Studies on Genetic Diversity in Various Qualitative and Quantitative Characters in Rice Germplasm

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One hundred and ninety five rice accessions were evaluated to study the diversity pattern among the genotypes. The genotypes were grouped under ten clusters. The distribution pattern indicated that maximum number of genotypes (28) were grouped into cluster II, followed by 27 in cluster III. The inter-cluster distance is higher than intra cluster indicating wide genetic diversity among the genotypes. The highest inter-cluster distances was observed between cluster VI and VII followed by cluster IV and VII showed wider diversity among the groups. The highest intra-cluster, distance was observed for cluster I followed by cluster IX. The accessions with IC 346231, 352813, 346237, 331640, 152036, 372020 can be used as potential donors for hybridization programme to develop variety with higher yield potential.

Key Words: Genetic Divergence, Germplasm, Rice

Introduction

Rice (*Oryza sativa* L.) is the principal staple food for more than 50% of the world's population. Rice is grown under diverse eco-geographical conditions in various tropical and sub-tropical countries, including India.

Landraces and wild species possess immense potential of most valuable gene which can be effectively utilized in the breeding programmes to develop high yielding rice varieties with quality and resistance to biotic and abiotic stresses (Saxena *et al*., 1988).

Materials and Methods

The experimental materials comprised 195 rice germplasm accessions (landraces) received from Directorate of Rice Research (DRR), Hyderabad. These genotypes were evaluated in Augumented Design during *Kharif* 2007 at Research farm, Indra Gandhi Krishi Vishwavidyala (IGKV), Raipur, Chhattishgarh (situated at $21^0$41' N latitude, 81^0 21' E longitude and at the height of 289.60 meters above the mean sea level). Twenty one days old seedlings from the nursery were transplanted. Each plot consisted of three rows of 5 m length. The spacing was maintained at 20x15 cm and the recommended practices were followed during the crop season. Five plants from middle of the row of each entry were randomly taken for observation on various 22 qualitative characters *viz.* coleoptile colour, early plant vigour, basel leaf sheath colour, leaf blade colour, leaf pubescence, flag leaf angle, ligule colour, ligule shape, collar colour, auricle colour, internode colour, panicle exertion, panicle type, stigma colour, apiculus colour, awning, hull colour, sterile lemma colour, seed coat colour, aroma and threshability. Eight quantitative characters *viz*. days to 50% flowering, plant height (cm), panicle length (cm), effective tillers per plant, no. of filled grains per plant, grain L:B ratio, 100 grain weight (g), and grain yield per plant (g). D^2 statistic was employed to measure the genetic distance between the genotypes (Mahalanobis, 1928).

Results and Discussion

A clear understanding of the extent of variability prevailing for each trait in germplasm is essential for the improvement of characters through selection. In hybridization programme, selection of genetically diverse parent is important to get wide range of recombinants. Based on qualitative descriptors, 195 accessions were classified for different characters (Table 1). Some of the qualitative characters with distinct characteristics are as follows: purple coleoptiles colour: IC325948., Purple line in basal leaf sheath colour: IC310484, IC326224, IC330649, IC331658, IC381993, IC347672., Leaf blade color with purple tips and purple margin : IC347637, IC347641, IC347643, IC346040., Purple ligule colour: IC330649, IC115503., Green collor colour: IC343382, IC347613, IC381993., Auricle color under others: IC326224, IC330036., Purple internode colour: IC330796, IC334049, IC347641., Yellow stigma colour.

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Table 1. Classification of rice germplasm accessions for qualitative characters

Characters		No. of accessions
Coleptile colour	Green	194
	Purple	1
Early plant vigour	Poor	19
	Good	105
	Very good	71
Basal leaf sheath colour	Green	164
	Purple line	7
	Light green	10
	Purple	14
Leaf blade colour	Light green	11
	Green	148
	Dark green	22
	Purple margin	9
	Purple	1
	Others	4
Leaf pubescence	Glabrous	115
	Intermediate	72
	Pubescent	8
Flag leaf angle	Erect	37
	Intermediate	133
	Horizontal	22
	Descending	3
Ligule colour	White	177
	Purple lines	16
	Purple	2
Ligule shape	Acute	9
	Cleft	186
Collar colour	Pale green	181
	Green	3
	Purple	11
Auricle colour	Pale green	184
	Purple	9
	Others	2
Internode colour	Green	124
	Light gold	64
	Purple line	4
	Purple	3
Panicle exertion	Well exerted	149
	Moderately exerted	10
	Just exerted	36
Panicle type	Compact	17
	Intermediate	135
	Open	43
Stigma colour	White	153
	Yellow	1
	Purple	41
Apiculous colour	White	20
	Straw	106
	Brown	5
	Red	33
	Red apex	9
	Purple	13
	Purple apex	8
	Others	1
Awning	Absent	169
	Short and partly awned	14
	Long and partly awned	8
	Long and fully awned	4
Hull colour	Straw	153
	Golden	2
	Brownish furrows on straw	13
	Purple furrow on straw	3
	Brown	18
	Black	6
Sterile lemma colour	Straw	171
	Red	23
	Purple	1
Seed coat colour	White	117
	Light brown	20
	Brown	6
	Red	52
Aroma	Absent	129
	Present	66
Threshability	Easy	78
	Intermediate	93
	Difficult	24

The analysis of variance (ANOVA) revealed highly significant differences among all the genotypes (Table 2) for all the characters studied of considerable amount of genetic variation. The magnitude of variation between genotypes was reflected by high mean value and range of genotype traits studied (Table 3). High genetic variability for different quantitative traits in rice has been reported earlier (Khan *et al.*, 2009; Ullah *et al.*, 2011; Seyoum *et al.*, 2012).

The results (Table 3) revealed that estimates of PCV were slightly higher than those of GCV for all traits studied. The extent of the environmental influence on traits is explained by the magnitude of the difference between PCV and GCV. Large differences between PCV and GCV values reflect high environmental influence on the expression of traits. In this study, slight difference indicated minimum environmental influence and consequently greater role of genetic factor on the expression of traits. High GCV and PCV values were observed for effective tiller per plant (26.2, 28.4), no. of grains per plant (50.97, 60.11) indicating the presence of ample variation for this character in the present material which indicate the possibility of yield improvements through selection on these traits.

Table. 2. Analysis of variation ANOVA

Source of variation	DF	50% flowering	Plant height (cm)	Effective tiller per plant	Panicle length	No. of filled grains /plant	Grain L : B ratio	100 grain weight (gm)	Grain weight per plant (g).
Replication	1	0.281	5045.476	0.5897	35.511	169824.2	4.029574	10.13308	367.54
Treatment	195	136.527**	243702.6**	11.405*	14.016*	362562.1*	0.467739**	01.11138*	141.38*
Error	195	104.226	1262.495	0.915	6.735	59230.44	0.162189	0.326485	18.277
Total	391								

Estimates of heritability and genetic advance were high for plant height (98.96, 44.2) in genotypes indicating the predominance of additive gene action for these traits, hence direct selection may be highly effective. Similar findings were reported by Thakur *et al.* (2000) and Seyoum *et al.* (2012). So these characters may be considered as important criteria for selection of the parent for hybridization program.

For quantitative characters, 195 genotypes were grouped into 10 clusters by using D^2 statistics in such a way that the genotypes within a cluster had a small or low D^2 values than those of in-between the characters. The composition of clusters has been presented in Table. 4. Cluster-II had largest number of genotypes (28) followed by cluster III (27) and cluster I (22) whereas, cluster VII had minimum number of genotypes with 12. The inter-cluster distance is higher than intra-cluster, indicating wide genetic diversity among the genotypes Table. 4. The highest inter-cluster distance varied from 4.573 to 1.965. The inter-cluster distance was observed between cluster VI and VII (4.573) (Table 5; Fig. 1). On the other hand minimum distance was observed between cluster III and IV (1.965), indicating close relationship between these clusters would not provide any good result. The greater the distance between clusters wider the genetic diversity between the genotypes. Highly divergent genotype would produce a broad spectrum of variability in the subsequent generations enabling further selection and improvement. The hybrids developed from the selected genotypes within the limit of compatibility of these clusters may produce desirable transgressive segregants or higher magnitude of heterosis. This would be useful in rice breeding programme to evolve miracle varieties with high yield potential and a similar finding was of Sarawgi and Rastogi (2000), Nayak *et al*. (2004) and Parikh *et al.* (2011).

The maximum intra cluster distance was observed for cluster I (2.127) followed by cluster IX (2.109) and cluster VI (2.079) (Table 5, Fig. 1). It was reported that genotypes within the cluster with high degree of divergence would produce more desirable breeding material for achieving

Table 3. Estimation of genetic variability, heritability, genetic advance, genetic advance in % and mean

Character	GCV	PCV	Heritability	GA	GA%	Mean
50% flowering	4.498	12.281	13.416	3.028	33.90	89.33
Plant height (cm)	216.29	217.42	98.969	712.64	44.27	160.96
Effective tiller/plant	26.23	28.43	85.14	4.38	49.80	8.73
Panicle length	7.14	12.05	35.08	2.33	8.74	26.72
No. of filled grains/plant	50.97	60.11	71.91	686.43	89.85	763.97
Grain length:width ratio	12.75	18.31	48.50	0.56	18.56	3.06
100-grain weight (g)	29.98	40.57	54.58	0.96	46.39	2.09
Grain weight/ plant (g)	51.59	58.75	77.10	14.25	93.76	15.21

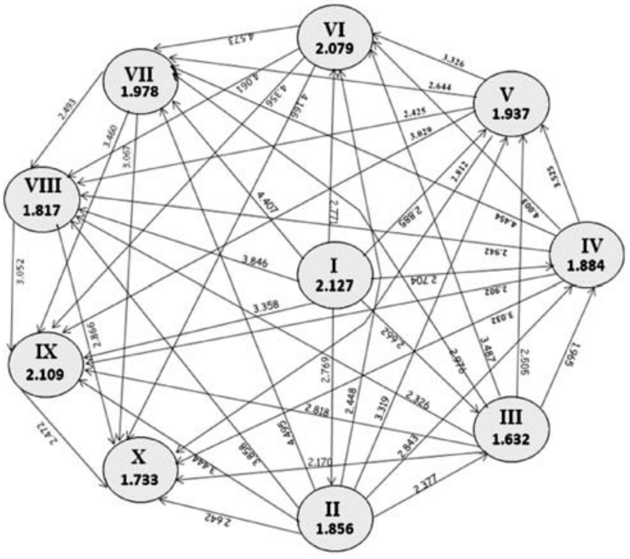

Fig. 1. Intra-and inter-cluster distance (D) in the rice germplasm

Table 4. Grouping of 195 genotypes into 10 clusters

Cluster	No. of genotypes	Genotypes with IC. No.
I	22	IC 316312, 320824, 321194, 326415, 326488, 330256, 330831, 331659, 331677, 332571, 334107, 337593, IC. No.344676, 344686, 344690, 347641, 352924, 352973, 372180, 372307, 325948, 320540.
II	28	IC 115503, 310499, 310500, 310501, 310502, 311850, 311863, 320843, 332622, 332640, 335936, 333010, 334049, 334132, 336076, 343382, 343475, 343492, 343503, 346918, 347637, 350758, 381993, 372181, 372293, 272302, 408352, 343476.
III	27	IC 306430, 311142, 311871, 316276, 316283, 320875, 330187, 331792, 332998, 334032, 334202, 340049, 340054, 340977, 343391, 346882, 351747, 342623, 342891, 372068, 360742, 363760, 381932, 381916, 381968, 381936, 396768.
IV	21	IC 310484, 310487, 311855, 311861, 330430, IC. No.332978, 336862, 340975, 343395, 346877, 346893, 346932, 347617, 347643, 347672, 340548, 340353, 342889, 350095, 350790, 320533.
V	21	IC 316273, 316277, 316378, 316279, 316311, 325162, 326224, 330836, 330649, 331658, 331785, 332975, 333018, 334111, 344735, 347638, 351697, 342864, 342622, 352764, 375774.
VI	12	IC 311864, 326477, 330699, 330807, 332019, 332040, 334046, 334321, 337616, 340072, 337002.
VII	12	IC 311856, 330226, 330251, 330260, 331646, 331640, 332031, 332043, 343982, 347613, 346039, 346234.
VIII	21	IC 152036, 310469, 319358, 319435, 330796, 330800, 330808, 331641, 332051, 333004, 352857, 352862, 352959, 353014, 346221, 346231, 346237, 350093, 350146, 352813, 352908.
IX	17	IC 325167, 326485, 330036, 330049, 330695, 332777, 334118, 334150, 334207, 337586, 351736, 351779, 356445, 340524, 342888, 372020, 382624.
X	14	IC 313549, 330055, 332049, 343546, 346843, 346865, 347669, 350292, 351738, 342618, 346040, 352836, 342864, 372845.

maximum genetic advance (Bose and Pradhan, 2005). The minimum intra-cluster distance was observed in III (1.632) followed by cluster X (1.733) and cluster VIII (1.817) indicating homogeneous nature of the genotypes with less deviation between the genotypes, therefore selection will be ineffective (Rajesh *et al*., 2010).

The cluster mean and coefficient of variation are presented in Table 6. The coefficient of variation was highest in number of filled grains/plant (423.31) followed by plant height (24.16) and lowest was recorded in grain L:B ratio (0.49). Cluster II showed highest mean value for days to 50% flowering, followed by cluster VI (95.50). Cluster X showed highest mean value for plant height (153.19) with high panicle length (30.31) and better effective tiller/plant (9.71), grain L:B ratio (2.86) and grain yield (12.62). Cluster V showed highest mean value for effective tiller/plant (12.53) with better L:B ratio (3.00) grain yield per plant (18.65). Cluster VII showed highest mean value for number of filled grains/plant (1743.92) with better panicle length (27.46), effective tiller per plant (9.97 and grain yield/plant (27.22). Cluster IX showed highest mean value for grain L:B ratio (3.91) with better panicle length (29.45). Cluster IV showed highest mean value for 100 grain weight (3.00) with better panicle length (27.86). Likewise cluster VIII showed highest mean value for grain yield/plant (28.16) with better effective tiller/plant (9.55), panicle length/plant (27.17), number of filled grains/plant (1023.76), 100 grain weight (2.76).

The results suggest that intercrossing of genotypes from different cluster showing good mean performance may help in obtaining high yield. Inclusion of more diverse parents in hybridization is believed to increase the chances of obtaining better heterosis and give broad spectrum of variability in segregating generation.

The better genotypes can be selected for most of characters on the basis of mean performance in the cluster. The best genotypes chosen for different characters is presented in Table 7.

The genotype IC346231 of cluster VIII showed highest grain yield per plant and 100 seed weight, the IC330226 of cluster VII showed highest number of filled grain per plant with better grain yield per plant. Maximum effective tiller per plant was found in IC316273 and maximum panicle length was found in IC326485 of cluster IX.

On the basis of divergence and cluster mean it may be suggested that maximum heterosis and good recombinants could be obtained in crosses between genotypes of cluster IX, VI, VII and V in varietal improvement programme. For bringing improvement in specific traits, genotypes with IC347669 for days to 50% flowering, IC381936 for plant height, IC316273 for effective tiller per plant, IC330036 for panicle length per plant, IC330226 for number of filled grain per plant, IC356445 for grain L:B ratio, IC340353 for 100 grain weight and IC346231 for grain yield per plant could be considered in rice improvement programme (Table 7). The traits days to flowering, plant height, 1000 grain weight are the major contributors of genetic divergence.

Table 5. Average of intra-cluster (diagonal bold) and inter-cluster distance (D values) among the ten clusters in rice for characters

	I	II	III	IV	V	VI	VII	VIII	IX	X
I	2.127	2.769	2.662	2.704	2.885	2.771	4.407	3.846	3.358	3.784
II		1.856	2.377	2.843	3.319	2.448	4.495	3.858	3.444	2.642
III			1.632	1.965	2.505	3.487	2.976	2.326	2.818	2.170
IV				1.884	3.525	4.003	4.454	2.942	2.902	3.032
V					1.937	3.326	2.644	2.425	3.029	2.812
VI						2.079	4.573	4.061	4.356	4.166
VII							1.978	2.493	3.460	3.067
VIII								1.817	3.052	2.866
IX									2.109	2.472
X										1.733

Table 6. Characters mean in different clusters of rice germplasm

	1	2	3	4	5	6	7	8
I	78.32	105.57	8.16	25.08	500.68	3.23	2.21	10.54
II	96.71	125.09	7.56	25.88	399.96	2.93	1.45	5.64
III	86.78	150.35	7.21	26.50	795.78	2.70	1.96	15.66
IV	87.05	147.61	6.43	27.86	395.10	2.98	3.00	11.66
V	86.14	136.05	12.53	25.09	965.70	3.00	1.96	18.65
VI	95.50	85.09	8.45	22.68	736.67	3.07	1.86	12.07
VII	87.42	146.28	9.97	27.46	1743.92	2.87	1.55	27.22
VIII	93.14	149.60	9.55	27.17	1023.76	2.81	2.76	28.16
IX	88.41	152.33	8.91	29.45	836.65	3.91	2.01	16.66
X	94.14	153.19	9.71	30.31	855.14	2.86	1.47	12.62
Grand mean	89.27	135.87	8.68	26.67	767.89	3.02	2.05	15.24
CV%	8.23	24.16	2.39	2.63	423.31	0.49	0.73	8.36

1. Days to 50% flowering 2. Plant height (cm) 3. Effective tillers/plant 4. Panicle length (cm) 5. No. of filled grains/plant 6. Grain L:B ratio 7.100-grain weight (g) 8. Grain yield/plant (g)

Table 7. Desirable genotypes for different traits

S. No.	Character	Desirable genotype with accession number
1	Days to 50% flowering	IC 347669(109), 334321(107), 320843(107), 337002(106).
2	Plant height (cm)	IC 381936(173.7), 340054(173.6), 330049(173.0), 351779(173.0), 343982(172.0).
3	Effective tillers/plant	IC 316273(19.7), 316279(17.3), 342622(14.7), 330836(14.3), 332043(14.3).
4	Panicle length (cm)	IC 313549(32.2), 326485(33.4), 330036(33.3), 330055(31.6), 343982(31.9), 347643(32.1), 347669(32.1).
5	No. of filled grains/plant	IC 311856(1687), 316279(1716), 330226(2296), 330251(1824), 332042(2196), 343982(2042).
6	Grain L:B ratio	IC 332040(4.0), 334207(4.3), 351779(4.0), 352924(4.0), 356445(5.0), 372020(4.0), 372307(4.1), 382624(4.8).
7	100 grain weight	IC 330430(3.49), 330796(3.21), 340353(3.99), 352959(3.77), 351779(3.55), 347672(3.46), 346231(3.69), 350790(3.73), 372180(3.4).
8	Grain yield/plant	IC No. 152036(32.76), 331640(33.06), 346231(40.79), 372020(32.60), 330226(30.35), 346237(34.77), 352813(37.73).

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