Genetic Divergence for Yield and Quality Traits in Rice (*Oryza sativa* L.)

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Abstract

An investigation was carried out with the forty eight genotypes of rice to study the nature and magnitude of genetic divergence using D^2 statistics. Seventeen yield and quality traits were recorded on the genotypes raised in the α-Design with three replications. The forty eight genotypes were grouped into five clusters based on Euclidean cluster analysis with cluster I containing the maximum of 18 genotypes. Maximum intra-cluster distance was observed in cluster I indicating greater genetic divergence between the genotypes belonging to this cluster. Days to maturity, gel consistency and days to 50 per cent flowering contributed 74.55 per cent of total divergence. Maximum inter-cluster distance was recorded between clusters II and III followed by clusters III and IV indicating wide genetic diversity and it may be used in rice hybridization programme for improving grain yield.

Rice (*Oryza sativa* L.) is one of the staple cereal crops of the world and it is one of the main sources of carbohydrate for nearly one half of the world population. Genetic variability is the basic requirement for making progress in crop breeding. Inclusion of genetically divergent parents in any breeding programme is essential to create new genetic stocks. Genetic diversity is the most important tool in the hands of the plant breeder in choosing the right type of parents for hybridization programme. The divergence can be studied by technique using D^2 statistics developed by Mahalanobis (1936). It is based on multivariate analysis and grouped into various cluster as given by Spark (1973). This is considered as the most effective method for qualifying the degree of genetic diversity among the genotypes included in the study. The present investigation aimed to estimate the magnitude of genetic divergence present in the 48 rice genotypes and to identify the diverse genotypes for future breeding programme.

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Materials and Methods

Forty eight diverse genotypes of rice from different geographical origin were transplanted in the α-Design with 3 replications, 6 blocks/replication and 8 entries/block at the Experimental Farm of the Department of the Crop Improvement, College of Agriculture, CSK HP Krishi Vishvavidyalaya, Palampur, during *Kharif* 2008. In each replication, single seedling was transplanted per hill in 6 rows with 20 x 15 cm spacing. The observations were recorded on five randomly taken plants from each plot for days to 50 per cent flowering, days to maturity, plant height at maturity, total tillers//plant at maturity, effective tillers/plant at maturity, grain yield/plant, spikelets/panicle, grains/panicle, panicle length, 1000-grain weight, protein content, amylose content, gel consistency (GC), grain length (L), grain breadth (B), length breadth ratio (L:B), gelatinization temperature (GT) rating. The analysis of genetic divergence was done using Mahalanobis (1936) D^2 statistics. The genotypes were grouped into different clusters by applying Euclidean clustering method (Spark, 1973). Intra and inter-cluster distances and mean performance of the clusters for the characters were also computed.

Results and Discussion

The analysis of variance revealed significant differences among the genotypes for all the characters (Table S1). Based on D^2 values, all the genotypes could be grouped into five clusters using non-hierarchical Euclidean cluster analysis (Table 1). The genotypes within each cluster were closer to each other than the genotypes in different clusters. Maximum number of genotypes (18) were included in cluster I followed by 12 in cluster II, seven each in cluster IV & V and four genotypes in cluster III. Genotypes from same geographic location fell into different clusters indicating that clustering of populations did not follow their geographic or location distribution. Average intra and inter-cluster distances have been shown in Table 3. Maximum intra-cluster distance was observed in cluster I (1.84) followed by cluster II (1.80)

indicating genetic diversity among the genotypes belonging to these clusters. The minimum intra-cluster distance was observed in clusters V, III and IV. The

Table 1: Distribution of 48 genotypes of rice among clusters on the basis of D^2 analysis

Clusters	No. of genotypes	Genotypes
I	18	AC-19177-1, AC-19187, AC-19229, Bhangou, AC-19291, NBPGR-141, AC-19329, NBPGR-195, AC-19130, NBPGR-209, Kalizhini, Deval, Matali, Chhohartu, HPR-1068, HPR-2143, RP-2421, Sukaradhan-1
II	12	Kindu, AC-19211-1, AC-19227, AC-19234-1, AC-19241-1, Basmati, AC-19306-2, Sundrudhan, Rohrudhan, Chawaaidhan, RJ-100, Jattoo
III	4	AC-19155-3, AC-19171, AC-19179, R-575
IV	7	AC-19175-1, AC-19236-1, AC-19241, Jhini, Kaludhan, AC-19261, Laldhan
V	7	AC-19217, Farmi, Totudhan, Lalnakanda-41, Lalzhini, Krishandhan, Achhoo(White)

Table 2: Average intra and inter-cluster values of D^2 and √D^2 among five clusters

Clusters	I	II	III	IV	V
I	**3.39**	2.59	4.60	4.19	3.80
	(1.84)	(1.60)	(2.14)	(2.05)	(1.95)
II	-	**3.24**	6.04	4.72	4.03
		(1.80)	(2.46)	(2.17)	(2.00)
III	-	-	**3.17**	4.49	5.45
			(1.78)	(2.12)	(2.33)
IV	-	-	-	**3.18**	4.29
				(1.78)	(2.07)
V	-	-	-	-	**2.87**
					(1.69)

Bold values are intra-cluster distance

Data in parenthesis are √D^2 values

of developing good segregants by crossing the genotypes of the same cluster showing low values for intra-cluster distance are very low. Therefore, the crosses should be made between the genotypes of clusters separated by large inter-cluster distances (Sandhyakishore *et al.*, 2007; Chandra *et al.*, 2007). Highest inter-cluster distance was observed between clusters II and III (2.46) suggesting wide diversity between these clusters. Therefore, genotypes belonging to these clusters may be used in hybridization programme for the improvement of rice. The least inter- cluster distance was observed between clusters I and II (1.60) followed by clusters I and V (1.95) indicating close relationship between the genotypes of these clusters and hence, may not be emphasized upon to be used in hybridization programme. Crosses involving parents belonging to the most divergent clusters would be expected to manifest maximum heterosis and wide variability of genetic architecture (Souroush *et al.*, 2004). The diversity was also supported by the appreciable amount of variation among the cluster means for different characters (Table S2). Cluster I showed the maximum cluster means for total tillers/plant at maturity, effective tillers/plant at maturity, L: B ratio and grain breadth. For spikelets/panicle, grains/panicle, GC and grain yield/plant; cluster II recorded the maximum values and cluster III showed maximum values for 1000-grain weight, protein content and grain length. Maximum values for days to maturity, days to 50 per cent flowering, plant height, amylose content and panicle length were recorded by cluster IV. Thus, these genotypes hold great promise as parents for obtaining promising elite lines through hybridization and to create further variability for these characters (Mishra and Pravin, 2004).

The contribution of individual trait to the divergence among genotypes is presented in Table 3. Days to maturity contributed maximum towards genetic divergence (37.32%) followed by gel consistency (25.00%) and days to 50 per cent flowering (12.32%). Similar kinds of observations were made by earlier workers (Sandhyakishore *et al.*, 2007 and Patil *et al.*, 2005). Remaining traits had very little or no contribution towards genetic divergenceand hence, they were of less importance. Since varieties with narrow genetic base are increasingly vulnerable to diseases and adverse climatic changes, availability of the genetically diverse genotypes for hybridization programme become more important. Since days to maturity contributed maximum towards the genetic divergence, we may go for direct selection of this trait for diversity purpose.

Table 3: Relative contribution (%) of individual trait to the divergence among genotypes

Traits	No. of times ranked first	Contri-bution (%)
Days to 50% flowering (No.)	138	12.23
Days to maturity (No.)	421	37.32
Plant height (cm)	52	4.61
Total tillers/plant at maturity (No.)	8	0.71
Effective tillers/plant at maturity (No.)	1	0.09
Panicle length (cm)	0	0.00
Spikelets/ panicle (No.)	35	3.10
Grains/ panicle (No.)	16	1.42
Grain yield/plant (g)	23	2.04
1000-grain weight (g)	44	3.90
Protein content (%)	0	0.00
Amylose content (%)	58	5.14
Gel consistency (mm)	282	25.00
Grain length (L) mm	32	2.84
Grain Breadth (B) mm	5	0.44
Length Breadth ratio (L:B)	7	0.62
Gelatinization temperature (GT) rating	6	0.53

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Table S1: Analysis of variance for yield, morphological and quality traits in rice

Sources of variation	df	Days to 50% flowering	Days to maturity	Plant height at maturity	Total tillers/ plant at maturity	Effective tillers/plant at maturity	Panicle length	Spikelets / panicle	Grains/ panicle	Grain yield/plant
Replication	2	2.194	1.049	11.00	1.268	0.543	4.599	37.015	14.205	1.110
Blocks within replications	15	1.661	0.298	13.980	0.447	0.498	1.231	25.518	33.0145	0.748
Genotypes	47	179.632*	322.175*	617.096*	4.678*	5.157*	6.478*	1356.706*	1468.234*	31.050*
Error	79	0.912	0.719	14.017	0.543	0.491	1.423	34.839	45.549	1.241

TableS1. Contd…

Sources of variation	Df	1000-grain weight	Protein content	Amylose content	Gel consistency	Grain length (L)	Grain breadth (B)	Length breadth ratio (L:B)	Gelatinization temperature (GT) rating
Replication	2	0.905	1.255	0.276	3.361	0.113	0.082*	0.078*	1.938*
Blocks within replications	15	1.005	1.202	0.555	10.945	0.016	0.012	0.015	0.132
Genotypes	47	33.911*	5.778*	23.509*	1510.856*	0.806*	0.106*	0.374*	1.544*
Error	79	1.082	2.185	0.666	15.187	0.037	0.007	0.012	0.289

*Significant at 5% level

Table S2 : Cluster means of five clusters for different traits of rice

Traits	I	II	III	IV	V	Mean	Range Maximum	Minimum
Days to 50% flowering (No.)	104.49**	106.79	117.76	120.77*	108.28	111.62	120.77	104.49
Days to maturity (No.)	132.75**	134.10	149.21	159.76*	135.64	142.29	159.76	132.75
Plant height (cm)	98.36	107.25	87.68**	112.08*	110.34	103.14	112.08	87.68
Total tillers/plant at maturity (No.)	8.12*	7.16**	7.74	7.84	5.76	7.32	8.12	7.16
Effective tillers/plant at maturity (No.)	7.66*	6.88	7.42	7.60	5.10**	6.93	7.66	5.10
Panicle length (cm)	20.85**	21.51	21.60	23.81*	21.52	21.86	23.81	20.85
Spikelets/panicle (No.)	104.21	130.69*	83.04**	85.31	96.81	100.01	130.69	83.04
Grains/ panicle (No.)	67.29	94.05*	31.88**	54.17	55.64	60.61	94.05	31.88
Grain yield/plant (g)	9.34	10.15*	4.91	6.03	4.30**	6.95	10.15	4.30
1000-grain weight (g)	24.12	21.50	28.01*	21.76	20.99**	23.28	28.01	20.99

Protein content (%)	13.16	13.07**	15.11*	13.39	14.88	13.92	15.11	13.07
Amylose content (%)	26.63	26.90	21.81**	27.14*	26.96	25.89	27.14	21.81
Gel consistency (mm)	44.92	69.77*	37.78	42.87	32.81**	45.63	69.77	32.81
Grain length (L) mm	5.97	5.60	6.75*	5.95	5.56**	5.97	6.75	5.56
Grain breadth (B) mm	2.43*	2.37	2.42	2.41	2.35**	2.40	2.43	2.35
Length breadth ratio (L:B)	2.49*	2.39	2.79	2.47	2.38**	2.50	2.49	2.38
Gelatinization temperature (GT) rating	5.77	6.06	6.80*	5.56	5.19**	5.88	6.80	5.19

*and**: maximum and minimum values, respectively.