Short Communication

Genetic diversity studies in selected elite genotypes and released varieties of Rice

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An experiment was undertaken by utilizing fifty selected elite genotypes and released varieties of rice for ten yields and yield contributing characters to assess genetic divergence at Zonal Agriculture Research Station, Igatpuri, Dist. Nashik during *kharif* 2020. Path coefficient analysis revealed that test weight exhibited highest positive direct effect on grain yieldplant[-1] and subsequently by spikelet fertility, number of panicles plant[-1], plant height, number of spikelet panicle[-1], panicle length and days to physiological maturity. Whereas, number of fertile spikelet panicle[-1] recorded the highest negative direct effect on grain yieldplant[-1]. The characters *viz;* number of panicles plant[-1], number of spikelet panicle[-1], spikelet fertility, test weight had exerted significant positive direct effect on grain yield plant[-1] and correlation of these characters with grain yield plant[-1] was positively significant. Fifty genotypes were grouped into eight clusters. ClusterII was biggest and consisted of 19 genotypes followed by cluster I with 11 genotypes. The cluster III and V both were consist of 8 genotypes. All remaining clusters *viz.* cluster IV, VI, VII and VIII were solitary. Intra cluster distance was ranged from zero (cluster IV, VI, VII and VIII) to 13.15 (cluster V). The highest intra cluster distance was observed in cluster V followed by cluster III, cluster II and cluster I. From the inter cluster D^2 values of the eight clusters, it can be seen that the highest divergence occurred between cluster VII and VIII followed by cluster I and VI, cluster VI and VII suggesting that the crosses involving varieties from these clusters would give wider and desirable recombination.

Rice (*Oryzasativa* L.) isone of the most important staple food crops for more than 60% of the world population and it has been the cheapest source of food, energy and protein. It belongs to family Poaceae (*Gramineae*) that includes other cereals such as wheat and corn. It provides 43% of calories of human diet in India; and contributes 20-25% of agricultural income due to its intensive cultivation. In Asia, majority of the population consumes rice in meal every day. In many countries, rice accounts for more than 70% of human calorific intake.

In India, rice is cultivated in an area of 43.79 MH with the production and productivity levels of 116.42 Mt and 2659 kg/ha, respectively (Anonymous, 2018), while in Maharashtra, rice is cultivated in an area of 1.54MH with the production of 3.51 Mt (Anonymous, 2019). West Bengal has the highest rice production, while Punjab has the highest productivity of rice in India.

Genetic diversity within crop species is essential to maintain high level of productivity. The importance of information about the degree of genetic divergence in rice and its utilization for the selection of desirable parents either for exploitation of hybrid vigour or to get desirable segregants has been put forth by many workers (Anand and Murthy, 1968). Arunachalam (1981) reported that the greater probability of getting heterotic hybrids and improved variation in the segregating population of varietal improvement programmes mainly depended on genetic diversity. Analysis of degree of divergence in a given experimental material

is of great value in identification of diverse genotypes for further use in hybridization programme to sustain variability. Mahalanobis D^2 statistic has proved to be a helpful tool for quantifying genetic divergence in a given population. Murthy and Arunachalam (1966) stated that multivariate analysis with Mahalanobis D^2 statistics is a tool to know the clustering pattern which helps to establish the relationship between genetic and divergence and to determine the contribution of different quantitative characters towards the divergence. Diverse genotypes could be obtained by collection from different eco-geographical regions or diversity could be induced by combination breeding.

The 50 genotypes of rice were sown on 15th June, 2020 in a Randomized Block Design with two replications. Each entry was represented by a quadral row of 3 m length and 0.8 m breadth with a spacing of 25 cm between rows and 15 cm between plants within a row. Two border rows were sown on both the sides of plots to reduce the border effects. 3-4 grains were dibbled hill[-1] to ensure better crop stand and a single seedling was kept hill[-1] after thinning of seedlings. All prescribed agronomic techniques were implemented as needed. The 11 quantitative character observations were made on five randomly selected plants from each plot in each replication. The analysis for divergence was done by following Mahalanobis (1936) D^2 statistics. The path coefficient analysis was carried out by the procedure suggested by Dewey and Lu (1959).

The data obtained from eleven characters were subjected to statistical analysis of variance revealed highly significant differences among the genotypes for all the characters studied (Table 1). The mean performances of 50 genotypes of Rice for eleven characters studied are presented in Table 2. The genotype Phule Samruddhi depicted highest grain yield per plant (34.60 g) and the genotype P-6 recorded lowest grain yield per plant (9.71 g) The genotype KJT-4 (94 days) was the earliest for flowering and days to physiological maturity 128 days). The genotype IGP local was found tall and Ratna was found short. Phule Samruddhi recorded the highest number of panicle per plant (17.50), however RTN-182-2 showed the lowest number of panicle (5.50). In relation to fertile spikelet per panicle the genotype IGP local showed highest better performance. Test weight was found highest in Phule Samruddhi and lowest in Bhandardara local.

Phenotypic and genotypic correlation coefficients of fifty genotypes of rice for grain yield with its component characters were studied. The results indicated that genotypic correlation coefficients were higher than phenotypic correlation coefficients between most of the characters (Table 3). This indicated that there was strong inherent association between various characters studied and the same was less influenced by environmental variations. A strong and significant and positive correlation was observed between grain yield per plant with panicle length, number of panicles per plant, number of spikelet per panicle, number of fertile spikelet per panicle, spikelet fertility and test weight. Similar kind of associations were revealed by Sawant *et al.* (1995) for panicle length and test weight, Sarawgi *et al.* (1997) for number of fertile spikelets panicle[-1], Sangeeta *et al.* (2001) for panicle length and number of panicles plant[-1] and Lingaiah *et al.* (2020) for test weight.

It was evident from Table 4 that grain yield plant[-1] was the result of panicle length, number of panicles plant[-1], number of spikelets panicle[-1], number of fertile spikelets panicle[-1], spikelet fertility, test weight as they were significantly correlated with it. These variables were interrelated, so that each factor influenced the grain yield by a direct contribution and indirect contributions through other variables with which it was correlated.

From the data, it can be concluded that the positive and highest direct effect on grain yield plant[-1] was exhibited by test weight (0.581). This highest positive direct effect was followed by spikelet fertility (0.276), number of panicles plant[-1] (0.263), plant height (0.051), number of spikelet panicle[-1] (0.036), panicle length (0.035) and days to physiological maturity (0.002). The highest negative direct effect on grain yield plant[-1]was exhibited by the number of fertile spikelet panicle[-1](-0.143) and subsequently by days to 50% flowering (-0.093) and number of infertile spikelet panicle[-1](-0.014). The yield contributing characters *viz.* number of panicles plant[-1], number of spikelet panicle[-1], spikelet fertility, test weight had exerted significant positive direct effect on grain yield plant[-1] and correlation of these characters with grain yield was positively significant. Thus, direct selection for these traits will be rewarding for yield improvement. These findings were in agreement with reports of Sawant *et al.* (1995) for test weight, panicle length, Sarawgi *et al.* (1997) for test weight, Sangeeta *et al.* (2001) for number of panicles plant[-1] and Satish *et al.* for test weight.

Based on genetic distances 50 genotypes were grouped into eight clusters (Table 5). Cluster II was biggest and consisted of 19 genotypes followed by cluster I with 11 genotypes..All the genotypes consisted in different clusters are same eco geographical region except one from Uttar Pradesh. In the present study, the genotypes belonging to the same geographical region or same location fell into different clusters, separated by high genetical distances. It confirmed the non existence of any relationship of genetic diversity with geographical diversity. Similar findings were reported by earlier by Chaturvedi and Maurya (2005), Reddy *et al.* (2006), Rai *et al.* (2014) and Raut *et al.* (2009).

The intra and inter cluster D^2 and D values were worked out from divergence analysis.(Table 6). Maximum intra cluster distance was observed in cluster V (D^2=172.92) followed by cluster III (D^2=101.00), cluster II (D^2=95.84) and cluster I(D^2=87.98). From the inter cluster D^2 values of the eight clusters, it can be seen that the highest divergence occurred between cluster VII and VIII followed by cluster I and VI, cluster VI and VII suggesting that the crosses involving varieties from these clusters would give wider and desirable recombination. Cluster mean for 11 characters revealed wide range of variability among the clusters for the characters, days to 50 % flowering, days to physiological maturity, number of panicles plant[-1], number of spikelet panicle[-1], spikelet fertility, test weight and grain yield per plant.

Table 1:   Analysis of variance for eleven characters of 50 rice genotypes

S. N.	Characters	Mean sum of Squares		
		Replication (df 1)	Genotype (df 49)	Error (df 49)
1	Days to 50%flowering	0.64	111.82**	2.88
2	Days to physiological maturity	1.21	130.31**	4.70
3	Plant height (cm)	0.61	905.18**	6.14
4	Panicle length (cm)	2.82	24.85**	1.37
5	Number of panicles plant[-1]	0.09	17.48**	0.60
6	Number of spikelet panicle[-1]	1.44	6705.14**	238.97
7	Number of fertile spikelet panicle[-1]	50.41	6897.87**	250.21
8	Number of infertile spikelet panicle[-1]	68.89	192.21**	28.34
9	Spikelet fertility (%)	7.25	110.23**	9.57
10	Test weight (g)	0.19	36.50**	1.13
11	Grain yield plant[-1]	6.46	92.81**	5.02

*,** Significant at 5 and 1 per cent, respectively.)

Table 2:   Character wise mean performance, range and genotype depicted

S. N.	Characters	Mean	Range	Name of genotype	
				Highest	Lowest
1	Days to 50%flowering	108.92	94.00 – 120.00	Ambemohar-157	KJT-4
2	Days to physiological maturity	142.03	128.00 – 157.00	Ambemohar-157	KJT-4
3	Plant height (cm)	83.55	50.40 - 134.10	IGP-Local-8	Ratna
4	Panicle length (cm)	21.54	14.00 – 28.20	Bhogavati	RTN-185-2
5	Number of panicles plant[-1]	11.09	5.50 - 17.50	Phule Samruddhi	RTN-185-2
6	Number of spikelet panicle[-1]	187.90	92.50 – 288.00	IGP local	Bhandardara local
7	Number of fertile spikelet panicle[-1]	159.17	70.00 - 261.50	IGP local	Bhandardara local
8	Number of infertile spikelet panicle[-1]	28.73	11.00 - 51.50	Jai Bangal	IGP local-10
9	Spikelet fertility (%)	83.26	58.81 - 94.22	Vikram	P-6
10	Test weight (g)	18.00	11.10 - 27.18	Phule Samruddhi	Bhandardara local
11	Grain yield plant[-1](g)	19.79	9.71 - 34.60	Phule Samruddhi	P-6

Table 3: Estimates of genotypic (above diagonal) and phenotype correlation coefficients (below diagonal) among grain yield plant⁻¹ and ten yield contributing characters in 50 rice genotypes

Characters	Days to 50% flowering	Days to physiological maturity	Plant height (cm)	Panicle length (cm)	No. of panicles plant⁻¹	No. of spikelets panicle⁻¹	No. of fertile spikelets panicle⁻¹	No. of infertile spikelets panicle⁻¹	Spikelet fertility (%)	Test weight (g)	Grain yield plant⁻¹
Days to 50% flowering	1.000	0.887**	0.354**	-0.005	-0.041	0.025	0.012	0.079	-0.061	0.073	-0.061
Days to physiological maturity	0.890**	1.000	0.391**	-0.119	-0.086	-0.034	-0.042	0.053	-0.054	0.050	-0.070
Plant height (cm)	0.355**	0.389**	1.000	-0.199*	-0.085	0.048	0.009	0.240	-0.103	0.073	-0.020
Panicle length (cm)	0.012	-0.090	-0.183	1.000	0.751**	0.603**	0.632**	-0.233*	0.497**	0.656**	0.677**
No. of panicles plant⁻¹	-0.016	-0.051	-0.072	0.709**	1.000	0.829**	0.839**	-0.134	0.591**	0.867**	0.868**
No. of spikelets panicle⁻¹	0.062	0.014	0.057	0.555**	0.800**	1.000	0.988**	-0.009	0.652**	0.824**	0.794**
No. of fertile spikelets panicle⁻¹	0.051	0.007	0.020	0.580**	0.816**	0.985**	1.000	-0.165	-0.756**	0.848**	0.840**
No. of infertile spikelets panicle⁻¹	0.061	0.039	0.204	-0.188	-0.158	0.007	-0.169	1.000	0.721**	-0.226*	-0.360**
Spikelet fertility (%)	-0.020	-0.010	-0.100	0.435**	0.573**	0.610**	0.732**	-0.739**	1.000	0.662**	0.760**
Test weight (g)	0.099	0.083	0.054	0.617**	0.840**	0.807**	0.831**	-0.203	0.625**	1.000	0.923**
Grain yield plant⁻¹	-0.011	-0.006	-0.010	0.650**	0.841**	0.772**	0.817**	-0.319*	0.707**	0.889**	1.000

Table 4: Estimates of genotypic direct (diagonal) and indirect effects (above and below diagonal) of contributing characters on grain yield in 50 rice genotypes

Characters	Days to 50% flowering	Days to physiological maturity	Plant height (cm)	Panicle Length (cm)	No. of Panicles plant⁻¹	No. of spikelets panicle⁻¹	No. of fertile spikelets panicle⁻¹	No. of infertile spikelets panicle⁻¹	Spikelet Fertility (%)	Test Weight (g)	Grain Yield plant⁻¹
Days to 50% flowering	-0.093	0.002	0.018	-0.0002	-0.011	0.001	-0.002	-0.001	-0.017	0.042	-0.061
Days to physiological maturity	-0.083	0.002	0.020	-0.004	-0.023	-0.001	0.006	-0.001	-0.015	0.029	-0.070
Plant height (cm)	-0.033	0.001	0.051	-0.007	-0.022	0.002	-0.001	-0.003	-0.034	0.028	-0.020
Panicle Length (cm)	0.001	-0.0002	-0.010	0.035	0.198	0.022	-0.090	0.003	0.137	0.381	0.677**
No. of Panicles plant⁻¹	0.004	-0.0002	-0.004	0.026	0.263	0.030	-0.120	0.002	0.163	0.504	0.868**
No. of spikelets panicle⁻¹	-0.002	-0.0001	0.002	0.021	0.219	0.036	-0.141	0.0001	0.180	0.479	0.794**
No. of fertile spikelets panicle⁻¹	-0.001	-0.0001	0.001	0.022	0.221	0.036	-0.143	0.002	0.209	0.493	0.840**
No. of infertile spikelets panicle⁻¹	-0.007	0.0001	0.012	-0.008	-0.035	-0.0003	0.024	-0.014	-0.199	-0.132	-0.360**
Spikelet Fertility (%)	0.006	-0.0001	-0.006	0.017	0.156	0.024	-0.108	0.010	0.276	0.385	0.760**
Test Weight (g)	-0.007	0.0001	0.002	0.023	0.228	0.030	-0.121	0.003	0.183	0.581	0.923**

*, ** = significant at 5% and 1% levels, respectively

Residual effect (R): 0.2874

Table 5: Composition of 50 Rice genotypes into different clusters by Tocher's method

Cluster Number	No.of Genotype	Name of genotype included in cluster
I	11	Vikram,Basmati370, IR36, KJT-3, Ratna, Manibhog, PAU-3079, KJT-4, China-26, Pawana, Darna
II	19	VDN-1-6-1, BhadasBhog, P-1, AlmuSathi, Kala Girga, T-3, Vasumati, RTN-24, Ambemohor157, W355, RDN 185-2, Krishna Sal, Adhaya, Tilsha, Nizamgod, Kala Namak, Phule Radha, SKL-8, IGP Local-3
III	8	Varanasi, PKV Khamang, PKV HMT, Bhandardara Local, LK-248, P-6, RTN-711, NK-3325
IV	1	IGP Local
V	8	Bhogawati, PKV-Kisan, SYE-5, SYE-2001, IGP Local-8, Pusa Basmati, Jay Bangal, VDN-5-5-1-2.
VI	1	IGP Local-10
VII	1	Phule Samruddhi
VIII	1	PKV Makrand

Table 6: Average intra and inter cluster distance (D^2) values for eight clusters in fifty Rice genotypes

Clusters	I	II	III	IV	V	VI	VII	VIII
I	9.38 (87.98)	18.98 (360.24)	15.61 (243.67)	20.32 (412.90)	16.48 (271.59)	21.74 (472.63)	18.70 (349.69)	16.59 (275.23)
II		9.79 (95.84)	16.10 (259.21)	11.93 (142.32)	15.07 (227.10)	12.00 (144.00)	17.22 (296.53)	21.45 (460.10)
III			10.05 (101.00)	20.95 (438.90)	19.23 (369.79)	17.69 (312.94)	24.44 (597.31)	14.21 (201.92)
IV				0.00 (0.00)	17.11 (292.75)	15.44 (238.39)	9.79 (95.84)	27.37 (749.12)
V					13.15 (172.92)	16.05 (257.60)	17.55 (308.00)	19.42 (377.14)
VI						0.00 (0.00)	21.49 (461.82)	20.48 (419.43)
VII							0.00 (0.00)	29.47 (868.48)
VIII								0.00 (0.00)

Diagonal: Intra cluster and above diagonal: inter cluster D values

Table 7: Cluster mean performances of the eight clusters for eleven characters in fifty rice genotypes

Cluster No.	Days to 50% flowering	Days to physiological maturity	Plant height (cm)	Panicle length (cm)	No. of panicles plant^{-1}	No. of spikelets panicle^{-1}	No. of fertile spikelets panicle^{-1}	No. of infertile spikelets panicle^{-1}	Spikelet fertility (%)	Test weight (g)	Grain yield plant^{-1}
I	101.86	134.18	59.20	23.40	13.50	220.91	193.91	27.00	86.76	20.36	24.58
II	113.32	145.68	100.82	20.53	10.42	179.74	148.24	31.50	81.17	17.03	17.51
III	114.00	145.94	63.09	21.51	9.56	156.88	127.88	29.00	79.69	15.79	15.86
IV	119.00	151.00	114.95	22.50	16.50	288.00	261.50	26.50	90.85	26.80	33.36
V	101.31	137.50	90.98	20.93	9.94	184.50	156.81	27.69	84.02	17.10	18.84
VI	116.50	153.50	101.40	18.20	7.50	119.50	108.50	11.00	90.71	20.82	23.37
VII	106.00	135.50	105.65	27.60	17.50	286.00	252.00	34.00	88.03	27.19	34.61
VIII	108.50	150.00	56.30	21.55	10.50	125.50	109.50	16.00	87.12	14.48	17.39

Author contributions

Conceptualization of experimentation (KDB, SRP & JSC); Designing of the experiments (KDB, SRP & JSC); Experimental materials (KDB, SRP & JSC); Execution of field experiments and data collection (KDB, SRP & JSC); Analysis of data and interpretation (KDB, SRP & JSC); Preparation of the manuscript (all authors).

Conflict of interest

The authors declare no conflict of interest.

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