.* 2012) [10]. However, biological yield contributed low towards genetic divergence. This finding is in consonance with Nagle *et al.* (2014) [8].

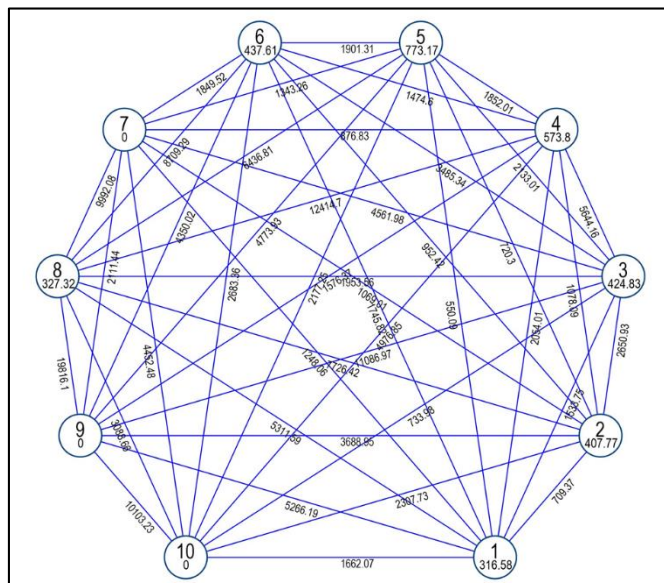


Fig 1: Diagrammatic representation of Intra and Inter cluster distance

Table 4: Average intra and inter cluster D^2 values of NPT lines of rice.

Column1	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster 7	Cluster 8	Cluster 9	Cluster 10
Cluster 1	316.58	709.37	1533.75	2054.01	550.09	1745.82	1248.06	5311.59	5266.19	1662.07
Cluster 2		407.77	2650.93	1078.09	720.3	952.42	1069.01	7726.42	3688.95	2307.73
Cluster 3			424.83	5644.16	2133.01	3485.34	4561.98	1953.56	11086.97	733.98
Cluster 4				573.8	1852.01	1474.6	876.83	12414.7	1576.37	4976.85
Cluster 5					773.17	1901.31	1343.26	6436.81	4773.93	2177.25
Cluster 6						437.61	1849.52	8709.29	4350.02	2683.36
Cluster 7							0	9992.08	2111.44	4452.48
Cluster 8								327.32	19816.1	3088.66
Cluster 9									0	10103.23
Cluster 10										0

Table 5: Cluster mean values showing importance of grouped characters.

	DTF	DTM	TPP	PTPP	PH	SL	PL	ST	FLL	FLW	BYPP	PWPP	NSPP	FSPP
Cluster 1	107.80	133.80	7.17	7.15	105.39	78.57	26.82	5.76	53.40	1.50	58.09	26.49	212.37	183.40
Cluster 2	106.35	133.67	7.37	7.36	100.64	76.08	24.57	5.86	48.88	1.35	59.61	27.79	193.50	170.42
Cluster 3	109.53	136.42	6.74	6.72	101.04	75.77	25.26	5.97	50.98	1.45	54.66	26.35	282.18	229.73
Cluster 4	103.24	129.79	7.69	7.68	100.02	74.67	25.35	5.44	47.81	1.44	57.17	26.55	181.74	164.43
Cluster 5	111.17	140.17	7.83	7.80	96.63	72.28	24.35	5.95	46.75	1.21	68.15	30.50	171.08	149.92
Cluster 6	102.56	129.67	7.84	7.84	94.44	70.73	23.71	5.47	44.44	1.47	54.16	25.22	165.44	149.89
Cluster 7	103.33	130.33	8.07	8.07	98.73	74.93	23.80	5.87	50.00	1.30	55.40	26.87	169.00	151.33
Cluster 8	121.83	154.00	8.90	8.87	109.70	86.07	23.63	5.53	54.33	1.25	56.20	22.73	201.83	189.33
Cluster 9	109.67	135.67	6.27	6.27	87.20	59.73	27.47	6.33	48.00	1.23	63.33	24.80	313.00	220.33
Cluster 10	98.67	125.33	6.93	6.93	121.73	92.80	28.93	6.80	55.67	1.57	66.20	26.40	328.00	125.67

	SF	SD	TGW	PI	HI	GL	GW	DGL	DGW	DLBR	HP	MP	HRR	GYPP
Cluster 1	86.86	7.93	24.30	73.99	33.89	8.80	2.58	6.33	2.16	2.94	77.13	73.27	68.07	19.80
Cluster 2	88.08	7.91	26.16	74.64	34.80	9.26	2.64	6.69	2.18	3.08	78.87	73.58	59.79	20.63
Cluster 3	81.79	11.20	19.76	73.52	36.28	8.59	2.46	6.22	2.06	3.03	78.24	72.09	62.62	19.39
Cluster 4	90.64	7.16	29.59	75.03	35.45	9.30	2.76	6.75	2.30	2.96	79.29	74.29	59.55	20.00
Cluster 5	88.05	6.98	24.93	73.48	32.99	9.37	2.66	6.61	2.25	2.97	79.08	74.08	68.67	22.38
Cluster 6	90.73	6.99	26.73	77.11	36.10	8.56	2.79	6.40	2.37	2.73	79.00	74.78	45.56	19.46
Cluster 7	89.51	7.08	28.43	79.31	38.47	8.27	3.07	6.03	2.57	2.33	80.67	76.67	71.67	21.33
Cluster 8	94.00	8.52	15.08	77.11	31.38	7.30	2.37	5.47	2.23	2.50	77.67	67.67	66.00	17.63
Cluster 9	70.34	11.52	34.03	72.36	28.33	9.27	2.50	6.57	2.27	2.90	80.67	71.67	63.67	18.03
Cluster 10	38.30	11.39	20.47	74.24	29.71	8.53	2.53	6.47	2.07	3.13	78.33	69.33	54.00	19.60

4. Conclusion

On the basis of D^2 values, the sixty-seven genotypes were grouped into 10 clusters out of which seven were polygenotypic and three were monogenotypic. The genotypes of cluster VIII and IX showed higher (19816.1) inter cluster distance followed by cluster IV and VIII (12414.7). Hence genotypes of these clusters may be crossed to broaden the genetic base of rice. Intra cluster distance has been found the highest of cluster V hence, the hybridization among the genotypes of cluster V may also result superior recombinants. However, the highest percentage contribution towards divergence was due to thousand grain weight followed by remaining characters viz. head rice recovery, grain length, decorticated grain length, days to 50% flowering, fertile spikelets/panicle, days to maturity, milling percentage, grain breadth, panicle length, biological yield/plant and harvest index. Thus, these characters must be considered for selecting the genotypes for yield and quality traits in segregating generation of rice. The results of this study suggested further hybridization programme should be planned involving the diverse genotype viz. JNPT-1065-3, JNPT-1066-52, JNPT-1065-1, JNPT-1065-2 and JNPT-1068-65 present in Cluster IV, Cluster V, Cluster VII and Cluster VIII on the basis of their greater inter-cluster distances and higher cluster mean values for the yield and quality attributing character

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