

Genetic divergence analyses in rice (*oryza sativa* L.) Germplasm lines

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Abstract

This study was carried out with 96 genotypes of rice representing diversity for yield and yield attributing traits. The main objective of the study was the estimation of nature and magnitude of variability; to estimate inter se genetic distance among the genotypes and grouping them into different clusters. In order to accomplish it divergence analysis (using Tocher's method) was carried out in order to assess the genetic divergence amongst the 96 germplasm lines. In this analysis germplasm lines arranged into 9 clusters of which cluster (1) was found to be the largest containing 35 genotypes followed by clusters (3),(2),(4),(9) and (6) which comprises of 19, 17, 10,7 and 5 genotypes respectively. Clusters (5),(7) and (8) comprises of one genotype each. Maximum intra cluster distance [10.92] was observed in cluster (6), containing 5 genotypes. Likewise, maximum inter cluster distance (75.73) was observed between clusters (6) and (9) indicating suitability of germplasm lines of these clusters for hybridization. In the study character grain yield per plant showed highest percent contribution towards genetic divergence followed by tillers per plant, effective tillers per plant and grains per panicle.

Keywords: Divergence, Tocher's method, Cluster, Cluster distance, Hybridization.

Introduction:

Rice belongs to genus ORYZA of Gramineae family. The genus oryza includes 24 species, of which 22 are wild and 2 namely *Oryza sativa* and *Oryza glaberrima* are cultivated. *O. sativa* is diploid species having 24 chromosomes. Rice being the staple food for more than 70% of Indian population occupies a pivotal place in Indian agriculture. Rice is grown, particularly in India in a wide range of agro climatic situations, ranging from the high altitude Himalayan valleys to the tropical coastal areas of Kerala. The principal systems of rice cultivation followed in India are 'dry', 'semidry' and 'wet'. However, 'wet' system is the one which is widely followed and most productive. This is practiced in areas of adequate supply of water either by rainfall or irrigation. The forth coming trend in rice is that, much more rice will be needed to be produced on less land with less labour and less water along with sustainable achievement and protection to environment. At the current rate

of population growth of 1.8%, the rice requirement of the country is estimated to be around 140 million tonnes by 2020. For achieving this production target in the next few decades, it has been advocated that hybrid rice may be of greater hope as it has hypothetical to produce about 20-30% higher yield than the pure line varieties. The important issue is how to balance the need for ever greater food production against very real concerns about protecting natural resources and the environment for the generations to come. Biological diversity and genetic resources have great role to play in achieving sustainable agricultural development and the ecological health of the earth. Plant breeding program with diverse genetic base could sustain a high level of crop yield. The narrow genetic base of semi-dwarf varieties is likely to make them vulnerable to different biotic and abiotic stresses. Therefore, to meet the ever-increasing demand of food grains, for higher production emphasis should be given to the genetic improvement of the

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existing varieties of rice. The major thrust area for such genetic improvement has been known to lay importance on selecting efficient breeding system and

identifying potential genotypes in hybridization program. This would depend to large extent on the knowledge of the genetic system controlling the various characters. With this backdrop the present investigation was undertaken to estimate the genetic distance amongst the genotypes and to identify the trait contributing towards maximum diversity.

Materials and methods

The present investigation was carried out at agricultural research farm, Institute of Agricultural sciences, Banaras Hindu University, Varanasi. The genotypes under study were a set of 96 diverse rice germplasm lines from IRRI. All the 96

genotypes were grown in *Kharif* season of 2010. The crop was directly sown under the irrigated conditions on 7th June 2010. Ninety six genotypes were grown in a completely randomized Block Design with two replications. Each plot consisted of two rows of 1.5m length. Spacing was maintained at 15 × 10 cm excluding the induced irrigation; the normal recommended agronomic practices were followed. Fertilizers were applied at the rate of 120 kg N, 80 kg P₂O₅ and 80 kg K₂O per hectare. Five plants were randomly selected from each entry in each replication and their means were used for the statistical analysis.

Result and Discussion

In this investigation in order to study genetic divergence 96 germplasm lines were subjected to divergence analysis using Tocher's method. In the study 9 clusters were obtained.

Table (1)

a) CLUSTER	b) GENOTYPES AS PER TOCHER'S METHOD	c) NUMBER
d) 1 e) f)	g) 7,13,14,16,17,20,21,22,23,29,32,36,38,39,41, h) 44,45,46,47,49,50,54,55,57,58,61,64,71,72, i) 77,81,82,83,84,95	j) 35
k) 2	l) 5,12,19,25,31,34,42,48,56,59,60,62,67,70,89, m) 90,94	n) 17
o) 3	p) 4,18,24,27,28,33,40,52,68,69,73,76,79,80,85,86, q) 87,88,96	r) 19
s) 4	t) 3,6,8,9,15,43,51,53,74,98	u) 10
v) 5	w) 93	x) 1
y) 6	z) 30,37,75,91,97	aa) 5
bb) 7	cc) 92	dd) 1
ee) 8	ff) 26	gg) 1
hh) 9	ii) 1,2,10,63,65,66,99	jj) 7

As per the findings a highest of 35 genotypes clustered in cluster (1) followed by clusters (3), (2), (4), (9) and (6) having 19,17,10,7 and 5 genotypes respectively. Through the cluster diagram D² values and D values are extracted as shown in Table (2).

Table 2: Average Intra and Inter cluster D^2 values (D values) among 9 clusters of 96 rice genotype

kk)	ll) 1 Cluster	mm) 2 Cluster	nn) 3 Cluster	oo) 4 Cluster	pp) 5 Cluster	qq) 6 Cluster	rr) 7 Cluster	ss) 8 Cluster	tt) 9 Cluster
uu) 1 Cluster	vv) 30.28 (5.50)	ww) 209.40 (14.47)	xx) 197.50 (14.05)	yy) 753.86 (27.46)	zz) 69.22 (8.32)	aaa) 1196.01 (34.58)	bbb) 375.32 (19.37)	ccc) 265.03 (16.28)	ddd) 1786.30 (42.26)
eee) 2 Cluster	fff)	ggg) 33.21 (5.76)	hhh) 715.47 (26.75)	iii) 217.20 (14.74)	jjj) 268.64 (16.39)	kkk) 2272.39 (47.67)	lll) 952.22 (30.86)	mmm) 796.83 (28.23)	nnn) 870.24 (29.49)
ooo) 3 Cluster	ppp)	qqq)	rrr) 42.83 (6.54)	sss) 1604.06 (40.05)	ttt) 207.14 (14.39)	uuu) 512.03 (22.63)	vvv) 159.63 (12.63)	www) 96.15 (9.81)	xxx) 3000.12 (54.77)
yyy) 4 Cluster	zzz)	aaaa)	bbbb)	cccc) 35.79 (5.98)	dddd) 856.34 (29.26)	eeee) 3721.42 (61.00)	fff) 1911.03 (43.72)	gggg) 1676.24 (40.94)	hhhh) 285.26 (16.89)
iiii) 5 Cluster	jjjj)	kkkk)	llll)	mmmm)	nnnn) 0.00 (0.00)	oooo) 1192.67 (34.54)	pppp) 251.78 (15.87)	qqqq) 377.60 (19.43)	rrrr) 1950.28 (44.16)
ssss) 6 Cluster	tttt)	uuuu)	vvvv)	wwww)	xxxx)	yyyy) 119.16 (10.92)	zzzz) 584.33 (24.17)	aaaaa) 528.29 (22.98)	bbbbb) 5704.46 (75.53)
ccccc) 7 Cluster	dddd)	eeeee)	ffff)	ggggg)	hhhhh)	iiii)	jjjjj) 0.00 (0.00)	kkkkk) 329.10 (18.14)	lllll) 3405.83 (58.36)
mmmmm) 8 Cluster	nnnnn)	ooooo)	ppppp)	qqqqq)	rrrrr)	sssss)	ttttt)	uuuuu) 0.00 (0.00)	vvvvv) 3032.11 (55.06)
wwwww) 9 Cluster	xxxxx)	yyyyy)	zzzzz)	aaaaaa)	bbbbbb)	cccccc)	dddddd)	eeeeee)	ffffff) 102.61 (10.13)

Among the clusters highest intra cluster distance of 10.92 (D values) has been found for Cluster 6 which comprises of LINES (30, 37, 75, 91 & 97). Cluster 6 is followed by Cluster 9 (10.13) which comprises of LINES (1,2,10,63,65,66 & 69). Similarly, lowest intra cluster distances [0] have been found for Clusters (5),(7) & (8) respectively which itself reveals that each of these clusters are formed of single genotype, namely LINE 93 (Cluster 5), LINE 92(Cluster 7) and LINE 26(Cluster 8).

The highest inter cluster distance (75.53) through Tocher method has been found between Cluster 6 (LINES 30, 37,75,91&97) and Cluster 9(LINES 1,2,10,63,65,66 & 69) followed by inter cluster distances (61.00),(58.36) & (55.06) between clusters 4 & 6, 7 & 9 and 8 & 9 respectively. High inter cluster distance would mean high phenotypic diversity for genotypes contained in clusters which would be mainly because of genetic diversity when environment influence is small. Therefore, the genotypes selected from distant clusters would be expected to yield wide spectrum of variability on hybridization in segregating generations.

Mean values of different traits for different clusters have been presented in Table(10). The highest mean values for different traits are observed to fall in different clusters. Cluster (5), (6) & (7) exhibited highest mean values for most of the traits. Cluster (5) exhibited highest values for total tillers per plant, test weight and grain L/B ratio. Cluster (6) recorded highest values for effective tillers per plant and grain yield and cluster (7) expressed highest mean values for chlorophyll content, panicle length and grains per panicle. Only maximum cluster mean value for plant height was exhibited by cluster (3).

Genotypes contained in clusters exhibiting high cluster mean for specific traits may be selected from the above mentioned clusters for breeding programme.

Lowest mean values for most of the traits except chlorophyll content are exhibited by Cluster 1. Therefore, genotypes in this cluster are expected to be contrasting for most of the traits against the genotypes exhibiting higher cluster mean. Based on the information from cluster means contrasting genotypes for different traits may be utilized for making divergent crosses. Lowest mean value for chlorophyll content is recorded from Cluster 6.

A perusal of cluster means indicated that their existed considerable differences in mean value of the different traits. Distribution of maximum and minimum mean values for

different traits in distinct cluster indicated the traits contributing to the total divergence. In this regard, grain yield per plant contributed maximum to the total divergence followed by tillers per plant, effective tillers per plant and grains per panicle. More than 80 percent contribution towards total divergence was mainly because of these four characters. In their findings Ahmed and Borah (1999) found out that tiller number, panicles per plant, grains per panicle, grain fertility and grain yield accounted for the major portion of genetic divergence; while Banumathy *et al.*(2010) reported maximum contribution was made by grain yield followed by days to 50% flowering, total grains per panicle and plant height; and Vennila *et al.*(2011) in their studies accounted maximum contribution to number of grains per panicle, plant height, grain length and grain breadth.

The major contributing character towards genetic divergence was found to be grain yield per plant (28.52%) followed by effective tillers per plant (19.59%), tillers per plant (18.24%) and grains per panicle (17.20%).

In Tocher's method of clustering maximum intra cluster distance was observed for cluster 6 containing five genotypes followed by cluster 9 and cluster 3. Cluster 5, 7 & 8 each contained single genotype namely, LINE 26, LINE 92 & LINE 93. All the single genotype clusters showed large inter cluster distances with cluster 9. Cluster 1 was the largest with respect to number and genotypes it accommodated 35 genotypes and exhibited low intra cluster distance indicating that a large number of genotypes were phenotypically similar with respect to number of traits in the present study.

The maximum inter cluster distance was observed between cluster 6 and cluster 9. This indicates that the hybridization between the genotypes of cluster 6 and cluster 9 would yield desirable segregates with accumulation of favorable genes in the segregating generations. Similar was suggested by Sarma, Richharia and Agarwal (1996). Following cluster 6 and 9 were the clusters 4 & 6, cluster 7 & 9 and cluster 8 & 9 respectively. The greater the distance between two clusters, wider the expected genetic distance between their genotypes. The genetic distance between the parents largely governs the variability spectrum generated in the segregating generation and also the F1 heterosis. Similar suggestions were given by Babu *et al.*(2003), Chauhan and Singh (2003).

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